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Phe Ala Val Val Thr Ile Leu Gln Cys Phe Leu Ile Ser Thr Leu Phe	
725 730 735 740	
tcc aga gcc aac ctg gca gca gcc tgt ggg ggc atc atc tac ttc acg	2609
Ser Arg Ala Asn Leu Ala Ala Ala Cys Gly Gly Ile Ile Tyr Phe Thr	
745 750 755	
ctg tac ctg ccc tac gtc ctg tgt gtg gca tgg cag gac tac gtg ggc	2657
Leu Tyr Leu Pro Tyr Val Leu Cys Val Ala Trp Gln Asp Tyr Val Gly	
760 765 770	
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Phe Thr Leu Lys Ile Phe Ala Ser Leu Leu Ser Pro Val Ala Phe Gly	
775 780 785	
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Phe Gly Cys Glu Tyr Phe Ala Leu Phe Glu Glu Gln Gly Ile Gly Val	
790 795 800	
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Gln Trp Asp Asn Leu Phe Glu Ser Pro Val Glu Glu Asp Gly Phe Asn	
805 810 815 820	
ctc acc act tcg gtc tcc atg atg ctg ttt gac acc ttc ctc tat ggg	2849
Leu Thr Thr Ser Val Ser Met Met Leu Phe Asp Thr Phe Leu Tyr Gly	
825 830 835	
gtg atg acc tgg tac att gag gct gtc ttt cca ggc cag tac gga att	2897
Val Met Thr Trp Tyr Ile Glu Ala Val Phe Pro Gly Gln Tyr Gly Ile	
840 845 850	
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Pro Arg Pro Trp Tyr Phe Pro Cys Thr Lys Ser Tyr Trp Phe Gly Glu	
855 860 865	
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Glu Ser Asp Glu Lys Ser His Pro Gly Ser Asn Gln Lys Arg Ile Ser	
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gaa atc tgc atg gag gag gaa ccc acc cac ttg aag ctg ggc gtg tcc	3041
Glu Ile Cys Met Glu Glu Glu Pro Thr His Leu Lys Leu Gly Val Ser	
885 890 895 900	
att cag aac ctg gta aaa gtc tac cga gat ggg atg aag gtg gct gtc	3089
Ile Gln Asn Leu Val Lys Val Tyr Arg Asp Gly Met Lys Val Ala Val	
905 910 915	
gat ggc ctg gca ctg aat ttt tat gag ggc cag atc acc tcc ttc ctg	3137
Asp Gly Leu Ala Leu Asn Phe Tyr Glu Gly Gln Ile Thr Ser Phe Leu	
920 925 930	
ggc cac aat gga gcg ggg aag acg acc acc atg tca atc ctg acc ggg	3185
Gly His Asn Gly Ala Gly Lys Thr Thr Met Ser Ile Leu Thr Gly	
935 940 945	
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Leu Phe Pro Pro Thr Ser Gly Thr Ala Tyr Ile Leu Gly Lys Asp Ile	
950 955 960	
cgc tct gag atg agc acc atc cgg cag aac ctg ggg gtc tgt ccc cag	3281
Arg Ser Glu Met Ser Thr Ile Arg Gln Asn Leu Gly Val Cys Pro Gln	
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His Asn Val Leu Phe Asp Met Leu Thr Val Glu Glu His Ile Trp Phe	
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Tyr Ala Arg Leu Lys Gly Leu Ser Glu Lys His Val Lys Ala Glu Met	
1000 1005 1010	
gag cag atg gcc ctg gat gtt ggt ttg cca tca agc aag ctg aaa agc	3425
Glu Gln Met Ala Leu Asp Val Gly Leu Pro Ser Ser Lys Leu Lys Ser	
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Lys Thr Ser Gln Leu Ser Gly Gly Met Gln Arg Lys Leu Ser Val Ala	
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Ala Gly Val Asp Pro Tyr Ser Arg Arg Gly Ile Trp Glu Leu Leu Leu	
1065 1070 1075	
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Lys Tyr Arg Gln Gly Arg Thr Ile Ile Leu Ser Thr His His Met Asp	
1080 1085 1090	
gaa gcg gac gtc ctg ggg gac agg att gcc atc atc tcc cat ggg aag	3665
Glu Ala Asp Val Leu Gly Asp Arg Ile Ala Ile Ile Ser His Gly Lys	
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Leu Cys Cys Val Gly Ser Ser Leu Phe Leu Lys Asn Gln Leu Gly Thr	
1110 1115 1120	
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Gly Tyr Tyr Leu Thr Leu Val Lys Lys Asp Val Glu Ser Ser Leu Ser	
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Ser Val Ser Gln Ser Ser Ser Asp Ala Gly Leu Gly Ser Asp His Glu	
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Ser Asp Thr Leu Thr Ile Asp Val Ser Ala Ile Ser Asn Leu Ile Arg	
1175 1180 1185	
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Lys His Val Ser Glu Ala Arg Leu Val Glu Asp Ile Gly His Glu Leu	
1190 1195 1200	
acc tat gtg ctg cca tat gaa gct gct aag gag gga gcc ttt gtg gaa	4001
Thr Tyr Val Leu Pro Tyr Glu Ala Ala Lys Glu Gly Ala Phe Val Glu	
1205 1210 1215 1220	
ctc ttt cat gag att gat gac cgg ctc tca gac ctg ggc att tct agt	4049
Leu Phe His Glu Ile Asp Asp Arg Leu Ser Asp Leu Gly Ile Ser Ser	
1225 1230 1235	

225	230	235	
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atc act gaa cca tac ttt aac ttc act tca att caa gaa tca atg aat Ile Thr Glu Pro Tyr Phe Asn Phe Thr Ser Ile Gln Glu Ser Met Asn 275 280 285			1346
gaa att cta ttt gaa gaa tac cag ttt caa gca gta tta aga gta aat Glu Ile Leu Phe Glu Glu Tyr Gln Phe Gln Ala Val Leu Arg Val Asn 290 295 300			1394
gct ggg gct ctc agt gca cat agg tat ttc cga gat aat cct tcc gaa Ala Gly Ala Leu Ser Ala His Arg Tyr Phe Arg Asp Asn Pro Ser Glu 305 310 315			1442
tta tgc tgt atc att gtt gat agt gga tat tcc ttt aca cat ata gtt Leu Cys Cys Ile Ile Val Asp Ser Gly Tyr Ser Phe Thr His Ile Val 320 325 330			1490
cct tat tgt aga agt aaa aag aaa aaa gaa gca att att cgg ata aat Pro Tyr Cys Arg Ser Lys Lys Lys Lys Glu Ala Ile Ile Arg Ile Asn 335 340 345 350			1538
gtg gga gga aaa ctc tta acc aat cat cta aag gag atc ata tct tac Val Gly Gly Lys Leu Leu Thr Asn His Leu Lys Glu Ile Ile Ser Tyr 355 360 365			1586
agg cag cta cat gtt atg gat gaa aca cat gtg att aat caa gtg aaa Arg Gln Leu His Val Met Asp Glu Thr His Val Ile Asn Gln Val Lys 370 375 380			1634
gaa gat gta tgc tat gtg tct cag gat ttt tat aga gac atg gat att Glu Asp Val Cys Tyr Val Ser Gln Asp Phe Tyr Arg Asp Met Asp Ile 385 390 395			1682
gca aag ttg aaa gga gaa gaa aat aca gta atg ata gac tat gtc ttg Ala Lys Leu Lys Gly Glu Glu Asn Thr Val Met Ile Asp Tyr Val Leu 400 405 410			1730
cct gac ttc agt aca att aaa aag ggc ttt tgt aag cca agg gaa gag Pro Asp Phe Ser Thr Ile Lys Lys Gly Phe Cys Lys Pro Arg Glu Glu 415 420 425 430			1778
atg gtg ttg agt gga aaa tac aaa tct ggg gaa caa att ctt cgt ttg Met Val Leu Ser Gly Lys Tyr Lys Ser Gly Glu Gln Ile Leu Arg Leu 435 440 445			1826
gcc aat gag aga ttt gct gtt ccg gaa ata ctc ttt aat cct tct gat Ala Asn Glu Arg Phe Ala Val Pro Glu Ile Leu Phe Asn Pro Ser Asp 450 455 460			1874
ata ggc att caa gaa atg gga att cca gaa gct att gtc tat tca att Ile Gly Ile Gln Glu Met Gly Ile Pro Glu Ala Ile Val Tyr Ser Ile 465 470 475			1922
caa aat cta cct gaa gaa atg cag ccg cat ttt ttt aag aac att gtc Gln Asn Leu Pro Glu Glu Met Gln Pro His Phe Phe Lys Asn Ile Val 1970			

480	485	490	
ttg aca gga gga aat tcc ctt ttc cca gga ttt agg gat cgg gtt tac			2018
Leu Thr Gly Gly Asn Ser Leu Phe Pro Gly Phe Arg Asp Arg Val Tyr			
495	500	505	510
tca gaa gtt cga tgt ctt act cca aca gat tat gat gtt tct gtt gtg			2066
Ser Glu Val Arg Cys Leu Thr Pro Thr Asp Tyr Asp Val Ser Val Val			
	515	520	525
ctg cct gaa aac cct att act tat gcc tgg gaa ggt gga aaa ttg ata			2114
Leu Pro Glu Asn Pro Ile Thr Tyr Ala Trp Glu Gly Gly Lys Leu Ile			
	530	535	540
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Ser Glu Asn Asp Asp Phe Glu Asp Met Val Val Thr Arg Glu Asp Tyr			
	545	550	555
gaa gaa aat gga cat agc gtc tgt gaa gag aaa ttt gat att taagcaa			2211
Glu Glu Asn Gly His Ser Val Cys Glu Glu Lys Phe Asp Ile			
	560	565	570
catttttgaa tgaaagtgt gaccataagg tttaatttca aagttccttt taaaagaggt			2271
taaggaactg tgttaccttt tgtcctaaga aaaaggcttg aatttatgta aatactttga			2331
tcgattgcta attttcaaag gcttcttagg taggttacta cagtaaaactg taactcagtc			2391
cacattttca tttaggagct agactaccat aacaatgctt atgctgtttc caagggtagg			2451
ttatttttca ttaaaagaag aatgaatgca ttttaagttt aattcttcat agctgaaagc			2511
acaaatttaa cggcttcact ggacagtttt ccttagaagg tagttttgtg tgactgtgac			2571
taaactattt tattttaaaa tgtcattott atttatacat tctaaagttg gaaagactga			2631
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Met Ser Arg Pro Ala Pro Gly Arg Arg Ala Ala Pro Thr Ala Thr	
1 5 10 15	
gcc gcc gcc gcc atg aac att ttc cgg ctg act ggg gac ctg tcc cac	157
Ala Ala Ala Ala Met Asn Ile Phe Arg Leu Thr Gly Asp Leu Ser His	
20 25 30	
ctg gcg gcc atc gtc atc ctg ctg ctg aag atc tgg aag acg cgc tcc	205



Leu	Ala	Ala	Ile	Val	Ile	Leu	Leu	Leu	Lys	Ile	Trp	Lys	Thr	Arg	Ser		
			35					40					45				
tgc	gcc	ggt	att	tct	ggg	aaa	agc	cag	ctt	ctg	ttt	gca	ctg	gtc	ttc	253	
Cys	Ala	Gly	Ile	Ser	Gly	Lys	Ser	Gln	Leu	Leu	Phe	Ala	Leu	Val	Phe		
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aca	act	cgt	tac	ctg	gat	ctt	ttt	act	tca	ttt	att	tca	ttg	tat	aac	301	
Thr	Thr	Arg	Tyr	Leu	Asp	Leu	Phe	Thr	Ser	Phe	Ile	Ser	Leu	Tyr	Asn		
		65				70					75						
aca	tct	atg	aag	gtt	atc	tac	ctt	gcc	tgc	tcc	tat	gcc	aca	gtg	tac	349	
Thr	Ser	Met	Lys	Val	Ile	Tyr	Leu	Ala	Cys	Ser	Tyr	Ala	Thr	Val	Tyr		
		80				85				90					95		
ctg	atc	tac	ctg	aaa	ttt	aag	gca	acc	tac	gat	gga	aat	cat	gat	acc	397	
Leu	Ile	Tyr	Leu	Lys	Phe	Lys	Ala	Thr	Tyr	Asp	Gly	Asn	His	Asp	Thr		
			100					105					110				
ttc	cga	gtg	gag	ttt	ctg	gtg	gtc	cct	gtg	gga	ggc	ctc	tca	ttt	tta	445	
Phe	Arg	Val	Glu	Phe	Leu	Val	Val	Pro	Val	Gly	Gly	Leu	Ser	Phe	Leu		
			115					120					125				
gtt	aat	cac	gat	ttc	tct	cct	ctt	gag	atc	ctc	tgg	acc	ttc	tcc	atc	493	
Val	Asn	His	Asp	Phe	Ser	Pro	Leu	Glu	Ile	Leu	Trp	Thr	Phe	Ser	Ile		
		130					135					140					
tac	ctg	gag	tcc	gtg	gct	atc	ctt	ccg	cag	ctg	ttt	atg	atc	agc	aag	541	
Tyr	Leu	Glu	Ser	Val	Ala	Ile	Leu	Pro	Gln	Leu	Phe	Met	Ile	Ser	Lys		
		145				150					155						
act	ggg	gag	gcc	gag	acc	atc	acc	acc	cac	tac	ctg	ttc	ttc	ctg	ggc	589	
Thr	Gly	Glu	Ala	Glu	Thr	Ile	Thr	Thr	His	Tyr	Leu	Phe	Phe	Leu	Gly		
		160			165				170					175			
ctc	tat	cgt	gct	ttg	tat	ctt	gtc	aac	tgg	atc	tgg	cgc	ttc	tac	ttt	637	
Leu	Tyr	Arg	Ala	Leu	Tyr	Leu	Val	Asn	Trp	Ile	Trp	Arg	Phe	Tyr	Phe		
			180					185					190				
gag	ggc	ttc	ttt	gac	ctc	att	gct	gtg	gtg	gcc	ggc	gta	gtc	cag	acc	685	
Glu	Gly	Phe	Phe	Asp	Leu	Ile	Ala	Val	Val	Ala	Gly	Val	Val	Gln	Thr		
		195						200				205					
atc	cta	tac	tgt	gac	ttc	ttc	tac	ttg	tac	att	aca	aaa	gta	ctc	aag	733	
Ile	Leu	Tyr	Cys	Asp	Phe	Phe	Tyr	Leu	Tyr	Ile	Thr	Lys	Val	Leu	Lys		
		210				215						220					
gga	aag	aag	ctc	agt	ttg	cca	gca	taa	gttgc	caaagaccat	caccagcatc					785	
Gly	Lys	Lys	Leu	Ser	Leu	Pro	Ala	*									
		225				230											
tgctccttcag	ggtgctcgga	cagaattcctt	accacagcaa	aggcataaga	tgcttgatac											845	
ggaaaatcag	aaacttaact	cttttggtgc	agatagtcac	cagtggctct	gtaaaaacgc											905	
agaggaaaag	agccagaagg	tttctgttta	atgcaccttg	ccttatcttt	ttttattact											965	
gtgtacaaaag	attttttttac	acaaagaaac	ttaatgctgt	attaataaat	tcagtgtgta											1025	
gcttcaattg	ggatagttcc	aaaagtgaag	attttgtag	gaataagtgc	aaattttttt											1085	
tttatttttaa	aaaattcttt	gaaactctta	agtctttgtg	tctgcaatga	aattgtactc											1145	
cttgacagtt	gatagattat	gtattcttcc	atccctcaaa	cttgcatcc	actatattta											1205	

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 Met Glu Leu Val Gln Val Leu Lys Arg  
 1 5  
 ggg ctg cag cag atc acc ggc cac ggc ggt ctc cga ggc tat cta cgg 161  
 Gly Leu Gln Gln Ile Thr Gly His Gly Gly Leu Arg Gly Tyr Leu Arg  
 10 15 20 25  
 gtt ttt ttc agg aca aat gat gcg aag gtt ggt aca tta gtg ggg gaa 209  
 Val Phe Phe Arg Thr Asn Asp Ala Lys Val Gly Thr Leu Val Gly Glu  
 30 35 40  
 gac aaa tat gga aac aaa tac tat gaa gac aac aag caa ttt ttt ggc 257  
 Asp Lys Tyr Gly Asn Lys Tyr Tyr Glu Asp Asn Lys Gln Phe Phe Gly  
 45 50 55  
 cgt cac cga tgg gtt gta tat act act gaa atg aat ggc aaa aac aca 305  
 Arg His Arg Trp Val Val Tyr Thr Thr Glu Met Asn Gly Lys Asn Thr  
 60 65 70  
 ttc tgg gat gtg gat gga agc atg gtg cct cct gaa tgg cat cgt tgg 353  
 Phe Trp Asp Val Asp Gly Ser Met Val Pro Pro Glu Trp His Arg Trp  
 75 80 85  
 ctt cac agt atg act gat gat cct cca aca aca aaa cca ctt act gct 401  
 Leu His Ser Met Thr Asp Asp Pro Pro Thr Thr Lys Pro Leu Thr Ala  
 90 95 100 105  
 cgt aaa ttc att tgg acg aac cat aaa ttc aac gtg act ggc acc cca 449  
 Arg Lys Phe Ile Trp Thr Asn His Lys Phe Asn Val Thr Gly Thr Pro  
 110 115 120  
 gaa caa tat gta cct tat tct acc act aga aag aag att cag gag tgg 497  
 Glu Gln Tyr Val Pro Tyr Ser Thr Thr Arg Lys Lys Ile Gln Glu Trp  
 125 130 135  
 atc cca cct tca aca cct tac aag taaagacaat gaagaacagt tgaaacatgc 551  
 Ile Pro Pro Ser Thr Pro Tyr Lys  
 140 145  
 aaaatatgga gcttttcatg taattactct ttactgttt accattcact ataattcaca 611  
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 ctacagggaaa ttctgttctc ttctgcggca cagagaaccc tgcttcaaag cagaagtagc 120  
 agttccggag tccagctggc taaaactcat cccagaggat a atg gca acc cat 173  
 Met Ala Thr His  
 1  
 gcc tta gaa atc gct ggg ctg ttt ctt ggt ggt gtt gga atg gtg ggc 221  
 Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val Gly Met Val Gly  
 5 10 15 20  
 aca gtg gct gtc act gtc atg cct cag tgg aga gtg tgc gcc ttc att 269  
 Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val Ser Ala Phe Ile  
 25 30 35  
 gaa aac aac atc gtg gtt ttt gaa aac ttc tgg gaa gga ctg tgg atg 317  
 Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu Gly Leu Trp Met  
 40 45 50  
 aat tgc gtg agg cag gct aac atc agg atg cag tgc aaa atc tat gat 365  
 Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile Tyr Asp  
 55 60 65  
 tcc ctg ctg gct ctt tct ccg gac cta cag gca gcc aga gga ctg atg 413  
 Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly Leu Met  
 70 75 80  
 tgt gct gct tcc gtg atg tcc ttc ttg gct ttc atg atg gcc atc ctt 461  
 Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met Met Ala Ile Leu  
 85 90 95 100  
 ggc atg aaa tgc acc agg tgc acg ggg gac aat gag aag gtg aag gct 509  
 Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala  
 105 110 115  
 cac att ctg ctg acg gct gga atc atc ttc atc atc acg ggc atg gtg 557  
 His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val  
 120 125 130  
 gtg ctc atc cct gtg agc tgg gtt gcc aat gcc atc atc aga gat ttc 605  
 Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe  
 135 140 145  
 tat aac tca ata gtg aat gtt gcc caa aaa cgt gag ctt gga gaa gct 653  
 Tyr Asn Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala  
 150 155 160

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ctc tac tta gga tgg acc acg gca ctg gtg ctg att gtt gga gga gct      701
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165                      170                      175                      180

ctg ttc tgc tgc gtt ttt tgt tgc aac gaa aag agc agt agc tac aga      749
Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr Arg
                      185                      190                      195

tac tcg ata cct tcc cat cgc aca acc caa aaa agt tat cac acc gga      797
Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His Thr Gly
                      200                      205                      210

aag aag tca ccg agc gtc tac tcc aga agt cag tat gtg tag ttgtgta      846
Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val *
                      215                      220                      225

tgtttttttta actttactat aaagccatgc aaatgacaaa aatctatatt actttctcaa      906

aatggacccc aaagaaactt tgatttactg ttcttaactg cctaacttta attacaggaa      966

ctgtgcatca gctatztatg attctataag ctatttcagc agaatgagat attaaatcca      1026

atgctttgat tgnctagaa agtatagtaa tttgttttct aaggtggttc aagcatctac      1086

tcttttnatc atttacttca aaatgacatt gctaaagact gcattattn actactgtaa      1146

tttctccacg gccatagcat tatgtacata ggtgagtgtg ccatttatta tcctcaccat      1206

tggngggccat gctttattat gggttttaat ttnaaaattg gaatgccccg gtcccattnc      1266

cacctggnat taantagggc ctccaacctt attgcctttt nnaggggggaa atcatggggg      1326

aggggggtgn aaggaggggg tncttgtna tntggmntaa aanccagggt tggggggttaa      1386

tggccccccn tttttnattg gcggtttaan atngaggntt nnatccggga ttgttanggg      1446

anttgattgn gttcctggtn tcgtggtttt nggccttggg ggttgggncc cnacctcent      1506

nacccttnt nccngggggg ttttttcccc tgggggntta ntacctntnt nnaanggggg      1566

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669

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catgagacat tgaattaagg agaatcatct tcatgcctga aaatttagca aaattccgac 1387
tatggcctcc aggggcaatt cctaaaagct gaatggataa taaaattgga ctgggaaagt 1447
aagtaggtgg ctggtcctca cctgttggg aatgggctat cctacttatg gctgttcttt 1507
gggtaatggg gattaaattg accccaaggg acccgatttt cntttgggtt ttcaaattgt 1567
tccagagttg ggaaaagccn ttccaagggtg gacatgggtg aatttactcc gtttctctg 1627
atttctnggt 1637

```

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<210> 252
<211> 2076
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (320) .. (1306)

```

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<220>
<221> misc_feature
<222> (1) ... (2076)
<223> n = a,t,c or g

```

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<400> 252
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cggaggtggc tgaagcatca taggccacaa tagcagttgt ctgagacagg gggggacgtg 120
tggcagatgt tacagccacc acctattgtg tgcagacaac agttagcctg agtcggctcc 180
gttacctgca ttcacagct ccagaatcct ccagctgct tggaggaact ggtgctccta 240
tgtggtgacc cgcaccatct catgccatgt gcagaatggc acctaccttc agcgagtgt 300
gcagaactgc ccctggccc atg agc tgt ccg ggg agc agc tac aga act gtg 352
Met Ser Cys Pro Gly Ser Ser Tyr Arg Thr Val
1 5 10

gtg aga ccc aca tac aag gtg atg tac aag ata gtg acc gcc cgt gag 400
Val Arg Pro Thr Tyr Lys Val Met Tyr Lys Ile Val Thr Ala Arg Glu
15 20 25

tgg agg tgc tgc cct ggg cac tca aga gtg agc tgc gag gaa gtt gca 448
Trp Arg Cys Cys Pro Gly His Ser Arg Val Ser Cys Glu Glu Val Ala
30 35 40

ggg tcc tct gcc tcc ttg gag ccc atg tgg tgc ggc agt acc atg cgg 496
Gly Ser Ser Ala Ser Leu Glu Pro Met Trp Ser Gly Ser Thr Met Arg
45 50 55

cgg atg gcg ctt cgg ccc aca gcc ttc tca ggt tgt ctc aac tgc agc 544
Arg Met Ala Leu Arg Pro Thr Ala Phe Ser Gly Cys Leu Asn Cys Ser
60 65 70 75

aaa gtg tca gag ctg aca gag cgg ctg aag gtg ctg gag gcc aag atg 592
Lys Val Ser Glu Leu Thr Glu Arg Leu Lys Val Leu Glu Ala Lys Met
80 85 90

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acc atg ctg act gtc ata gag cag cca gta cct cca aca cca gct acc	640
Thr Met Leu Thr Val Ile Glu Gln Pro Val Pro Pro Thr Pro Ala Thr	
95 100 105	
cct gag gac cct gcc ccg ctc tgg ggt ccc cct cct gcc cag ggc agc	688
Pro Glu Asp Pro Ala Pro Leu Trp Gly Pro Pro Pro Ala Gln Gly Ser	
110 115 120	
ccc gga gat gga ggc ctc cag gac caa gtc ggt gct tgg ggg ctt ccc	736
Pro Gly Asp Gly Gly Leu Gln Asp Gln Val Gly Ala Trp Gly Leu Pro	
125 130 135	
ggg ccc acc ggc ccc aag gga gat gcc ggc agt cgg ggc cca atg ggg	784
Gly Pro Thr Gly Pro Lys Gly Asp Ala Gly Ser Arg Gly Pro Met Gly	
140 145 150 155	
atg aga ggc cca cca gga gac cca ttg ctg tcc aac acc ttc act gag	832
Met Arg Gly Pro Pro Gly Asp Pro Leu Leu Ser Asn Thr Phe Thr Glu	
160 165 170	
acc aac aac cac tgg ccc cag gga ccc act ggg cct cca ggc cct cca	880
Thr Asn Asn His Trp Pro Gln Gly Pro Thr Gly Pro Pro Gly Pro Pro	
175 180 185	
ggg ccc atg ggt ccc cct ggg cct cct ggc ccc aca ggt gtc cct ggg	928
Gly Pro Met Gly Pro Pro Gly Pro Pro Gly Pro Thr Gly Val Pro Gly	
190 195 200	
agt cct ggt cac ata gga ccc cca ggc ccc act gga ccc aaa gga atc	976
Ser Pro Gly His Ile Gly Pro Pro Gly Pro Thr Gly Pro Lys Gly Ile	
205 210 215	
tct ggc cac cca gga gag aag ggc gag aga gga ctg cgt ggg gag cct	1024
Ser Gly His Pro Gly Glu Lys Gly Glu Arg Gly Leu Arg Gly Glu Pro	
220 225 230 235	
ggc ccc caa ggc tct gct ggg cag cgg ggg gaa cct ggc cct aag gga	1072
Gly Pro Gln Gly Ser Ala Gly Gln Arg Gly Glu Pro Gly Pro Lys Gly	
240 245 250	
gac cct ggt gag aag agc cac tgg ggg gag ggg ttg cac cag cta cgc	1120
Asp Pro Gly Glu Lys Ser His Trp Gly Glu Gly Leu His Gln Leu Arg	
255 260 265	
gag gct ttg aag att tta gct gag agg gtt tta atc ttg gaa aca atg	1168
Glu Ala Leu Lys Ile Leu Ala Glu Arg Val Leu Ile Leu Glu Thr Met	
270 275 280	
att ggg ctc tat gaa cca gag ctg ggg tct ggg gcg ggc cct gcc ggc	1216
Ile Gly Leu Tyr Glu Pro Glu Leu Gly Ser Gly Ala Gly Pro Ala Gly	
285 290 295	
aca ggc acc ccc agc ctc ctt cgg ggc aag agg ggc gga cat gca acc	1264
Thr Gly Thr Pro Ser Leu Leu Arg Gly Lys Arg Gly Gly His Ala Thr	
300 305 310 315	
aac tac cgg atc gtg gcc ccc agg agc cgg gac gag aga ggc tgagggt	1313
Asn Tyr Arg Ile Val Ala Pro Arg Ser Arg Asp Glu Arg Gly	
320 325	
ggtggcggcc cctgaggcag accaggccag gcttccctc ctacctggac tcggccagct	1373
gcctccaggg accgcccgtc catatttatt aatgtcctca gggtccttc tgccatctag	1433

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gccttagggg taagcaggtc tcagtcctgg caccatgcac atgtctgagg ctgagcaagg 1493
gctgagagga gaggcttggg cctcagtttc cctctgtgaa gtggggggag gcaggccttc 1553
aaggagggat agaggtacaa ggcttcgtct catctgctgt ctgagcatcc aggcccaaag 1613
gcaactgaggg agtcaggagc tggggctcgg cacatgcaga gatgacaggg cagggggcag 1673
tcttcctccc cctccccgac caaacctcgg ggagccctcc tgtgcccctc cctccttggt 1733
gtccagtgtc gggctcccca ccccgaggtc aggctgcccc atcctctgac tggatcaccc 1793
ggggcttctt gcctcagttc ttccctctga gccccaggc cctcccgcat ctcaggttgg 1853
ggatggggac atggagagga aggggccgcc tactcctgca aatgcttggt acagatgcca 1913
ggaggtagat gtgtgctggc caataaaggc ccctacctga ttccccgcag aaaaaaagtc 1973
gacgcggccg cgaattcgga tcctcgagag atctcttttt ttgggtttgg tggggtatct 2033
tcatcatcga atagatagtt atatacatca tcgcctttcg atg 2076

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```

<210> 253
<211> 2858
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (137)..(1207)

```

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<220>
<221> misc_feature
<222> (1)...(2858)
<223> n = a,t,c or g

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<400> 253
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tcaaaagtgg cagagtgtat tcaatgattc tcaggagcac ttggaaagat tttactgtaa 120
cccagaaaat gataga      atg aga atg aag tat gga gga caa gaa ttt tgg 169
                        Met Arg Met Lys Tyr Gly Gly Gln Glu Phe Trp
                        1          5          10
gca gat ttg aat gcc atg aac gtg tat gaa aca act gaa ttt gac caa 217
Ala Asp Leu Asn Ala Met Asn Val Tyr Glu Thr Thr Glu Phe Asp Gln
      15          20          25
cta cga agg ctg tcc aca cca ccc tct agc aat gtc aac tct att tac 265
Leu Arg Arg Leu Ser Thr Pro Pro Ser Ser Asn Val Asn Ser Ile Tyr
      30          35          40
cac aca gtc tgg aaa ttc ttc tgt agg gac cac ttt gga tgg aga gag 313
His Thr Val Trp Lys Phe Phe Cys Arg Asp His Phe Gly Trp Arg Glu
      45          50          55
tat ccc gag tct gtc att cga ttg att gaa gaa gcc aac tct cgg ggt 361
Tyr Pro Glu Ser Val Ile Arg Leu Ile Glu Glu Ala Asn Ser Arg Gly
      60          65          70          75

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ctg aaa gag gtt cga ttt atg atg tgg aat aac cac tac atc ctc cac	409
Leu Lys Glu Val Arg Phe Met Met Trp Asn Asn His Tyr Ile Leu His	
80 85 90	
aat tca ttc ttc agg aga gag ata aaa agg aga ccc ctc ttc cgc tcc	457
Asn Ser Phe Phe Arg Arg Glu Ile Lys Arg Arg Pro Leu Phe Arg Ser	
95 100 105	
tgt ttt ata ctg ctt cca tat tta cag aca ctt ggt ggg gtt ccc aca	505
Cys Phe Ile Leu Leu Pro Tyr Leu Gln Thr Leu Gly Gly Val Pro Thr	
110 115 120	
caa gct cct cca cct ctt gaa gca act tca tca tca caa att atc tgc	553
Gln Ala Pro Pro Pro Leu Glu Ala Thr Ser Ser Ser Gln Ile Ile Cys	
125 130 135	
cca gat ggg gtc act tca gca aac ttt tac cct gaa act tgg gtt tat	601
Pro Asp Gly Val Thr Ser Ala Asn Phe Tyr Pro Glu Thr Trp Val Tyr	
140 145 150 155	
atg cat cca tct cag gac ttc atc caa gtc cct gtt tct gca gag gat	649
Met His Pro Ser Gln Asp Phe Ile Gln Val Pro Val Ser Ala Glu Asp	
160 165 170	
aaa agt tat cgg atc att tac aat ctt ttt cat aag act gtg cct gag	697
Lys Ser Tyr Arg Ile Ile Tyr Asn Leu Phe His Lys Thr Val Pro Glu	
175 180 185	
ttt aaa tac aga att ttg cag ata ttg aga gtc caa aac cag ttt ctt	745
Phe Lys Tyr Arg Ile Leu Gln Ile Leu Arg Val Gln Asn Gln Phe Leu	
190 195 200	
tgg gag aaa tat aaa agg aaa aag gaa tat atg aac agg aaa atg ttt	793
Trp Glu Lys Tyr Lys Arg Lys Lys Glu Tyr Met Asn Arg Lys Met Phe	
205 210 215	
ggc cgt gac agg ata ata aat gag aga cat tta ttt cat gga aca tcc	841
Gly Arg Asp Arg Ile Ile Asn Glu Arg His Leu Phe His Gly Thr Ser	
220 225 230 235	
cag gat gtg gta gat gga atc tgc aaa cac aac ttt gac cct cga gtc	889
Gln Asp Val Val Asp Gly Ile Cys Lys His Asn Phe Asp Pro Arg Val	
240 245 250	
tgt gga aag cat gct aca atg ttt gga caa ggc agt tat ttt gca aag	937
Cys Gly Lys His Ala Thr Met Phe Gly Gln Gly Ser Tyr Phe Ala Lys	
255 260 265	
aag gca agc tac tct cat aac ttt tct aag aag tcc tcc aaa gga gtc	985
Lys Ala Ser Tyr Ser His Asn Phe Ser Lys Lys Ser Ser Lys Gly Val	
270 275 280	
cac ttc atg ttt ctg gcc aaa gtg ctg acg ggc aga tac aca atg ggc	1033
His Phe Met Phe Leu Ala Lys Val Leu Thr Gly Arg Tyr Thr Met Gly	
285 290 295	
agt cat ggc atg aga agg ccc ccg cca gtc aat cct ggc agt gtc acc	1081
Ser His Gly Met Arg Arg Pro Pro Pro Val Asn Pro Gly Ser Val Thr	
300 305 310 315	
agt gac ctt tat gac tct tgt gtg gat aat ttc ttt gag cct cag att	1129
Ser Asp Leu Tyr Asp Ser Cys Val Asp Asn Phe Phe Glu Pro Gln Ile	
320 325 330	

ttt gtc att ttt aat gat gac cag agt tac cct tat ttt gtt atc caa	1177
Phe Val Ile Phe Asn Asp Asp Gln Ser Tyr Pro Tyr Phe Val Ile Gln	
335 340 345	
tat gaa gaa gtc agt aac act gtt tcc att t gaaaaatcctt ggtactgcta	1228
Tyr Glu Glu Val Ser Asn Thr Val Ser Ile	
350 355	
aattatttga tatgaactca atccagcatt tgtagcaggt tttgaatggg tgggactggg	1288
tggggaacag cattggacat taatagggca cttttcagac ccatttttta aagtgctaga	1348
aaatgctttt tttaaaaaaa aaatacaagt tttaaaatga ccacttactc ttttaattatt	1408
tactaattgc tagtgactc agtgtggaaa agactacaga ttacacactc ttttcattca	1468
cacttgta ca tatagacagc aatgttatta ggagcattaa attaaaaaac tgaacagcct	1528
aatttaaagtg tggcttgggc ctggtagaag tttgaccaa tggaatggag gctgtgagca	1588
atgtgaggat tctattttatt tatttacgtt tgataaaact tactggaact agtactacca	1648
tgcgtattcc ctgtcccaa gcatcactgc tttggtatag tataagttca tgaaattctg	1708
gtgggtagaa agaaattttt atttctatca gcagtactaa aatgtatcag ccaaccagag	1768
aacatcagtg actttaactt ctgcagagtt tgcccagaa ttcagagttc tatttagagg	1828
aagttaaaac aacaacaaaa aacaaccatt tgaaaaattt ttgtcaccag caaaactttt	1888
cactaattag tgatatgaaa tgtgattttt gtgttgtaa acttcagctt tggaaaactc	1948
agtctctttc attatcatcc attccaattt gaaggagttg ggcagctaatt ttggttaaag	2008
gcagtcttga gggttagaag tattacttcc ttttcgggtt ccagacctag cttgtgactg	2068
aaagttttag aaaaaggaag tacatctata gccgaattga taaggttatt actgtgtttt	2128
gcacaaaagta tattagcaaa agtatttgct ggaattattg gtagatggca gtcccactcc	2188
tacacctgct ttgtcagata cagctgggtt ccctggctga ctctgtacct tacttacact	2248
acttacttaa tagaaacaca aacttgaaa ttgtgccagt ggtccagctg gagcacaacg	2308
tttggtgaat atgctgtttc ctcatgtcag agaggtagca actaggtaaa ctcttataa	2368
aaagcaaata cctggattta caaaagtga agtagttgtt cacaaaagaa ttcgccatgg	2428
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agtctgttta ttaagcactt atcagggctt ccacacactt atttattttg ccctagttaa	2608
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tcaattataa cttgtaaacc agtgactcct aatctttttc aagttaagac accttaccat	2728
tgcttatttg gttttatgag acttgttcct tttttctcc ctaaggaaaa agaaagcttt	2788
atgacatatt tattttttta ataaaactaa gcaaaaaataa aacttatggt aattctttta	2848
aaaaaaaaa	2858

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<220>  
<221> CDS  
<222> (296)..(4498)
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675

atg gat cca att aca cgt caa gta gga caa cat att gaa atg gaa cca	826
Met Asp Pro Ile Thr Arg Gln Val Gly Gln His Ile Glu Met Glu Pro	
165 170 175	
gag tgg gaa gca gcc ttc aca cta caa atg aaa tta aca cat gtc att	874
Glu Trp Glu Ala Ala Phe Thr Leu Gln Met Lys Leu Thr His Val Ile	
180 185 190	
tca atg atg cag gac tgg tgt gct tca gat gaa aaa gtg tta atc gaa	922
Ser Met Met Gln Asp Trp Cys Ala Ser Asp Glu Lys Val Leu Ile Glu	
195 200 205	
gct tac aag aaa tgt ctc gct gta ctg atg cag tgt cat ggt ggt tat	970
Ala Tyr Lys Lys Cys Leu Ala Val Leu Met Gln Cys His Gly Gly Tyr	
210 215 220 225	
act gat ggt gaa cag cca atc aca cta agc att tgt gga cat tca gtg	1018
Thr Asp Gly Glu Gln Pro Ile Thr Leu Ser Ile Cys Gly His Ser Val	
230 235 240	
gaa act atc aga tac tgt gtt tcc caa gaa aaa gtt agc att cac ctc	1066
Glu Thr Ile Arg Tyr Cys Val Ser Gln Glu Lys Val Ser Ile His Leu	
245 250 255	
cca gtt tct cgc tta ctt gca ggt tta cat gta tta tta agc aaa agt	1114
Pro Val Ser Arg Leu Leu Ala Gly Leu His Val Leu Leu Ser Lys Ser	
260 265 270	
gaa gtg gca tat aaa ttt cca gag ctc cta cct cta agt gaa ctt agc	1162
Glu Val Ala Tyr Lys Phe Pro Glu Leu Leu Pro Leu Ser Glu Leu Ser	
275 280 285	
cca ccc atg ttg ata gaa cac cct ctt aga tgt ctt gtt ctg tgt gcc	1210
Pro Pro Met Leu Ile Glu His Pro Leu Arg Cys Leu Val Leu Cys Ala	
290 295 300 305	
caa gta cat gcc gga atg tgg aga aga aat ggg ttc tct cta gta aac	1258
Gln Val His Ala Gly Met Trp Arg Arg Asn Gly Phe Ser Leu Val Asn	
310 315 320	
cag att tat tac tac cat aat gtg aaa tgc aga cgt gag atg ttt gac	1306
Gln Ile Tyr Tyr Tyr His Asn Val Lys Cys Arg Arg Glu Met Phe Asp	
325 330 335	
aag gat gta gta atg ctt cag aca ggt gtc tcc atg atg gat cca aat	1354
Lys Asp Val Val Met Leu Gln Thr Gly Val Ser Met Met Asp Pro Asn	
340 345 350	
cat ttc ctg atg atc atg ctc agc cgc ttt gaa ctt tat cag att ttc	1402
His Phe Leu Met Ile Met Leu Ser Arg Phe Glu Leu Tyr Gln Ile Phe	
355 360 365	
agt act cca gac tat gga aaa aga ttt agt tct gag att acc cat aag	1450
Ser Thr Pro Asp Tyr Gly Lys Arg Phe Ser Ser Glu Ile Thr His Lys	
370 375 380 385	
gat gtt gtt cag cag aac aat act cta ata gaa gaa atg cta tac ctc	1498
Asp Val Val Gln Gln Asn Asn Thr Leu Ile Glu Glu Met Leu Tyr Leu	
390 395 400	
att ata atg ctt gtt gga gag aga ttt agt cct gga gtt gga cag gta	1546
Ile Ile Met Leu Val Gly Glu Arg Phe Ser Pro Gly Val Gly Gln Val	
405 410 415	

aat gct aca gat gaa atc aag cga gag att atc cat cag ttg agt atc Asn Ala Thr Asp Glu Ile Lys Arg Glu Ile Ile His Gln Leu Ser Ile 420 425 430	1594
aag cct atg gct cat agt gaa ttg gta aag tct tta cct gaa gat gag Lys Pro Met Ala His Ser Glu Leu Val Lys Ser Leu Pro Glu Asp Glu 435 440 445	1642
aac aag gag act ggc atg gag agt gta atc gaa gca gtt gcc cat ttc Asn Lys Glu Thr Gly Met Glu Ser Val Ile Glu Ala Val Ala His Phe 450 455 460 465	1690
aag aaa cct gga tta aca gga cga ggc atg tat gaa ctg aaa cca gaa Lys Lys Pro Gly Leu Thr Gly Arg Gly Met Tyr Glu Leu Lys Pro Glu 470 475 480	1738
tgt gcc aaa gag ttc aac ttg tat ttc tat cac ttt tca agg gca gaa Cys Ala Lys Glu Phe Asn Leu Tyr Phe Tyr His Phe Ser Arg Ala Glu 485 490 495	1786
cag tcc aag gca gaa gaa gcg caa cgg aaa ttg aaa aga caa aat aga Gln Ser Lys Ala Glu Glu Ala Gln Arg Lys Leu Lys Arg Gln Asn Arg 500 505 510	1834
gaa gat aca gca ctc cca cct ccg gtg ttg cct cca ttc tgc cct ctg Glu Asp Thr Ala Leu Pro Pro Pro Val Leu Pro Pro Phe Cys Pro Leu 515 520 525	1882
ttt gca agc ctg gtt aac att ttg cag tca gat gtc atg ttg tgc atc Phe Ala Ser Leu Val Asn Ile Leu Gln Ser Asp Val Met Leu Cys Ile 530 535 540 545	1930
atg gga aca att ctg caa tgg gct gtg gaa cat aat gga tat gcc tgg Met Gly Thr Ile Leu Gln Trp Ala Val Glu His Asn Gly Tyr Ala Trp 550 555 560	1978
tca gag tcc atg ctg caa agg gtg tta cat tta att ggc atg gca cta Ser Glu Ser Met Leu Gln Arg Val Leu His Leu Ile Gly Met Ala Leu 565 570 575	2026
caa gaa gaa aaa caa cat tta gag aat gtc acg gaa gag cat gta gta Gln Glu Glu Lys Gln His Leu Glu Asn Val Thr Glu Glu His Val Val 580 585 590	2074
aca ttt acc ttc act cag aag ata tca aaa cct ggt gaa gcg cca aaa Thr Phe Thr Phe Thr Gln Lys Ile Ser Lys Pro Gly Glu Ala Pro Lys 595 600 605	2122
aat tct cct agc ata cta gct atg ctg gaa aca cta caa aat gct ccc Asn Ser Pro Ser Ile Leu Ala Met Leu Glu Thr Leu Gln Asn Ala Pro 610 615 620 625	2170
tac cta gaa gtc cac aaa gac atg att cgg tgg ata ttg aag act ttt Tyr Leu Glu Val His Lys Asp Met Ile Arg Trp Ile Leu Lys Thr Phe 630 635 640	2218
aat gct gtt aaa aag atg agg gag agt tca cct acc agt ccc gtg gca Asn Ala Val Lys Lys Met Arg Glu Ser Ser Pro Thr Ser Pro Val Ala 645 650 655	2266
gag aca gaa gga acc ata atg gaa gag agt tca agg gac aaa gac aaa Glu Thr Glu Gly Thr Ile Met Glu Glu Ser Ser Arg Asp Lys Asp Lys 660 665 670	2314

gct gag agg aag aga aaa gca gag att gcc aga ctg cgc aga gaa aag Ala Glu Arg Lys Arg Lys Ala Glu Ile Ala Arg Leu Arg Arg Glu Lys 675 680 685	2362
atc atg gct cag atg tct gaa atg cag cgg cat ttt att gat gaa aac Ile Met Ala Gln Met Ser Glu Met Gln Arg His Phe Ile Asp Glu Asn 690 695 700 705	2410
aaa gaa ctc ttt cag cag aca tta gaa ctg gat gcc tca acc tct gct Lys Glu Leu Phe Gln Gln Thr Leu Glu Leu Asp Ala Ser Thr Ser Ala 710 715 720	2458
gtt ctt gat cat agc cct gtg gct tca gat atg aca ctt aca gca ctg Val Leu Asp His Ser Pro Val Ala Ser Asp Met Thr Leu Thr Ala Leu 725 730 735	2506
ggc ccc gca caa act cag gtt cct gaa caa aga caa ttc gtt aca tgt Gly Pro Ala Gln Thr Gln Val Pro Glu Gln Arg Gln Phe Val Thr Cys 740 745 750	2554
ata ttg tgt caa gag gag caa gaa gtt aaa gtg gaa agc agg gca atg Ile Leu Cys Gln Glu Glu Gln Val Lys Val Glu Ser Arg Ala Met 755 760 765	2602
gtc ttg gca gca ttt gtt cag aga tca act gta tta tca aaa aac aga Val Leu Ala Ala Phe Val Gln Arg Ser Thr Val Leu Ser Lys Asn Arg 770 775 780 785	2650
agt aaa ttt att caa gat cca gaa aaa tat gat cca tta ttc atg cac Ser Lys Phe Ile Gln Asp Pro Glu Lys Tyr Asp Pro Leu Phe Met His 790 795 800	2698
cct gat ctg tct tgt gga aca cac act agt agc tgt ggg cac att atg Pro Asp Leu Ser Cys Gly Thr His Thr Ser Ser Cys Gly His Ile Met 805 810 815	2746
cat gcc cat tgt tgg caa agg tat ttt gat tcc gtt caa gct aaa gaa His Ala His Cys Trp Gln Arg Tyr Phe Asp Ser Val Gln Ala Lys Glu 820 825 830	2794
cag cga agg caa cag aga tta cgc tta cat acg agc tat gat gta gaa Gln Arg Arg Gln Gln Arg Leu Arg Leu His Thr Ser Tyr Asp Val Glu 835 840 845	2842
aac gga gaa ttc ctt tgc ccc ctt tgt gaa tgc ttg agt aat act gtt Asn Gly Glu Phe Leu Cys Pro Leu Cys Glu Cys Leu Ser Asn Thr Val 850 855 860 865	2890
att cct ctg ctg ctt cct cca aga aat att ttt aac aac agg tta aat Ile Pro Leu Leu Leu Pro Pro Arg Asn Ile Phe Asn Asn Arg Leu Asn 870 875 880	2938
ttt tca gac caa cca aat ctg act cag tgg att aga aca ata tct cag Phe Ser Asp Gln Pro Asn Leu Thr Gln Trp Ile Arg Thr Ile Ser Gln 885 890 895	2986
caa ata aaa gca tta cag ttt ctt agg aaa gaa gaa agt act cct aat Gln Ile Lys Ala Leu Gln Phe Leu Arg Lys Glu Glu Ser Thr Pro Asn 900 905 910	3034
aat gcc tct aca aag aat tca gaa aat gtg gat gaa tta cag ctc cct Asn Ala Ser Thr Lys Asn Ser Glu Asn Val Asp Glu Leu Gln Leu Pro 915 920 925	3082

gaa ggg ttc agg cct gat ttt cgt cct aag atc cct tat tct gag agc	3130
Glu Gly Phe Arg Pro Asp Phe Arg Pro Lys Ile Pro Tyr Ser Glu Ser	
930 935 940 945	
ata aaa gaa atg cta acg aca ttt gga act gct acc tac aag gtg gga	3178
Ile Lys Glu Met Leu Thr Thr Phe Gly Thr Ala Thr Tyr Lys Val Gly	
950 955 960	
cta aag gtt cat ccc aat gaa gag gat cct cgt gtt ccc ata atg tgt	3226
Leu Lys Val His Pro Asn Glu Glu Asp Pro Arg Val Pro Ile Met Cys	
965 970 975	
tgg ggt agc tgc gcg tac acc atc caa agc ata gaa aga att ttg agt	3274
Trp Gly Ser Cys Ala Tyr Thr Ile Gln Ser Ile Glu Arg Ile Leu Ser	
980 985 990	
gat gaa gat aaa cca ttg ttt ggt cct tta cct tgc aga ctg gat gac	3322
Asp Glu Asp Lys Pro Leu Phe Gly Pro Leu Pro Cys Arg Leu Asp Asp	
995 1000 1005	
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Cys Gln Asp Phe Ser Gly Ile Ser Leu Gly Thr Gly Asp Leu His Ile	
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 Gly Arg Gln Gly Phe Ala Gln Ser Leu Leu Lys Lys Met Ser His Arg  
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 Pro Glu Asp Ala Gln Gly Val Glu Glu Arg Glu Ala Leu Ala Arg Met  
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 Glu Lys Tyr Leu Arg Ser Val Leu Ala Val Glu Asn Leu Leu Thr Leu  
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 Lys Gly Arg Trp Glu Ser Gln Gln Asp Val Ser Gln Thr Thr Val Ser  
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 Arg Gly Ile Ala Pro Ala Pro Ala Leu Ser Val Ser Pro Gln Asn Asn  
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Pro Val Lys Ser Phe Val Pro Gln Met Pro Lys Leu Leu Lys Ser Leu	
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Phe Pro Val Arg Asp Glu Lys Arg Gly Lys Arg Pro Ser Pro Leu Ala	
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His Gln Pro Val Pro Arg Ile Met Val Gln Ser Ala Ser Pro Asp Ile	
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Arg Val Thr Arg Met Glu Glu Ala Gln Pro Glu Met Gly Pro Asp Val	
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Leu Val Gln Thr Met Gly Ala Pro Ala Leu Lys Ile Cys Asp Lys Pro	
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Ala Lys Val Pro Ser Pro Pro Pro Val Ile Ala Val Thr Ala Val Thr	
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Thr Ala Pro Glu Ala Glu Pro Glu Ala Pro Ile Ser His Pro Pro Pro	
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Lys Asn Asp Gly Ser Ile Gly Gly Lys Gln Tyr Phe Arg Cys Asn Pro	
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Thr Ala Ala Leu Ala Lys Ala Asp Arg Ser His Lys Asn Pro Glu Asn	
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 cacgcaatcg cgtttccgga gagacctggc tgctgtgtcc cgcggcttgc gctccgtagt 180  
 ggactccgcg ggccttcggc agatgcaggc ctggggtagt ctcctttctg gactgagaag 240  
 agaaga atg gag aag ccc ctc ttc cca tta gtg cct ttg cat tgg ttt 288  
 Met Glu Lys Pro Leu Phe Pro Leu Val Pro Leu His Trp Phe  
 1 5 10  
 ggc ttt ggc tac aca gca ctg gtt gtt tct ggt ggg atc gtt ggc tat 336  
 Gly Phe Gly Tyr Thr Ala Leu Val Val Ser Gly Gly Ile Val Gly Tyr  
 15 20 25 30  
 gta aaa aca ggc agc gtg ccg tcc ctg gct gca ggg ctg ctc ttc ggc 384  
 Val Lys Thr Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly  
 35 40 45  
 agt cta gcc ggc ctg ggt gct tac cag ctg tat cag gat cca agg aac 432  
 Ser Leu Ala Gly Leu Gly Ala Tyr Gln Leu Tyr Gln Asp Pro Arg Asn  
 50 55 60  
 gtt tgg ggt ttc cta gcc gct aca tct gtt act ttt gtt ggt gtt atg 480  
 Val Trp Gly Phe Leu Ala Ala Thr Ser Val Thr Phe Val Gly Val Met  
 65 70 75  
 gga atg aga tcc tac tac tat gga aaa ttc atg cct gta ggt tta att 528  
 Gly Met Arg Ser Tyr Tyr Tyr Gly Lys Phe Met Pro Val Gly Leu Ile  
 80 85 90  
 gca ggt gcc agt ttg ctg atg gcc gcc aaa gtt gga gtt cgt atg ttg 576  
 Ala Gly Ala Ser Leu Leu Met Ala Ala Lys Val Gly Val Arg Met Leu  
 95 100 105 110

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atg aca tct gat tag cagaagtcac gttccagctt ggactcatga aggattaaaa 631
Met Thr Ser Asp *
115

atctgcatct tccactatct tcaatgtatt aagagaaata agtgcagcat ttttgcacat 691

gacattttac ctaaaaaaaaa aaagacacca aatttggcgg aggggggggaa aatcagttgt 751

taccattata accctacaaa ggggggggagc atgtaacatg agcttattga gaccatcata 811

aagaccgatt cttggatatg gattttatct ctttctgtat ctataggaaa atctcagggg 871

taaaaggtta ggggttgaca ttgaaaaccc tgaaacccca ttccctgctc aaaggaacag 931

ggggaaaaaaa aatctcttga gagattaaaa aaatcttttt tttggctcat tttaaaccac 991

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<213> Homo sapiens

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ccgcggctgc ggcgcagggt ccctcggcct gagtcggg atg gag ctg cct gct 173
Met Glu Leu Pro Ala
1 5

gtg aac ctg aag gtg att ctc cta ggt cac tgg ctg ctg aca acc tgg 221
Val Asn Leu Lys Val Ile Leu Leu Gly His Trp Leu Leu Thr Thr Trp
10 15 20

ggc tgc att gta ttc tca ggc tcc tat gcc tgg gcc aac ttc acc atc 269
Gly Cys Ile Val Phe Ser Gly Ser Tyr Ala Trp Ala Asn Phe Thr Ile
25 30 35

ctg gcc ttg ggc gtg tgg gct gtg gct cag cgg gac tcc atc gac gcc 317
Leu Ala Leu Gly Val Trp Ala Val Ala Gln Arg Asp Ser Ile Asp Ala
40 45 50

ata agc atg ttt ctg ggt ggc ttg ctg gcc acc atc ttc ctg gac atc 365
Ile Ser Met Phe Leu Gly Gly Leu Leu Ala Thr Ile Phe Leu Asp Ile
55 60 65

gtg cac atc agc atc ttc tac ccg cgg gtc agc ctc acg gac acg ggc 413
Val His Ile Ser Ile Phe Tyr Pro Arg Val Ser Leu Thr Asp Thr Gly
70 75 80 85

cgc ttt ggc gtg ggc atg gcc atc ctc agc ttg ctg ctc aag ccg ctc 461
Arg Phe Gly Val Gly Met Ala Ile Leu Ser Leu Leu Leu Lys Pro Leu

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90

95

100

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tcc tgc tgc ttc gtc tac cac atg tac cgg gag cgc ggg ggt gag ctc      509
Ser Cys Cys Phe Val Tyr His Met Tyr Arg Glu Arg Gly Gly Glu Leu
      105                      110                      115

ctg gtc cac act ggt ttc ctt ggg tct tct cag gac cgt agt gcc tac      557
Leu Val His Thr Gly Phe Leu Gly Ser Ser Gln Asp Arg Ser Ala Tyr
      120                      125                      130

cag acg att gac tca gca gag gcg ccc gca gat ccc ttt gca gtc cca      605
Gln Thr Ile Asp Ser Ala Glu Ala Pro Ala Asp Pro Phe Ala Val Pro
      135                      140                      145

gag ggc agg agt caa gat gcc cga ggg tac tga agccagcc acgctgcgcc      656
Glu Gly Arg Ser Gln Asp Ala Arg Gly Tyr *
      150                      155                      160

cgggccctgcc ccgggccttc ctcgctgctg ggaggtcggt ctagggatgc tctgacctc      716

cgtctcttgga acctaagatg gaatgtgtcc ccagctcagg gattgcctga accaagaggc      776

caggagcccc catgggccgc ccagtaccat gcacactcct gtcccgaaact ccctgaggcc      836

tccccctcct tcagggcacc cactgggtcc caggctggaa ccagggtctc tctttacctc      896

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gaagccctga gagcttcagg tctgtctcag ccgaggagc agtctgacat gggagtgagg      1076

ccccgtcctt ctactgcct ggtcacatgg tgcctagga tgcagggtc gagggcagag      1136

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gcgatt   atg gac ccg gcc gag gcg gtg ctg caa gag aag gca ctc aag      168
          Met Asp Pro Ala Glu Ala Val Leu Gln Glu Lys Ala Leu Lys
          1           5           10

ttt atg tgc tct atg ccc agg tct ctg tgg ctg ggc tgc tcc agc ctg      216
Phe Met Cys Ser Met Pro Arg Ser Leu Trp Leu Gly Cys Ser Ser Leu
  15           20           25           30

gcg gac agc atg cct tcg ctg cga tgc ctg tat aac cca ggg act ggc      264

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Ala Leu Thr Ala Phe Met Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn	
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ggc gaa ccc cct agg aag ata ata cca gag aag aat tcg ctt aga cag	360
Gly Glu Pro Pro Arg Lys Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln	
65 70 75	
aca tac aac agc tgt gcc aga ctc tgc tta aac caa gaa aca gta tgt	408
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Leu Ala Ser Thr Ala Met Lys Thr Glu Asn Cys Val Ala Lys Thr Lys	
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ctt gcc aat ggc act tcc agt atg att gtg ccc aag caa cgg aaa ctc	504
Leu Ala Asn Gly Thr Ser Ser Met Ile Val Pro Lys Gln Arg Lys Leu	
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Ser Ala Ser Tyr Glu Lys Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu	
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Gln Trp Ser Glu Ser Asp Gln Val Glu Phe Val Glu His Leu Ile Ser	
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Gln Met Cys His Tyr Gln His Gly His Ile Asn Ser Tyr Leu Lys Pro	
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Met Leu Gln Arg Asp Phe Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp	
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cat att gct gag aac att ctg tca tac ctg gat gcc aaa tca cta tgt	744
His Ile Ala Glu Asn Ile Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys	
195 200 205	
gct gct gaa ctt gtg tgc aag gaa tgg tac cga gtg acc tct gat ggc	792
Ala Ala Glu Leu Val Cys Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly	
210 215 220	
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Met Leu Trp Lys Lys Leu Ile Glu Arg Met Val Arg Thr Asp Ser Leu	
225 230 235	
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Trp Arg Gly Leu Ala Glu Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys	
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aac aaa cct cct gac ggg aat gct cct ccc aac tct ttt tat aga gca	936
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Leu Tyr Pro Lys Ile Ile Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp	
275 280 285	
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Cys	Lys	Arg	Ile	Leu	Thr	Gly	His	Thr	Gly	Ser	Val	Leu	Cys	Leu	Gln		
			335				340						345			350	
tat	gat	gag	aga	gtg	atc	ata	aca	gga	tca	tcg	gat	tcc	acg	gtc	aga	1224	
Tyr	Asp	Glu	Arg	Val	Ile	Ile	Thr	Gly	Ser	Ser	Asp	Ser	Thr	Val	Arg		
			355						360						365		
gtg	tgg	gat	gta	aat	aca	ggc	gaa	atg	cta	aac	acg	ttg	att	cac	cat	1272	
Val	Trp	Asp	Val	Asn	Thr	Gly	Glu	Met	Leu	Asn	Thr	Leu	Ile	His	His		
			370						375						380		
tgt	gaa	gca	gtt	ctg	cac	ttg	cgt	ttc	aat	aat	ggc	atg	atg	gtg	acc	1320	
Cys	Glu	Ala	Val	Leu	His	Leu	Arg	Phe	Asn	Asn	Gly	Met	Met	Val	Thr		
			385						390						395		
tgc	tcc	aaa	gat	cgt	tcc	att	gct	gta	tgg	gat	atg	gcc	tcc	cca	act	1368	
Cys	Ser	Lys	Asp	Arg	Ser	Ile	Ala	Val	Trp	Asp	Met	Ala	Ser	Pro	Thr		
			400						405						410		
gac	att	acc	ctc	cgg	agg	gtg	ctg	gtc	gga	cac	cga	gct	gct	gtc	aat	1416	
Asp	Ile	Thr	Leu	Arg	Arg	Val	Leu	Val	Gly	His	Arg	Ala	Ala	Val	Asn		
			415						420						425		430
gtt	gta	gac	ttt	gat	gac	aag	tac	att	gtt	tct	gca	tct	ggg	gat	aga	1464	
Val	Val	Asp	Phe	Asp	Asp	Lys	Tyr	Ile	Val	Ser	Ala	Ser	Gly	Asp	Arg		
			435						440						445		
act	ata	aag	gta	tgg	aac	aca	agt	act	tgt	gaa	ttt	gta	agg	acc	tta	1512	
Thr	Ile	Lys	Val	Trp	Asn	Thr	Ser	Thr	Cys	Glu	Phe	Val	Arg	Thr	Leu		
			450						455						460		
aat	gga	cac	aaa	cga	ggc	att	gcc	tgt	ttg	cag	tac	agg	gac	agg	ctg	1560	
Asn	Gly	His	Lys	Arg	Gly	Ile	Ala	Cys	Leu	Gln	Tyr	Arg	Asp	Arg	Leu		
			465						470						475		
gta	gtg	agt	ggc	tca	tct	gac	aac	act	atc	aga	tta	tgg	gac	ata	gaa	1608	
Val	Val	Ser	Gly	Ser	Ser	Asp	Asn	Thr	Ile	Arg	Leu	Trp	Asp	Ile	Glu		
			480						485						490		
tgt	ggc	gca	tgt	tta	cga	gtg	tta	gaa	ggc	cat	gag	gaa	ttg	gtg	cgt	1656	
Cys	Gly	Ala	Cys	Leu	Arg	Val	Leu	Glu	Gly	His	Glu	Glu	Leu	Val	Arg		
			495						500						505		510
tgt	att	cga	ttt	gat	aac	aag	agg	ata	gtc	agt	ggg	gcc	tat	gat	gga	1704	
Cys	Ile	Arg	Phe	Asp	Asn	Lys	Arg	Ile	Val	Ser	Gly	Ala	Tyr	Asp	Gly		
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aaa	att	aaa	gtg	tgg	gat	ctt	gtg	gct	gct	ttg	gac	ccc	cgt	gct	cct	1752	
Lys	Ile	Lys	Val	Trp	Asp	Leu	Val	Ala	Ala	Leu	Asp	Pro	Arg	Ala	Pro		
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gca	ggg	aca	ctc	tgt	cta	cgg	acc	ctt	gtg	gag	cat	tcc	gga	aga	gtt	1800	

Ala Gly Thr Leu Cys Leu Arg Thr Leu Val Glu His Ser Gly Arg Val	
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Phe Arg Leu Gln Phe Asp Glu Phe Gln Ile Val Ser Ser Ser His Asp	
560 565 570	
gac aca atc ctc atc tgg gac ttc cta aat gat cca gct gcc caa gct	1896
Asp Thr Ile Leu Ile Trp Asp Phe Leu Asn Asp Pro Ala Ala Gln Ala	
575 580 585 590	
gaa ccc ccc cgt tcc cct tct cga aca tac acc tac atc tcc aga taa	1944
Glu Pro Pro Arg Ser Pro Ser Arg Thr Tyr Thr Tyr Ile Ser Arg *	
595 600 605	
ataaccatac actgacctca tacttgccca ggtatcgaaa tcgattatgt acataacact	2004
gtgggtagga gacgggatat tagctgtaag gtgttgctag ttcatggaac tttctcctgc	2064
cgtttggtgc accaactcct gtaaagccga ggaagcagac aatgtgagac agggctgaag	2124
ctgccacagt gtggacagtg cctttcacca aggtagccag cctcagttct agatgattct	2184
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gcgatt atg gac ccg gcc gag gcg gtg ctg caa gag aag gca ctc aag	168
Met Asp Pro Ala Glu Ala Val Leu Gln Glu Lys Ala Leu Lys	
1 5 10	
ttt atg tgc tct atg ccc agg tct ctg tgg ctg ggc tgc tcc agc ctg	216
Phe Met Cys Ser Met Pro Arg Ser Leu Trp Leu Gly Cys Ser Ser Leu	
15 20 25 30	
gcg gac agc atg cct tcg ctg cga tgc ctg tat aac cca ggg act ggc	264
Ala Asp Ser Met Pro Ser Leu Arg Cys Leu Tyr Asn Pro Gly Thr Gly	
35 40 45	
gca ctc aca gct ttc cag aca tac aac agc tgt gcc aga ctc tgc tta	312
Ala Leu Thr Ala Phe Gln Thr Tyr Asn Ser Cys Ala Arg Leu Cys Leu	
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aac caa gaa aca gta tgt tta gca agc act gct atg aag act gag aat	360
Asn Gln Glu Thr Val Cys Leu Ala Ser Thr Ala Met Lys Thr Glu Asn	
65 70 75	



tgt gtg gcc aaa aca aaa ctt gcc aat ggc act tcc agt atg att gtg	408
Cys Val Ala Lys Thr Lys Leu Ala Asn Gly Thr Ser Ser Met Ile Val	
80 85 90	
ccc aag caa cgg aaa ctc tca gca agc tat gaa aag gaa aag gaa ctg	456
Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr Glu Lys Glu Lys Glu Leu	
95 100 105 110	
tgt gtc aaa tac ttt gag cag tgg tca gag tca gat caa gtg gaa ttt	504
Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser Asp Gln Val Glu Phe	
115 120 125	
gtg gaa cat ctt ata tcc caa atg tgt cat tac caa cat ggg cac ata	552
Val Glu His Leu Ile Ser Gln Met Cys His Tyr Gln His Gly His Ile	
130 135 140	
aac tcg tat ctt aaa cct atg ttg cag aga gat ttc ata act gct ctg	600
Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg Asp Phe Ile Thr Ala Leu	
145 150 155	
cca gct cgg gga ttg gat cat att gct gag aac att ctg tca tac ctg	648
Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile Leu Ser Tyr Leu	
160 165 170	
gat gcc aaa tca cta tgt gct gct gaa ctt gtg tgc aag gaa tgg tac	696
Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys Lys Glu Trp Tyr	
175 180 185 190	
cga gtg acc tct gat ggc atg ctg tgg aag aag ctt atc gag aga atg	744
Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu Ile Glu Arg Met	
195 200 205	
gtc agg aca gat tct ctg tgg aga ggc ctg gca gaa cga aga gga tgg	792
Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala Glu Arg Arg Gly Trp	
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Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro Asp Gly Asn Ala Pro Pro	
225 230 235	
aac tct ttt tat aga gca ctt tat cct aaa att ata caa gac att gag	888
Asn Ser Phe Tyr Arg Ala Leu Tyr Pro Lys Ile Ile Gln Asp Ile Glu	
240 245 250	
aca ata gaa tct aat tgg aga tgt gga aga cat agt tta cag aga att	936
Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg His Ser Leu Gln Arg Ile	
255 260 265 270	
cac tgc cga agt gaa aca agc aaa gga gtt tac tgt tta cag tat gat	984
His Cys Arg Ser Glu Thr Ser Lys Gly Val Tyr Cys Leu Gln Tyr Asp	
275 280 285	
gat cag aaa ata gta agc ggc ctt cga gac aac aca atc aag atc tgg	1032
Asp Gln Lys Ile Val Ser Gly Leu Arg Asp Asn Thr Ile Lys Ile Trp	
290 295 300	
gat aaa aac aca ttg gaa tgc aag cga att ctc aca ggc cat aca ggt	1080
Asp Lys Asn Thr Leu Glu Cys Lys Arg Ile Leu Thr Gly His Thr Gly	
305 310 315	
tca gtc ctc tgt ctc cag tat gat gag aga gtg atc ata aca gga tca	1128
Ser Val Leu Cys Leu Gln Tyr Asp Glu Arg Val Ile Ile Thr Gly Ser	
320 325 330	

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Ser Asp Ser Thr Val Arg Val Trp Asp Val Asn Thr Gly Glu Met Leu	
335 340 345 350	
aac acg ttg att cac cat tgt gaa gca gtt ctg cac ttg cgt ttc aat	1224
Asn Thr Leu Ile His His Cys Glu Ala Val Leu His Leu Arg Phe Asn	
355 360 365	
aat ggc atg atg gtg acc tgc tcc aaa gat cgt tcc att gct gta tgg	1272
Asn Gly Met Met Val Thr Cys Ser Lys Asp Arg Ser Ile Ala Val Trp	
370 375 380	
gat atg gcc tcc cca act gac att acc ctc cgg agg gtg ctg gtc gga	1320
Asp Met Ala Ser Pro Thr Asp Ile Thr Leu Arg Arg Val Leu Val Gly	
385 390 395	
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His Arg Ala Ala Val Asn Val Val Asp Phe Asp Asp Lys Tyr Ile Val	
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Ser Ala Ser Gly Asp Arg Thr Ile Lys Val Trp Asn Thr Ser Thr Cys	
415 420 425 430	
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Glu Phe Val Arg Thr Leu Asn Gly His Lys Arg Gly Ile Ala Cys Leu	
435 440 445	
cag tac agg gac agg ctg gta gtg agt ggc tca tct gac aac act atc	1512
Gln Tyr Arg Asp Arg Leu Val Val Ser Gly Ser Ser Asp Asn Thr Ile	
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Arg Leu Trp Asp Ile Glu Cys Gly Ala Cys Leu Arg Val Leu Glu Gly	
465 470 475	
cat gag gaa ttg gtg cgt tgt att cga ttt gat aac aag agg ata gtc	1608
His Glu Glu Leu Val Arg Cys Ile Arg Phe Asp Asn Lys Arg Ile Val	
480 485 490	
agt ggg gcc tat gat gga aaa att aaa gtg tgg gat ctt gtg gct gct	1656
Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val Trp Asp Leu Val Ala Ala	
495 500 505 510	
ttg gac ccc cgt gct cct gca ggg aca ctc tgt cta cgg acc ctt gtg	1704
Leu Asp Pro Arg Ala Pro Ala Gly Thr Leu Cys Leu Arg Thr Leu Val	
515 520 525	
gag cat tcc gga aga gtt ttt cga cta cag ttt gat gaa ttc cag att	1752
Glu His Ser Gly Arg Val Phe Arg Leu Gln Phe Asp Glu Phe Gln Ile	
530 535 540	
gtc agt agt tca cat gat gac aca atc ctc atc tgg gac ttc cta aat	1800
Val Ser Ser Ser His Asp Asp Thr Ile Leu Ile Trp Asp Phe Leu Asn	
545 550 555	
gat cca gct gcc caa gct gaa ccc ccc cgt tcc cct tct cga aca tac	1848
Asp Pro Ala Ala Gln Ala Glu Pro Pro Arg Ser Pro Ser Arg Thr Tyr	
560 565 570	
acc tac atc tcc aga taa ataacc atacactgac ctcatacttg cccaggtatc	1902
Thr Tyr Ile Ser Arg *	
575 580	

gaaatcgatt atgtacataa cactgtgggt aggagacggg atattagctg taagggtgtg 1962  
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 gcgatt atg gac ccg gcc gag gcg gtg ctg caa gag aag gca ctc aag 168  
 Met Asp Pro Ala Glu Ala Val Leu Gln Glu Lys Ala Leu Lys  
 1 5 10  
 ttt atg atg gag ttt cgc tct tgg tgc cca ggc tgg aat aca atg gcg 216  
 Phe Met Met Glu Phe Arg Ser Trp Cys Pro Gly Trp Asn Thr Met Ala  
 15 20 25 30  
 cga tct cgg ctc acc gca acc tcc acc tcc cgg gtt caa tgc tct atg 264  
 Arg Ser Arg Leu Thr Ala Thr Ser Thr Ser Arg Val Gln Cys Ser Met  
 35 40 45  
 ccc agg tct ctg tgg ctg ggc tgc tcc agc ctg gcg gac agc atg cct 312  
 Pro Arg Ser Leu Trp Leu Gly Cys Ser Ser Leu Ala Asp Ser Met Pro  
 50 55 60  
 tcg ctg cga tgc ctg tat aac cca ggg act ggc gca ctc aca gct ttc 360  
 Ser Leu Arg Cys Leu Tyr Asn Pro Gly Thr Gly Ala Leu Thr Ala Phe  
 65 70 75  
 atg aat tcc tca gag aga gaa gac tgt aat aat ggc gaa ccc cct agg 408  
 Met Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn Gly Glu Pro Pro Arg  
 80 85 90  
 aag ata ata cca gag aag aat tcg ctt aga cag aca tac aac agc tgt 456  
 Lys Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser Cys  
 95 100 105 110  
 gcc aga ctc tgc tta aac caa gaa aca gta tgt tta gca agc act gct 504  
 Ala Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser Thr Ala  
 115 120 125  
 atg aag act gag aat tgt gtg gcc aaa aca aaa ctt gcc aat ggc act 552  
 Met Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn Gly Thr  
 130 135 140

tcc agt atg att gtg ccc aag caa cgg aaa ctc tca gca agc tat gaa Ser Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr Glu 145 150 155	600
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gat caa gtg gaa ttt gtg gaa cat ctt ata tcc caa atg tgt cat tac Asp Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His Tyr 175 180 185 190	696
caa cat ggg cac ata aac tcg tat ctt aaa cct atg ttg cag aga gat Gln His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg Asp 195 200 205	744
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tgc aag gaa tgg tac cga gtg acc tct gat ggc atg ctg tgg aag aag Cys Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys 240 245 250	888
ctt atc gag aga atg gtc agg aca gat tct ctg tgg aga ggc ctg gca Leu Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala 255 260 265 270	936
gaa cga aga gga tgg gga cag tat tta ttc aaa aac aaa cct cct gac Glu Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro Asp 275 280 285	984
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ata caa gac att gag aca ata gaa tct aat tgg aga tgt gga aga cat Ile Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg His 305 310 315	1080
agt tta cag aga att cac tgc cga agt gaa aca agc aaa gga gtt tac Ser Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser Lys Gly Val Tyr 320 325 330	1128
tgt tta cag tat gat gat cag aaa ata gta agc ggc ctt cga gac aac Cys Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly Leu Arg Asp Asn 335 340 345 350	1176
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atc ata aca gga tca tcg gat tcc acg gtc aga gtg tgg gat gta aat Ile Ile Thr Gly Ser Ser Asp Ser Thr Val Arg Val Trp Asp Val Asn 385 390 395	1320

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Thr Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala Val Leu	
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His Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys Asp Arg	
415 420 425 430	
tcc att gct gta tgg gat atg gcc tcc cca act gac att acc ctc cgg	1464
Ser Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr Leu Arg	
435 440 445	
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Arg Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp Phe Asp	
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Asp Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys Val Trp	
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Asn Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His Lys Arg	
480 485 490	
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Gly Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser Gly Ser	
495 500 505 510	
tct gac aac act atc aga tta tgg gac ata gaa tgt ggt gca tgt tta	1704
Ser Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala Cys Leu	
515 520 525	
cga gtg tta gaa ggc cat gag gaa ttg gtg cgt tgt att cga ttt gat	1752
Arg Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg Phe Asp	
530 535 540	
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Asn Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val Trp	
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gat ctt gtg gct gct ttg gac ccc cgt gct cct gca ggg aca ctc tgt	1848
Asp Leu Val Ala Ala Leu Asp Pro Arg Ala Pro Ala Gly Thr Leu Cys	
560 565 570	
cta cgg acc ctt gtg gag cat tcc gga aga gtt ttt cga cta cag ttt	1896
Leu Arg Thr Leu Val Glu His Ser Gly Arg Val Phe Arg Leu Gln Phe	
575 580 585 590	
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Asp Glu Phe Gln Ile Val Ser Ser Ser His Asp Asp Thr Ile Leu Ile	
595 600 605	
tgg gac ttc cta aat gat cca gct gcc caa gct gaa ccc ccc cgt tcc	1992
Trp Asp Phe Leu Asn Asp Pro Ala Ala Gln Ala Glu Pro Pro Arg Ser	
610 615 620	
cct tct cga aca tac acc tac atc tcc aga taa ataaccat aactgacct	2043
Pro Ser Arg Thr Tyr Thr Tyr Ile Ser Arg *	
625 630	
catacttgcc caggtatcga aatcgattat gtacataaca ctgtgggtag gagacgggat	2103
attagctgta aggtgttgct agttcatgga actttctcct gccgtttggg tcaccaactc	2163

ctgtaaagcc gaggaagcag acaatgtgag acagggctga agctgccaca gtgtggacag 2223  
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 gcccggaagc tacagcagcg gcgcggagac tgcggggcgg gcc atg gcg gcg aac 295  
 Met Ala Ala Asn  
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 ctg agc cgg aac ggg cca gcg ctg caa gag gcc tac gtg cgg gtg gtc 343  
 Leu Ser Arg Asn Gly Pro Ala Leu Gln Glu Ala Tyr Val Arg Val Val  
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 acc gag aag tcc ccg acc gac tgg gct ctc ttt acc tat gaa ggc aac 391  
 Thr Glu Lys Ser Pro Thr Asp Trp Ala Leu Phe Thr Tyr Glu Gly Asn  
 25 30 35  
 agc aat gac atc cgc gtg gct ggc aca ggg gag ggt ggc ctg gag gag 439  
 Ser Asn Asp Ile Arg Val Ala Gly Thr Gly Glu Gly Gly Leu Glu Glu  
 40 45 50  
 atg gtg gag gag ctc aac agc ggg aag gtg atg tac gcc ttc tgc aga 487  
 Met Val Glu Glu Leu Asn Ser Gly Lys Val Met Tyr Ala Phe Cys Arg  
 55 60 65  
 gtg aag gac ccc aac tct gga ctg ccc aaa ttt gtc ctc atc aac tgg 535  
 Val Lys Asp Pro Asn Ser Gly Leu Pro Lys Phe Val Leu Ile Asn Trp  
 70 75 80  
 aca ggc gag ggc gtg aac gat gtg cgg aag gga gcc tgt gcc agc cac 583  
 Thr Gly Glu Gly Val Asn Asp Val Arg Lys Gly Ala Cys Ala Ser His  
 85 90 95 100  
 gtc agc acc atg gcc agc ttc ctg aag ggg gcc cat gtg acc atc aac 631  
 Val Ser Thr Met Ala Ser Phe Leu Lys Gly Ala His Val Thr Ile Asn  
 105 110 115  
 gca cgg gcc gag gag gat gtg gag cct gag tgc atc atg gag aag gtg 679  
 Ala Arg Ala Glu Glu Asp Val Glu Pro Glu Cys Ile Met Glu Lys Val

120	125	130	
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ttc cag gac gtg gga ccc cag gcc cca gtg ggc tct gtg tac cag aag Phe Gln Asp Val Gly Pro Gln Ala Pro Val Gly Ser Val Tyr Gln Lys 150 155 160			775
acc aat gcc gtg tct gag att aaa agg gtt ggt aaa gac agc ttc tgg Thr Asn Ala Val Ser Glu Ile Lys Arg Val Gly Lys Asp Ser Phe Trp 165 170 175 180			823
gcc aaa gca gag aag gag gag gag aac cgt cgg ctg gag gaa aag cgg Ala Lys Ala Glu Lys Glu Glu Glu Asn Arg Arg Leu Glu Glu Lys Arg 185 190 195			871
cgg gcc gag gag gca cag cgg cag ctg gag cag gag cgc cgg gag cgt Arg Ala Glu Glu Ala Gln Arg Gln Leu Glu Gln Glu Arg Arg Glu Arg 200 205 210			919
gag ctg cgt gag gct gca cgc cgg gag cag cgc tat cag gag cag ggt Glu Leu Arg Glu Ala Ala Arg Arg Glu Gln Arg Tyr Gln Glu Gln Gly 215 220 225			967
ggc gag gcc agc ccc cag agg acg tgg gag cag cag caa gaa gtg gtt Gly Glu Ala Ser Pro Gln Arg Thr Trp Glu Gln Gln Gln Glu Val Val 230 235 240			1015
tca agg aac cga aat gag cag gag tct gcc gtg cac ccg agg gag att Ser Arg Asn Arg Asn Glu Gln Glu Ser Ala Val His Pro Arg Glu Ile 245 250 255 260			1063
ttc aag cag aag gag agg gcc atg tcc acc acc tcc atc tcc agt cct Phe Lys Gln Lys Glu Arg Ala Met Ser Thr Thr Ser Ile Ser Ser Pro 265 270 275			1111
cag cct ggc aag ctg agg agc ccc ttc ctg cag aag cag ctc acc caa Gln Pro Gly Lys Leu Arg Ser Pro Phe Leu Gln Lys Gln Leu Thr Gln 280 285 290			1159
cca gag acc cac ttt ggc aga gag cca gct gct gcc atc tca agg ccc Pro Glu Thr His Phe Gly Arg Glu Pro Ala Ala Ala Ile Ser Arg Pro 295 300 305			1207
agg gca gat ctc cct gct gag gag ccg gcg ccc agc act cct cca tgt Arg Ala Asp Leu Pro Ala Glu Glu Pro Ala Pro Ser Thr Pro Pro Cys 310 315 320			1255
ctg gtg cag gca gaa gag gag gct gtg tat gag gaa cct cca gag cag Leu Val Gln Ala Glu Glu Glu Ala Val Tyr Glu Glu Pro Pro Glu Gln 325 330 335 340			1303
gag acc ttc tac gag cag ccc cca ctg gtg cag cag caa ggt gct ggc Glu Thr Phe Tyr Glu Gln Pro Pro Leu Val Gln Gln Gln Gly Ala Gly 345 350 355			1351
tct gag cac att gac cac cac att cag ggc cag ggg ctc agt ggg caa Ser Glu His Ile Asp His His Ile Gln Gly Gln Gly Leu Ser Gly Gln 360 365 370			1399
ggg ctc tgt gcc cgt gcc ctg tac gac tac cag gca gcc gac gac aca Gly Leu Cys Ala Arg Ala Leu Tyr Asp Tyr Gln Ala Ala Asp Asp Thr 1447			

375	380	385	
gag atc tcc ttt gac ccc gag aac ctc atc acg ggc atc gag gtg atc			1495
Glu Ile Ser Phe Asp Pro Glu Asn Leu Ile Thr Gly Ile Glu Val Ile			
390	395	400	
gac gaa ggc tgg tgg cgt ggc tat ggg ccg gat ggc cat ttt ggc atg			1543
Asp Glu Gly Trp Trp Arg Gly Tyr Gly Pro Asp Gly His Phe Gly Met			
405	410	415	420
ttc cct gcc aac tac gtg gag ctc att gag tga ggctgagg gcacatcttg			1594
Phe Pro Ala Asn Tyr Val Glu Leu Ile Glu *			
425	430		
cccttccct ctcagacatg gcttccttat tgctggaaga ggaggcctgg gagttgacat			1654
tcagcactct tccaggaata ggacccccag tgaggatgag gcctcagggc tccctccggc			1714
ttggcagact cagcctgtca ccccaaatgc agcaatggcc tggatgattcc cacacatcct			1774
tcctgcatcc cccgaccctc ccagacagct tggctcttgc ccctgacagg atactgagcc			1834
aagccctgcc tgtggccaag ccctgagtgg ccactgccaa gctgcgggga agggctcctga			1894
gcagggggcat ctgggaggct ctggctgctt tctgcattta ttgcctttt ttctttttct			1954
cttgccttcta aggggtggtg gccaccactg tttagaatga cccttgggaa cagtgaacgt			2014
agagaattgt ttttagcaga gtttgtgacc aaagtcagag tggatcatgg tggtttgga			2074
gcaggggaatt tgtcttggtg gagcctgctc tgtgctcccc actccatttc tctgtccctc			2134
tgcttgggct atgggaagtg gggatgcaga tggccaagct cccaccctgg gtattcaaaa			2194
acggcagaca caacatgttc ctccacgcgg ctactcgat gcctgcaggc ccagtggtgt			2254
gcctcaactg attctgactt caggaaaagt aacacagagt ggccttggcc tgttgtcttc			2314
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aaaa			2378

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caccaaacc aaaaaagag atctctcgag gatccgaatt cgcggccggc tctaccgcta	120
ggaagaggcc gcgtggggcg aaggcggcgc ttggctggtg gggcccgcg cggtatttc	180
ccggcgggcg agagcggatc tatcttggga tccc	232
atg gct ttc ttt act ggg	
Met Ala Phe Phe Thr Gly	
1 5	



```

ctc tgg ggc ccc ttc acc tgt gta agc aga gtg ctg agc cat cac tgt      280
Leu Trp Gly Pro Phe Thr Cys Val Ser Arg Val Leu Ser His His Cys
      10                      15                      20

ttc agc acc act ggg agt ctg agt gcg att cag aag atg acg cgg gta      328
Phe Ser Thr Thr Gly Ser Leu Ser Ala Ile Gln Lys Met Thr Arg Val
      25                      30                      35

cga gtg gtg gac aac agt gcc ctg ggg aac agc cca tac cat cgg gct      376
Arg Val Val Asp Asn Ser Ala Leu Gly Asn Ser Pro Tyr His Arg Ala
      40                      45                      50

cct cgc tgc atc cat gtc tat aag aag aat gga gtg ggc aag gtg ggc      424
Pro Arg Cys Ile His Val Tyr Lys Lys Asn Gly Val Gly Lys Val Gly
      55                      60                      65                      70

gac cag ata cta ctg gcc atc aag gga cag aag aaa aag gcg ctc att      472
Asp Gln Ile Leu Leu Ala Ile Lys Gly Gln Lys Lys Lys Ala Leu Ile
      75                      80                      85

gtg ggg cac tgc atg cct ggc ccc cga atg acc ccc aga ttt gac tcc      520
Val Gly His Cys Met Pro Gly Pro Arg Met Thr Pro Arg Phe Asp Ser
      90                      95                      100

aac aac gtg gtc ctc att gag gac aac ggg aac cct gtg ggg aca cga      568
Asn Asn Val Val Leu Ile Glu Asp Asn Gly Asn Pro Val Gly Thr Arg
      105                      110                      115

att aag aca ccc atc ccc acc agc ctg cgc aag cgg gaa ggc gag tat      616
Ile Lys Thr Pro Ile Pro Thr Ser Leu Arg Lys Arg Glu Gly Glu Tyr
      120                      125                      130

tcc aag gtg ctg gcc att gct cag aac ttt gtg tga gttg agcccaggcc      666
Ser Lys Val Leu Ala Ile Ala Gln Asn Phe Val *
      135                      140                      145

tctggttgca ggactcgtga atggagcagt tctgagaacc acccttttgc taagggagct      726

tgaggagccac atggctgctc ccttcacact gggtaacagt gtagtatcct gtgagagaat      786

aaatgtattc atttatgtgt ttttcagag ctttctggga tgtgggaaaa taaattacac      846

tgaagcagtt gaaaggtggc ttacccgagt ctggccacac ggggtagcat tctttacatg      906

gagcagcctt ggtgccaggg tctgagccct tgcttttctg gtttggaccc tataagttca      966

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gcc agc ccc acc tca ggc ccc cag gag tgt gca aag ggc tcc acg gtg	96
Ala Ser Pro Thr Ser Gly Pro Gln Glu Cys Ala Lys Gly Ser Thr Val	
20 25 30	
tgg tgt cag gat ctg cag aca gct gcc agg tgc ggg gct gtg ggg tac	144
Trp Cys Gln Asp Leu Gln Thr Ala Ala Arg Cys Gly Ala Val Gly Tyr	
35 40 45	
tgc caa ggg gcc gta tgg aac aaa ccc acc gcg aag tct ctg ccc tgc	192
Cys Gln Gly Ala Val Trp Asn Lys Pro Thr Ala Lys Ser Leu Pro Cys	
50 55 60	
gac gta tgc cag gac ata gca gcc gcc gct ggc aat ggg ctg aac cct	240
Asp Val Cys Gln Asp Ile Ala Ala Ala Ala Gly Asn Gly Leu Asn Pro	
65 70 75 80	
gac gcc acg gag tct gac atc ctg gct ttg gtg atg aag acc tgt gag	288
Asp Ala Thr Glu Ser Asp Ile Leu Ala Leu Val Met Lys Thr Cys Glu	
85 90 95	
tgg ctc ccc agc cag gag tct tca gcc gga tgc aag tgg atg gtg gat	336
Trp Leu Pro Ser Gln Glu Ser Ser Ala Gly Cys Lys Trp Met Val Asp	
100 105 110	
gcc cac agt tgc gcc atc ctg agc atg ctc cgt ggg gcc ccg gac agt	384
Ala His Ser Ser Ala Ile Leu Ser Met Leu Arg Gly Ala Pro Asp Ser	
115 120 125	
gcc ccg gca cag gtg tgc aca gcg ctc agc ctc tgt gag ccg ctg cag	432
Ala Pro Ala Gln Val Cys Thr Ala Leu Ser Leu Cys Glu Pro Leu Gln	
130 135 140	
agg cac ctg gcc acc ctg agg cca ctc tcc aaa gag gac acc ttt gag	480
Arg His Leu Ala Thr Leu Arg Pro Leu Ser Lys Glu Asp Thr Phe Glu	
145 150 155 160	
gct gtg gct ccg ttc atg gcc aat ggg ccc ctt acc ttc cac ccc cgc	528
Ala Val Ala Pro Phe Met Ala Asn Gly Pro Leu Thr Phe His Pro Arg	
165 170 175	
cag gcg cct gaa gga gct ctg tgc caa gac tgt gta cgg cag gtc tcc	576
Gln Ala Pro Glu Gly Ala Leu Cys Gln Asp Cys Val Arg Gln Val Ser	
180 185 190	
cga ctc cag gag gct gtc cgg tcc aac ttg acc ttg gcc gac ttg aac	624
Arg Leu Gln Glu Ala Val Arg Ser Asn Leu Thr Leu Ala Asp Leu Asn	
195 200 205	
atc cag gag cag tgt gag tcc ttg ggg cct ggc ctg gcc gtc ctc tgc	672
Ile Gln Glu Gln Cys Glu Ser Leu Gly Pro Gly Leu Ala Val Leu Cys	
210 215 220	
aag aac tac ctc ttc cag ttt ttt gtc cct gct gac caa gca ctg agg	720
Lys Asn Tyr Leu Phe Gln Phe Phe Val Pro Ala Asp Gln Ala Leu Arg	
225 230 235 240	
ctt ctc ccc ccg cag gag ctc tgc agg aag ggg gga ttc tgt gag gag	768
Leu Leu Pro Pro Gln Glu Leu Cys Arg Lys Gly Gly Phe Cys Glu Glu	
245 250 255	

cta ggg gca cct gcc cgt ttg act caa gta gtg gcc atg gac ggg gtc Leu Gly Ala Pro Ala Arg Leu Thr Gln Val Val Ala Met Asp Gly Val 260 265 270	816
ccc tcc ctg gag ctg ggg ttg cca agg aaa cag agc gag atg cag atg Pro Ser Leu Glu Leu Gly Leu Pro Arg Lys Gln Ser Glu Met Gln Met 275 280 285	864
aag gcc ggt gtg acc tgt gag gtg tgc atg aac gtg gtg cag aag ctg Lys Ala Gly Val Thr Cys Glu Val Cys Met Asn Val Val Gln Lys Leu 290 295 300	912
gac cac tgg ctc atg tcc aac agc tct gag ctc atg atc acc cat gcc Asp His Trp Leu Met Ser Asn Ser Ser Glu Leu Met Ile Thr His Ala 305 310 315 320	960
ctg gag cgc gtg tgc tgc gta atg cct gcc tct atc acg aag gag tgc Leu Glu Arg Val Cys Ser Val Met Pro Ala Ser Ile Thr Lys Glu Cys 325 330 335	1008
atc atc ttg gtg gac acc tac agc ccc tcc ttg gtg cag ctt gtg gcc Ile Ile Leu Val Asp Thr Tyr Ser Pro Ser Leu Val Gln Leu Val Ala 340 345 350	1056
aaa atc acc cca gag aag gtg tgc aag ttc atc cgt ctg tgt ggc aac Lys Ile Thr Pro Glu Lys Val Cys Lys Phe Ile Arg Leu Cys Gly Asn 355 360 365	1104
cgg agg cgg gcc cgg gca gtc cat gat gcc tat gcc atc gtg ccg tcc Arg Arg Arg Ala Arg Ala Val His Asp Ala Tyr Ala Ile Val Pro Ser 370 375 380	1152
cca gag tgg gac gcg gag aac cag ggc agc ttc tgc aat ggg tgc aag Pro Glu Trp Asp Ala Glu Asn Gln Gly Ser Phe Cys Asn Gly Cys Lys 385 390 395 400	1200
agg ctg ctc acg gtg tcc tcc cac aac ctg gag agc aag agc acc aag Arg Leu Leu Thr Val Ser Ser His Asn Leu Glu Ser Lys Ser Thr Lys 405 410 415	1248
cga gac atc ctg gtg gcc ttc aag ggt ggc tgc agc atc ctg ccg ctg Arg Asp Ile Leu Val Ala Phe Lys Gly Gly Cys Ser Ile Leu Pro Leu 420 425 430	1296
ccc tat atg atc cag tgc aag cac ttc gtc acc cag tac gag ccc gtg Pro Tyr Met Ile Gln Cys Lys His Phe Val Thr Gln Tyr Glu Pro Val 435 440 445	1344
ctc att gag agt ctc aag gac atg atg gac ccc gtg gct gtg tgc aag Leu Ile Glu Ser Leu Lys Asp Met Met Asp Pro Val Ala Val Cys Lys 450 455 460	1392
aag gtg ggg gcc tgc cac ggc ccc agg acc cca ctg ctg ggc acc gac Lys Val Gly Ala Cys His Gly Pro Arg Thr Pro Leu Leu Gly Thr Asp 465 470 475 480	1440
cag tgt gcc ctg ggc cca agc ttc tgg tgc agg agc cag gag gcc gcc Gln Cys Ala Leu Gly Pro Ser Phe Trp Cys Arg Ser Gln Glu Ala Ala 485 490 495	1488
aag ctg tgc aac gct gtg caa cac tgc cag aag cat gta tgg aaa gag Lys Leu Cys Asn Ala Val Gln His Cys Gln Lys His Val Trp Lys Glu 500 505 510	1536

atg cac ctc cac gct ggg gaa cac gcg tga c cgtggctgcc agagaccag 1587  
 Met His Leu His Ala Gly Glu His Ala \*  
 515 520

agcctgctag cgaggcccat gaggtgggtg ccttcccat cccatttca caaatgaaaa 1647  
 actgaagctc tgaggaggga ggctgggaag gagcagagct gaagttcaaa accaagtatt 1707  
 cctgatcccg aaagcctctc tcttaacaac ggtgccgcac agctttgccc ttgaaagcat 1767  
 ctctactgga ccggaacaca ctcattgtgcc ccgctccctg acccagccaa gcctgccttt 1827  
 tcatctccaa ggctgagatg ttgccggggg tcccatgaga gcctgcccatt gggctcaggt 1887  
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 c 1948

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 gcc agc ccc acc tca ggc ccc cag gag tgt gca aag ggc tcc acg gtg 96  
 Ala Ser Pro Thr Ser Gly Pro Gln Glu Cys Ala Lys Gly Ser Thr Val  
 20 25 30  
 tgg tgt cag gat ctg cag aca gct gcc agg tgc ggg gct gtg ggg tac 144  
 Trp Cys Gln Asp Leu Gln Thr Ala Ala Arg Cys Gly Ala Val Gly Tyr  
 35 40 45  
 tgc caa ggg gcc gta tgg aac aaa ccc acc gcg aag tct ctg ccc tgc 192  
 Cys Gln Gly Ala Val Trp Asn Lys Pro Thr Ala Lys Ser Leu Pro Cys  
 50 55 60  
 gac gta tgc cag gac ata gca gcc gcc gct ggc aat ggg ctg aac cct 240  
 Asp Val Cys Gln Asp Ile Ala Ala Ala Ala Gly Asn Gly Leu Asn Pro  
 65 70 75 80  
 gac gcc acg gag tct gac atc ctg gct ttg gtg atg aag acc tgt gag 288  
 Asp Ala Thr Glu Ser Asp Ile Leu Ala Leu Val Met Lys Thr Cys Glu  
 85 90 95  
 tgg ctc ccc agc cag gag tct tca gcc gga tgc aag tgg atg gtg gat 336  
 Trp Leu Pro Ser Gln Glu Ser Ser Ala Gly Cys Lys Trp Met Val Asp  
 100 105 110  
 gcc cac agt tcg gcc atc ctg agc atg ctc cgt ggg gcc ccg gac agt 384  
 Ala His Ser Ser Ala Ile Leu Ser Met Leu Arg Gly Ala Pro Asp Ser  
 115 120 125  
 gcc ccg gca cag gtg tgc aca gcg ctc agc ctc tgt gag ccg ctg cag 432

Ala Pro Ala Gln Val Cys Thr Ala Leu Ser Leu Cys Glu Pro Leu Gln	
130 135 140	
agg cac ctg gcc acc ctg agg cca ctc tcc aaa gag gac acc ttt gag	480
Arg His Leu Ala Thr Leu Arg Pro Leu Ser Lys Glu Asp Thr Phe Glu	
145 150 155 160	
gct gtg gct ccg ttc atg gcc aat ggg ccc ctt acc ttc cac ccc cgc	528
Ala Val Ala Pro Phe Met Ala Asn Gly Pro Leu Thr Phe His Pro Arg	
165 170 175	
cag gcg cct gaa gga gct ctg tgc caa gac tgt gta cgg cag ctt gtg	576
Gln Ala Pro Glu Gly Ala Leu Cys Gln Asp Cys Val Arg Gln Leu Val	
180 185 190	
gcc aaa atc acc cca gag aag gtg tgc aag ttc atc cgt ctg tgt ggc	624
Ala Lys Ile Thr Pro Glu Lys Val Cys Lys Phe Ile Arg Leu Cys Gly	
195 200 205	
aac cgg agg cgg gcc cgg gca gtc cat gat gcc tat gcc atc gtg ccg	672
Asn Arg Arg Arg Ala Arg Ala Val His Asp Ala Tyr Ala Ile Val Pro	
210 215 220	
tcc cca gag tgg gac gcg gag aac cag ggc agc ttc tgc aat ggg tgc	720
Ser Pro Glu Trp Asp Ala Glu Asn Gln Gly Ser Phe Cys Asn Gly Cys	
225 230 235 240	
aag agg ctg ctc acg gtg tcc tcc cac aac ctg gag agc aag agc acc	768
Lys Arg Leu Leu Thr Val Ser Ser His Asn Leu Glu Ser Lys Ser Thr	
245 250 255	
aag cga gac atc ctg gtg gcc ttc aag ggt ggc tgc agc atc ctg ccg	816
Lys Arg Asp Ile Leu Val Ala Phe Lys Gly Gly Cys Ser Ile Leu Pro	
260 265 270	
ctg ccc tat atg atc cag tgc aag cac ttc gtc acc cag tac gag ccc	864
Leu Pro Tyr Met Ile Gln Cys Lys His Phe Val Thr Gln Tyr Glu Pro	
275 280 285	
gtg ctc att gag agt ctc aag gac atg atg gac ccc gtg gct gtg tgc	912
Val Leu Ile Glu Ser Leu Lys Asp Met Met Asp Pro Val Ala Val Cys	
290 295 300	
aag aag gtg ggg gcc tgc cac ggc ccc agg acc cca ctg ctg ggc acc	960
Lys Lys Val Gly Ala Cys His Gly Pro Arg Thr Pro Leu Leu Gly Thr	
305 310 315 320	
gac cag tgt gcc ctg ggc cca agc ttc tgg tgc agg agc cag gag gcc	1008
Asp Gln Cys Ala Leu Gly Pro Ser Phe Trp Cys Arg Ser Gln Glu Ala	
325 330 335	
gcc aag ctg tgc aac gct gtg caa cac tgc cag aag cat gta tgg aaa	1056
Ala Lys Leu Cys Asn Ala Val Gln His Cys Gln Lys His Val Trp Lys	
340 345 350	
gag atg cac ctc cac gct ggg gaa cac gcg tga ccgtggct gccagagacc	1107
Glu Met His Leu His Ala Gly Glu His Ala *	
355 360	
cagagcctgc tagcgaggcc catgagggtgg gtgccttccc catccccatt tcacaaatga	1167
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 ctttcatctc caaggctgag atgttgccgg gggccccatg agagcctgcc catgggctca 1407  
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 ccgc 1471

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 aca gct ggt tat aag acc ctt ctc aag tgc ctc tca ggt aaa ttc tgc 96  
 Thr Ala Gly Tyr Lys Thr Leu Leu Lys Cys Leu Ser Gly Lys Phe Cys  
 20 25 30  
 cgc cgg gag ctg att ggc atc atg ggc ccc tca ggg gct ggc aag tct 144  
 Arg Arg Glu Leu Ile Gly Ile Met Gly Pro Ser Gly Ala Gly Lys Ser  
 35 40 45  
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 Thr Phe Met Asn Ile Leu Ala Gly Tyr Arg Glu Ser Gly Met Lys Gly  
 50 55 60  
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 Gln Ile Leu Val Asn Gly Arg Pro Arg Glu Leu Arg Thr Phe Arg Lys  
 65 70 75 80  
 atg tcc tgc tac atc atg caa gat gac atg ctg ctg ccg cac ctc acg 288  
 Met Ser Cys Tyr Ile Met Gln Asp Asp Met Leu Leu Pro His Leu Thr  
 85 90 95  
 gtg ttg gaa gcc atg atg gtc tct gct aac ctg aag ctg agt gag aag 336  
 Val Leu Glu Ala Met Met Val Ser Ala Asn Leu Lys Leu Ser Glu Lys  
 100 105 110  
 cag gag gtg aag aag gag ctg gtg aca gag atc ctg acg gca ctg ggc 384  
 Gln Glu Val Lys Lys Glu Leu Val Thr Glu Ile Leu Thr Ala Leu Gly  
 115 120 125  
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 Leu Met Ser Cys Ser His Thr Arg Thr Ala Leu Leu Ser Gly Gly Gln  
 130 135 140  
 agg aag cgt ctg gcc atc gcc ctg gag ctg gtc aac aac ccg cct gtc 480  
 Arg Lys Arg Leu Ala Ile Ala Leu Glu Leu Val Asn Asn Pro Pro Val  
 145 150 155 160  
 atg ttc ttt gat gag ccc acc agt ggt ctg gat agc gcc tct tgt ttc 528  
 Met Phe Phe Asp Glu Pro Thr Ser Gly Leu Asp Ser Ala Ser Cys Phe

165	170	175	
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atc tgc acc atc cac cag ccc agt gcc aag ctc ttt gag atg ttt gac Ile Cys Thr Ile His Gln Pro Ser Ala Lys Leu Phe Glu Met Phe Asp 195 200 205			624
aag tgc atc ttc aaa ggc gtg gtc acc aac ctg atc ccc tat cta aag Lys Cys Ile Phe Lys Gly Val Val Thr Asn Leu Ile Pro Tyr Leu Lys 210 215 220			672
gga ctc ggc ttg cat tgc ccc acc tac cac aac ccg gct gac ttc atc Gly Leu Gly Leu His Cys Pro Thr Tyr His Asn Pro Ala Asp Phe Ile 225 230 235 240			720
atc gag gtg gcc tct ggc gag tat gga gac ctg aac ccc atg ttg ttc Ile Glu Val Ala Ser Gly Glu Tyr Gly Asp Leu Asn Pro Met Leu Phe 245 250 255			768
agg gct gtg cag aat ggg ctg tgc gct atg gct gag aag aag agc agc Arg Ala Val Gln Asn Gly Leu Cys Ala Met Ala Glu Lys Lys Ser Ser 260 265 270			816
cct gag aag aac gag gtc cct gcc cca tgc cct cct tgt cct ccg gaa Pro Glu Lys Asn Glu Val Pro Ala Pro Cys Pro Pro Cys Pro Pro Glu 275 280 285			864
gtg gat ccc att gaa agc cac acc ttt gcc acc agc acc ctc aca cag Val Asp Pro Ile Glu Ser His Thr Phe Ala Thr Ser Thr Leu Thr Gln 290 295 300			912
ttc tgc atc ctc ttc aag agg acc ttc ctg tcc atc ctc agg gac acg Phe Cys Ile Leu Phe Lys Arg Thr Phe Leu Ser Ile Leu Arg Asp Thr 305 310 315 320			960
gtg gtg tgt ccg gtg gtc tac tgc agc att gtg tac tgg atg acg ggc Val Val Cys Pro Val Val Tyr Cys Ser Ile Val Tyr Trp Met Thr Gly 325 330 335			1008
cag ccc gct gag acc agc cgc ttc ctg ctc ttc tca gcc ctg gcc acc Gln Pro Ala Glu Thr Ser Arg Phe Leu Leu Phe Ser Ala Leu Ala Thr 340 345 350			1056
gcc acc gcc ttg gtg gcc caa tct ttg ggg ctg ctg atc gga gct gct Ala Thr Ala Leu Val Ala Gln Ser Leu Gly Leu Leu Ile Gly Ala Ala 355 360 365			1104
tcc aac tcc cta cag gtg gcc act ttt gtg ggc cca gtt acc gcc atc Ser Asn Ser Leu Gln Val Ala Thr Phe Val Gly Pro Val Thr Ala Ile 370 375 380			1152
cct gtc ctc ttg ttc tcc ggc ttc ttt gtc agc ttc aag acc atc ccc Pro Val Leu Leu Phe Ser Gly Phe Phe Val Ser Phe Lys Thr Ile Pro 385 390 395 400			1200
act tac ctg caa tgg agc tcc tat ctc tcc tat gtc agg tat ggc ttt Thr Tyr Leu Gln Trp Ser Ser Tyr Leu Ser Tyr Val Arg Tyr Gly Phe 405 410 415			1248
gag ggt gtg atc ctg acg atc tat ggc atg gag cga gga gac ctg aca Glu Gly Val Ile Leu Thr Ile Tyr Gly Met Glu Arg Gly Asp Leu Thr 420 425 430 435 440 445			1296

420	425	430	
tgt tta gag gaa cgc tgc ccg ttc cgg gag cca cag agc atc ctc cga Cys Leu Glu Glu Arg Cys Pro Phe Arg Glu Pro Gln Ser Ile Leu Arg 435 440 445			1344
gcg ctg gat gtg gag gat gcc aag ctc tac atg gac ttc ctg gtc ttg Ala Leu Asp Val Glu Asp Ala Lys Leu Tyr Met Asp Phe Leu Val Leu 450 455 460			1392
ggc atc ttc ttc cta gcc ctg cgg ctg ctg gcc tac ctt gtg ctg cgt Gly Ile Phe Phe Leu Ala Leu Arg Leu Leu Ala Tyr Leu Val Leu Arg 465 470 475 480			1440
tac cgg gaa tgt ggc ttt tgt tct ctg gac agt tct gct gac ctc atc Tyr Arg Glu Cys Gly Phe Cys Ser Leu Asp Ser Ser Ala Asp Leu Ile 485 490 495			1488
cgc cat gtc tac ttc cac tgc tac cac acc aag ctg aaa cag tgg ggg Arg His Val Tyr Phe His Cys Tyr His Thr Lys Leu Lys Gln Trp Gly 500 505 510			1536
ctg cag gcc ttg caa agc cag gct gac ctt ggc ccc tgc atc ctg gac Leu Gln Ala Leu Gln Ser Gln Ala Asp Leu Gly Pro Cys Ile Leu Asp 515 520 525			1584
ttc cag agc cgg aac gtc atc cct gat atc cct gac cac ttc ctg tgt Phe Gln Ser Arg Asn Val Ile Pro Asp Ile Pro Asp His Phe Leu Cys 530 535 540			1632
ctg tgg gag cac tgt gag ttg ccc ctg gca cag aat tcc ttc gac aat Leu Trp Glu His Cys Glu Leu Pro Leu Ala Gln Asn Ser Phe Asp Asn 545 550 555 560			1680
cct gag tgg ttt tat cgg cat gtg gaa gca cac agt ctg tgc tgt gaa Pro Glu Trp Phe Tyr Arg His Val Glu Ala His Ser Leu Cys Cys Glu 565 570 575			1728
tac gaa gca gtc ggc aag gac aac ccg gtg gtg ctg tgt ggc tgg aaa Tyr Glu Ala Val Gly Lys Asp Asn Pro Val Val Leu Cys Gly Trp Lys 580 585 590			1776
ggc tgt acc tgc acc ttc aag gac cgc agt aaa ctt cga gag cac ctc Gly Cys Thr Cys Thr Phe Lys Asp Arg Ser Lys Leu Arg Glu His Leu 595 600 605			1824
cgc agc cat acc cag gag aaa gtg gta gcc tgc ccc acc tgt ggg ggc Arg Ser His Thr Gln Glu Lys Val Val Ala Cys Pro Thr Cys Gly Gly 610 615 620			1872
atg ttt gcc aac aat acc aag ttc tta gat cac atc cgt cgc cag acc Met Phe Ala Asn Asn Thr Lys Phe Leu Asp His Ile Arg Arg Gln Thr 625 630 635 640			1920
tca ttg gat cag cag cac ttc cag tgt tct cac tgt tcc aag aga ttt Ser Leu Asp Gln Gln His Phe Gln Cys Ser His Cys Ser Lys Arg Phe 645 650 655			1968
gcc aca gag cgg cta ttg cgg gac cac atg cgc aac cat gtg aat cac Ala Thr Glu Arg Leu Leu Arg Asp His Met Arg Asn His Val Asn His 660 665 670			2016
tat aag tgc cct ctg tgt gac atg acc tgc ccg ctg cct tcc tcc ctc Tyr Lys Cys Pro Leu Cys Asp Met Thr Cys Pro Leu Pro Ser Ser Leu			2064



675	680	685	
cgc aac cac atg cgc ttt Arg Asn His Met Arg Phe 690	cgt cac agt gag gac cgg Arg His Ser Glu Asp Arg 695	ccc ttt aaa tgt Pro Phe Lys Cys 700	2112
gac tgt tgt gac tac agc Asp Cys Cys Asp Tyr Ser 705	tgc aag aat ctt att gac Cys Lys Asn Leu Ile Asp 710	ctc cag aag cac Leu Gln Lys His 715	2160
ctg gat acc cac agc gag Leu Asp Thr His Ser Glu 725	gag cca gcc tac agg Glu Pro Ala Tyr Arg 730	tgt gat ttt gag aac Cys Asp Phe Glu Asn 735	2208
tgc acc ttc agt gcc cga Cys Thr Phe Ser Ala Arg 740	tcc ctc tgc tct atc Ser Leu Cys Ser Ile 745	aag tcc cat tac cgc Lys Ser His Tyr Arg 750	2256
aaa gta cat gaa gga gac Lys Val His Glu Gly Asp 755	tct gag cca agg tac Ser Glu Pro Arg Tyr 760	aaa tgt cat gtg tgt Lys Cys His Val Cys 765	2304
gac aaa tgc ttc aca cgg Asp Lys Cys Phe Thr Arg 770	ggc aac aac ctc acc Gly Asn Asn Leu Thr 775	gtg cac ctt cgc aag Val His Leu Arg Lys 780	2352
aag cac cag ttc aag tgg Lys His Gln Phe Lys Trp 785	ccc tca ggg cat ccc Pro Ser Gly His Pro 790	cgt ttt cgg tac aag Arg Phe Arg Tyr Lys 795	2400
gaa cat gaa gat ggc tat Glu His Glu Asp Gly Tyr 805	atg cgg ctg cag ctg Met Arg Leu Gln Leu 810	gtt cgc tac gag agt Val Arg Tyr Glu Ser 815	2448
gta gag ctg aca cag caa Val Glu Leu Thr Gln Gln 820	ctg ctg cgg caa cca Leu Leu Arg Gln Pro 825	caa gag gga tcg ggc Gln Glu Gly Ser Gly 830	2496
ctg gga acg tcg ctg aac Leu Gly Thr Ser Leu Asn 835	gag agc agc ctg cag Glu Ser Ser Leu Gln 840	ggc att att cta gaa Gly Ile Ile Leu Glu 845	2544
aca gtg cca ggg gag cca Thr Val Pro Gly Glu Pro 850	gga cgt aag gaa gag Gly Arg Lys Glu Glu 855	gaa gag gag ggc aag Glu Glu Glu Gly Lys 860	2592
ggt agc gaa ggg aca gcc Gly Ser Glu Gly Thr Ala 865	ctc tca gcc tct cag Leu Ser Ala Ser Gln 870	gac aac ccc agt tct Asp Asn Pro Ser Ser 875	2640
gtc atc cac gtg gtg aat Val Ile His Val Val Asn 885	cag acc aat gcc caa Gln Thr Asn Ala Gln 890	ggc cag caa gag att Gly Gln Gln Glu Ile 895	2688
gtc tac tat gtg ctg tct Val Tyr Tyr Val Leu Ser 900	gaa gcc cca ggg gag Glu Ala Pro Gly Glu 905	cct ccc cca gtc cct Pro Pro Pro Val Pro 910	2736
gag cca cct tca ggg ggc Glu Pro Pro Ser Gly Gly 915	atc atg gaa aag ctt Ile Met Glu Lys Leu 920	caa gga ata gct gag Gln Gly Ile Ala Glu 925	2784
gag cca gag atc cag atg Glu Pro Glu Ile Gln Met 930	gtt tga aggccgcaga Val *	gccagaccat ttcttcccca	2838

930

935

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ggtcctgaag tttgagccag gcaagtggca gtgcccctag tgggcagccg ttgccaatgg 2898
atgccttttag gagggtgcc gagagcagtg tggccactc tggcctgggt ttgcatcatt 2958
ctgcagactc taaagacttc cctttttctgc cagactacat tttgtgggga gcctgaggac 3018
tctggattct ttgaggggat cctggatgtg tgtgttcttg ttaaagaggc tgttatcagg 3078
cttaactata accctcaaga tctgcttgac agtgattaaa tccttagctc acatccattc 3138
ccatctttcg ggctccttag gcccaaggat ggcatgtgac tggccctgc aagggtcctt 3198
tctttgtcac cagccaaggc attgataacc aagtagccat tttcctctta aggtttcctc 3258
tacaacccca aggactttca tgattatcct cagggacagg attggaggca ttgagcgtgt 3318
ttattaacaa attgtttttg gtaataaaat aaatgcttgg actcttaaaa aaaaaaaaa 3376

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<210> 268  
 <211> 2780  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(2040)

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<400> 268
atg gac cgc gtg acc aga tac ccc atc ctg ggc atc cct cag gca cac 48
Met Asp Arg Val Thr Arg Tyr Pro Ile Leu Gly Ile Pro Gln Ala His
1 5 10 15

cgt ggc acc ggc ctg gtg ctg gat gga gac acc agc tac aca tac cat 96
Arg Gly Thr Gly Leu Val Leu Asp Gly Asp Thr Ser Tyr Thr Tyr His
20 25 30

ctg gtg tgc atg ggc ccc gag gcc agc ggc tgg ggc cag gat gag ccg 144
Leu Val Cys Met Gly Pro Glu Ala Ser Gly Trp Gly Gln Asp Glu Pro
35 40 45

cag aca tgg ccc act gac cac agg gcc cag cag ggc gtg cag agg cag 192
Gln Thr Trp Pro Thr Asp His Arg Ala Gln Gln Gly Val Gln Arg Gln
50 55 60

ggg gtg tcc tac agc gtg cat gcc tac act ggc cag ccg tcc cca cgg 240
Gly Val Ser Tyr Ser Val His Ala Tyr Thr Gly Gln Pro Ser Pro Arg
65 70 75 80

ggg ctc cac tcg gag aac agg gag gat gag ggt tgg cag gtt tac cgc 288
Gly Leu His Ser Glu Asn Arg Glu Asp Glu Gly Trp Gln Val Tyr Arg
85 90 95

ctg ggc acc agg gat gcc cac cag gga cgt cca aca tgg gca ctc cgc 336
Leu Gly Thr Arg Asp Ala His Gln Gly Arg Pro Thr Trp Ala Leu Arg
100 105 110

cca gag gac ggg gag gac aag gag atg aag acc tac cgc ctg gat gct 384
Pro Glu Asp Gly Glu Asp Lys Glu Met Lys Thr Tyr Arg Leu Asp Ala
115 120 125

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ggg gac gct gac ccc agg agg ctg tgt gac ctg gag cgg gag cgc tgg Gly Asp Ala Asp Pro Arg Arg Leu Cys Asp Leu Glu Arg Glu Arg Trp 130 135 140	432
gcc gtc atc cag ggc cag gca gtc agg aag agc agc acc gtg gcc acg Ala Val Ile Gln Gly Gln Ala Val Arg Lys Ser Ser Thr Val Ala Thr 145 150 155 160	480
ctc cag ggc act cct gac cac gga gac ccc agg acc ccc ggc cca cct Leu Gln Gly Thr Pro Asp His Gly Asp Pro Arg Thr Pro Gly Pro Pro 165 170 175	528
cgg tcc acg ccc ctg gag gag aac gtg gtt gac agg gag cag att gac Arg Ser Thr Pro Leu Glu Glu Asn Val Val Asp Arg Glu Gln Ile Asp 180 185 190	576
ttc ctg gca gcg aga cag cag ttc ctg agt ctg gag cag gcg aac aag Phe Leu Ala Ala Arg Gln Gln Phe Leu Ser Leu Glu Gln Ala Asn Lys 195 200 205	624
ggg gcc cct cat agc tcc ccg gcc agg ggg acc ccc gca ggc aca acc Gly Ala Pro His Ser Ser Pro Ala Arg Gly Thr Pro Ala Gly Thr Thr 210 215 220	672
cca ggg gcc agc cag gcc ccc aag gcc ttc aac aag ccc cac ctg gcc Pro Gly Ala Ser Gln Ala Pro Lys Ala Phe Asn Lys Pro His Leu Ala 225 230 235 240	720
aac ggg cac gtg gtt ccc atc aag ccc cag gtg aag ggg gtg gtc agg Asn Gly His Val Val Pro Ile Lys Pro Gln Val Lys Gly Val Val Arg 245 250 255	768
gaa gag aac aag gtg cgt gct gtg ccc acc tgg gcc agt gtc caa gtt Glu Glu Asn Lys Val Arg Ala Val Pro Thr Trp Ala Ser Val Gln Val 260 265 270	816
gtg gat gac cct ggc tcc ttg gcc tca gtg gag tcc ccg ggg acc ccc Val Asp Asp Pro Gly Ser Leu Ala Ser Val Glu Ser Pro Gly Thr Pro 275 280 285	864
aag gag acg ccc atc gag cgg gag atc cgt ctg gct cag gag cgt gag Lys Glu Thr Pro Ile Glu Arg Glu Ile Arg Leu Ala Gln Glu Arg Glu 290 295 300	912
gca gac ctg cga gag cag agg ggg ctt cgg cag gca acc gac cac cag Ala Asp Leu Arg Glu Gln Arg Gly Leu Arg Gln Ala Thr Asp His Gln 305 310 315 320	960
gag ctg gtg gaa atc ccc acc agg ccg ctg ctg acc aag ctg agc ctg Glu Leu Val Glu Ile Pro Thr Arg Pro Leu Leu Thr Lys Leu Ser Leu 325 330 335	1008
atc aca gcc cca cgg cgg gag aga ggg cgc ccg tcc ctc tac gtg cag Ile Thr Ala Pro Arg Arg Glu Arg Gly Arg Pro Ser Leu Tyr Val Gln 340 345 350	1056
cgg gac ata gta cag gag aca cag cgt gag gaa gac cac cgg cgg gag Arg Asp Ile Val Gln Glu Thr Gln Arg Glu Glu Asp His Arg Arg Glu 355 360 365	1104
ggc ctg cac gtg ggc cgg gcg tcc aca ccc gac tgg gtc tcg gag ggt Gly Leu His Val Gly Arg Ala Ser Thr Pro Asp Trp Val Ser Glu Gly 370 375 380	1152

ccc cag ccc gga ctc cgg aga gcc ctc agc tca gat tcc atc ctc agc Pro Gln Pro Gly Leu Arg Arg Ala Leu Ser Ser Asp Ser Ile Leu Ser 385 390 395 400	1200
ccg gcc cca gat gcc cgt gcg gcc gac cca gct cca gaa gtg agg aag Pro Ala Pro Asp Ala Arg Ala Ala Asp Pro Ala Pro Glu Val Arg Lys 405 410 415	1248
gtg aac cgc atc cca cct gat gcc tac cag ccg tac ctg agc ccc ggg Val Asn Arg Ile Pro Pro Asp Ala Tyr Gln Pro Tyr Leu Ser Pro Gly 420 425 430	1296
acc ccc cag cta gaa ttc tca gcc ttc gga gca ttc ggc aag ccc agc Thr Pro Gln Leu Glu Phe Ser Ala Phe Gly Ala Phe Gly Lys Pro Ser 435 440 445	1344
agt ctc tcc aca gcg gag gcc aag gct gcg act tca cca aag gcc acg Ser Leu Ser Thr Ala Glu Ala Lys Ala Ala Thr Ser Pro Lys Ala Thr 450 455 460	1392
atg tcc ccg agg cat ctc tca gaa tcc tct gga aaa ccc ctg agc aca Met Ser Pro Arg His Leu Ser Glu Ser Ser Gly Lys Pro Leu Ser Thr 465 470 475 480	1440
aag caa gag gca tcg aag ccc cct cgg gga tgc ccg caa gcc aac agg Lys Gln Glu Ala Ser Lys Pro Pro Arg Gly Cys Pro Gln Ala Asn Arg 485 490 495	1488
ggg gtc gtg cgg tgg gag tac ttc cgc ctg cgt cct ctg cgg ttc agg Gly Val Val Arg Trp Glu Tyr Phe Arg Leu Arg Pro Leu Arg Phe Arg 500 505 510	1536
gcc cca gac gag ccc cag cag gcc caa gtc ccc cat gtc tgg ggc tgg Ala Pro Asp Glu Pro Gln Gln Ala Gln Val Pro His Val Trp Gly Trp 515 520 525	1584
gag gtg gct ggg gcc cct gca ctg agg ctg cag aag tcc cag tca tct Glu Val Ala Gly Ala Pro Ala Leu Arg Leu Gln Lys Ser Gln Ser Ser 530 535 540	1632
gat ctg ctg gaa agg gag agg gag agt gtc ctg cgc cgg gag caa gag Asp Leu Leu Glu Arg Glu Arg Glu Ser Val Leu Arg Arg Glu Gln Glu 545 550 555 560	1680
gtg gca gag gag cgg aga aat gct ctc ttc cca gag gtc ttc tcc cca Val Ala Glu Glu Arg Arg Asn Ala Leu Phe Pro Glu Val Phe Ser Pro 565 570 575	1728
acg cca gat gag aac tct gac cag aac tcc agg agc tcc tcc cag gca Thr Pro Asp Glu Asn Ser Asp Gln Asn Ser Arg Ser Ser Ser Gln Ala 580 585 590	1776
tcc ggc atc acg ggc agt tac tcg gtg tct gag tct ccc ttc ttc agc Ser Gly Ile Thr Gly Ser Tyr Ser Val Ser Glu Ser Pro Phe Phe Ser 595 600 605	1824
ccc atc cac cta cac tca aac gtg gcg tgg aca gtg gaa gat cca gtg Pro Ile His Leu His Ser Asn Val Ala Trp Thr Val Glu Asp Pro Val 610 615 620	1872
gac agt gct cct ccc ggg cag aga aag aag gag caa tgg tac gct ggc Asp Ser Ala Pro Pro Gly Gln Arg Lys Lys Glu Gln Trp Tyr Ala Gly 625 630 635 640	1920

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atc aac ccc tcg gac ggt atc aac tca gag gtc ctg gaa gcc ata cgg      1968
Ile Asn Pro Ser Asp Gly Ile Asn Ser Glu Val Leu Glu Ala Ile Arg
      645                      650                      655

gtg acc cgt cac aag aac gcc atg gca gag cgc tgg gaa tcc cgc atc      2016
Val Thr Arg His Lys Asn Ala Met Ala Glu Arg Trp Glu Ser Arg Ile
      660                      665                      670

tac gcc agt gag gag gat gac tga gcctcgggat ggggcgcca cccctgccc      2070
Tyr Ala Ser Glu Glu Asp Asp *
      675                      680

tgccctgacc ctctgtgggaa ctgccaagac catcgccaag cccccaccct aggaaatggg      2130

tcctaggtcc aggatccaag aaccacagct catctgccaa caatcccacc atgggcacat      2190

ttgggactgt tgggtttttc gtttcggttt ctatcttctt ttagaaatgt ttctgccttt      2250

ggggtctaaa gcttttgggg atgaaatggg acccctgctg attctttctg cttctaagac      2310

tttgccaaat gccctgggtc taagaaagaa agagaccgc tcctccactt tcaggtgtaa      2370

tttgcttccg ctagtctgag ggcagagggg ccggtcctaa agggtggcac agatcgcagc      2430

accttgaggg gctgcgggtc tgaggaggga gacactcagc tcctccctct gagaagtccc      2490

aagctgagag gggagacctg cccctttcca accctgggaa accatccagt ctgaggaggg      2550

aggccaaact cccagtgtct ggggtccctg tgcagccctc aaacccttca ccttggtgca      2610

cccagccaca cctggtggac acaaagctct cacatcgata ggatcccatg aggatggtcc      2670

ccttcacctg ggagaaaagt gaccagttt aggagctgga ggggggtctt tgtccccac      2730

cccaaaactg ccttgaaata aacctggagt gagctgccaa aaaaaaaaaa      2780

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<210> 269  
 <211> 600  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (114) .. (536)

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<400> 269
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ttggtaccga gctcggtatcc actagtccag tgtggtggaa ttcggcgttc aag   atg      116
                                   Met
                                   1

tcg aag cga gga cgt ggt ggg tcc tct ggt gcg aaa ttc cgg att tcc      164
Ser Lys Arg Gly Arg Gly Gly Ser Ser Gly Ala Lys Phe Arg Ile Ser
      5                      10                      15

ttg ggt ctt ccg gta gga gct gta atc aat tgt gct gac aac aca gga      212
Leu Gly Leu Pro Val Gly Ala Val Ile Asn Cys Ala Asp Asn Thr Gly
      20                      25                      30

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gcc aaa aac ctg tat atc atc tcc gtg aag ggg atc aag gga cgg ctg      260
Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly Arg Leu
      35              40              45

aac aga ctt ccc gct gct ggt gtg ggt gac atg gtg atg gcc aca gtc      308
Asn Arg Leu Pro Ala Ala Gly Val Gly Asp Met Val Met Ala Thr Val
      50              55              60              65

aag aaa ggc aaa cca gag ctc aga aaa aag gta cat cca gca gtg gtc      356
Lys Lys Gly Lys Pro Glu Leu Arg Lys Lys Val His Pro Ala Val Val
              70              75              80

att cga caa cga aag tca tac cgt aga aaa gat ggc gtg ttt ctt tat      404
Ile Arg Gln Arg Lys Ser Tyr Arg Arg Lys Asp Gly Val Phe Leu Tyr
              85              90              95

ttt gaa gat aat gca gga gtc ata gtg aac aat aaa ggc gag atg aaa      452
Phe Glu Asp Asn Ala Gly Val Ile Val Asn Asn Lys Gly Glu Met Lys
      100              105              110

ggt tct gcc att aca gga cca gta gca aag gag tgt gca gac ttg tgg      500
Gly Ser Ala Ile Thr Gly Pro Val Ala Lys Glu Cys Ala Asp Leu Trp
      115              120              125

ccc cgg att gca tcc aat gct ggc agc att gca tga ttct ccagtatat      550
Pro Arg Ile Ala Ser Asn Ala Gly Ser Ile Ala *
      130              135              140

ttgtaaaaaa taaaaaaaaa ctaaacccat taaaaagtaa aaaaaaaaaa      600

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<210> 270  
 <211> 2203  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (244) .. (1359)

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<400> 270
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ccgaggaggg tgatgaccct gggagtctgg gtcttgctg aggccttccg tccctgaaag      120

acccaggtc tgtctcccat gtcattcacc tcgttgctgt gttttctcag accccagagt      180

cagaaggagt gagaaccctg acccctaata cactgcata cagccaatag gagcccagcc      240

acc  atg gcg gag ctg cag gag gtg cag atc aca gag gag aag cca ctg      288
      Met Ala Glu Leu Gln Glu Val Gln Ile Thr Glu Glu Lys Pro Leu
              1              5              10              15

ttg cca gga cag acg cct gag gcg gcc aag gag gct gag tta gct gcc      336
Leu Pro Gly Gln Thr Pro Glu Ala Ala Lys Glu Ala Glu Leu Ala Ala
              20              25              30

cga atc ctc ctg gac cag gga cag act cac tct gtg gag aca cca tac      384
Arg Ile Leu Leu Asp Gln Gly Gln Thr His Ser Val Glu Thr Pro Tyr
              35              40              45

ggc tct gtc act ttc act gtc tat ggc acc ccc aaa ccc aaa cgc cca      432

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Gly	Ser	Val	Thr	Phe	Thr	Val	Tyr	Gly	Thr	Pro	Lys	Pro	Lys	Arg	Pro	
		50					55					60				
gcg	atc	ctt	acc	tac	cac	gat	gtg	gga	ctc	aac	tat	aaa	tct	tgc	ttc	480
Ala	Ile	Leu	Thr	Tyr	His	Asp	Val	Gly	Leu	Asn	Tyr	Lys	Ser	Cys	Phe	
		65				70					75					
cag	cca	ctg	ttt	cag	ttc	gag	gac	atg	cag	gaa	atc	att	cag	aac	ttt	528
Gln	Pro	Leu	Phe	Gln	Phe	Glu	Asp	Met	Gln	Glu	Ile	Ile	Gln	Asn	Phe	
		80			85					90					95	
gtg	cgg	gtt	cat	gtg	gat	gcc	cct	gga	atg	gaa	gag	gga	gcc	cct	gtg	576
Val	Arg	Val	His	Val	Asp	Ala	Pro	Gly	Met	Glu	Glu	Gly	Ala	Pro	Val	
				100				105					110			
ttc	cct	ttg	gga	tat	cag	tac	cca	tct	ctg	gac	cag	ctt	gca	gac	atg	624
Phe	Pro	Leu	Gly	Tyr	Gln	Tyr	Pro	Ser	Leu	Asp	Gln	Leu	Ala	Asp	Met	
			115					120					125			
atc	cct	tgc	gtc	ctg	cag	tac	cta	aat	ttc	tct	aca	ata	att	gga	gtt	672
Ile	Pro	Cys	Val	Leu	Gln	Tyr	Leu	Asn	Phe	Ser	Thr	Ile	Ile	Gly	Val	
		130					135					140				
ggt	gtt	gga	gct	gga	gcc	tac	atc	ctg	gcg	aga	tat	gct	ctt	aac	cac	720
Gly	Val	Gly	Ala	Gly	Ala	Tyr	Ile	Leu	Ala	Arg	Tyr	Ala	Leu	Asn	His	
		145				150					155					
ccg	gac	act	gtt	gaa	ggt	ctt	gtc	ctc	atc	aac	att	gat	ccc	aat	gcc	768
Pro	Asp	Thr	Val	Glu	Gly	Leu	Val	Leu	Ile	Asn	Ile	Asp	Pro	Asn	Ala	
		160			165					170					175	
aag	ggt	tgg	atg	gat	tgg	gca	gcc	cac	aag	cta	aca	ggc	ctc	acc	tcc	816
Lys	Gly	Trp	Met	Asp	Trp	Ala	Ala	His	Lys	Leu	Thr	Gly	Leu	Thr	Ser	
			180						185					190		
tgc	agt	ccg	gag	atg	atc	ctt	gga	cat	ctt	ttc	agc	cag	gaa	gag	ctc	864
Cys	Ser	Pro	Glu	Met	Ile	Leu	Gly	His	Leu	Phe	Ser	Gln	Glu	Glu	Leu	
			195					200					205			
tct	gga	aat	tct	gag	ttg	ata	caa	aag	tac	aga	aat	atc	att	aca	cat	912
Ser	Gly	Asn	Ser	Glu	Leu	Ile	Gln	Lys	Tyr	Arg	Asn	Ile	Ile	Thr	His	
		210					215					220				
gca	ccc	aac	ctg	gat	aac	att	gaa	ttg	tac	tgg	aac	agc	tac	aac	aac	960
Ala	Pro	Asn	Leu	Asp	Asn	Ile	Glu	Leu	Tyr	Trp	Asn	Ser	Tyr	Asn	Asn	
		225				230					235					
cgc	cga	gac	ctg	aac	ttt	gag	cgt	gga	ggt	gat	atc	acc	ctc	agg	tgt	1008
Arg	Arg	Asp	Leu	Asn	Phe	Glu	Arg	Gly	Gly	Asp	Ile	Thr	Leu	Arg	Cys	
		240			245					250					255	
cct	gtg	atg	ctg	gtg	gta	gga	gac	caa	gca	cct	cat	gaa	gat	gca	gtg	1056
Pro	Val	Met	Leu	Val	Val	Gly	Asp	Gln	Ala	Pro	His	Glu	Asp	Ala	Val	
				260				265						270		
gtg	gaa	tgt	aac	tca	aaa	ctg	gac	ccc	acc	cag	acc	tcg	ttc	ctc	aag	1104
Val	Glu	Cys	Asn	Ser	Lys	Leu	Asp	Pro	Thr	Gln	Thr	Ser	Phe	Leu	Lys	
			275					280					285			
atg	gct	gac	tcc	gga	ggt	cag	ccc	cag	ctg	act	cag	cca	ggc	aag	ctg	1152
Met	Ala	Asp	Ser	Gly	Gly	Gln	Pro	Gln	Leu	Thr	Gln	Pro	Gly	Lys	Leu	
		290					295					300				
acc	gag	gcc	ttc	aag	tac	ttc	ctg	caa	ggc	atg	ggc	tac	atg	gcc	tca	1200

Thr	Glu	Ala	Phe	Lys	Tyr	Phe	Leu	Gln	Gly	Met	Gly	Tyr	Met	Ala	Ser		
305						310					315						
tcc	tgc	atg	act	cgg	ctg	tcc	cgg	tct	cgt	aca	gcc	tct	ctg	acc	agt	1248	
Ser	Cys	Met	Thr	Arg	Leu	Ser	Arg	Ser	Arg	Thr	Ala	Ser	Leu	Thr	Ser		
320					325				330					335			
gca	gaa	tcc	gtt	gat	ggg	aac	cgg	tcc	cgc	tct	cgc	acc	ctg	tcc	cag	1296	
Ala	Glu	Ser	Val	Asp	Gly	Asn	Arg	Ser	Arg	Ser	Arg	Thr	Leu	Ser	Gln		
				340				345					350				
agc	aga	gag	tct	gga	act	ctt	tct	tcg	ggg	ccc	ccg	ggg	cac	acc	atg	1344	
Ser	Arg	Glu	Ser	Gly	Thr	Leu	Ser	Ser	Gly	Pro	Pro	Gly	His	Thr	Met		
			355				360					365					
gag	gtc	tcc	tgt	tga	atggcccttg	ttgccctaga	gtgggaccca	gccctcacct								1399	
Glu	Val	Ser	Cys	*													
			370														
ccccagagc	taacctggga	ggtgctgaag	gggcattggg	ccaccgtaag	caaggga	aaaa										1459	
agggcagatc	atgcggggag	atgacctga	tctttgattg	ctaccctaac	cttgaccttt											1519	
aacctgtgat	tccccccagc	tcttggaaga	gatgtcctaa	tatctcttag	ggacctcagac											1579	
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agaaacatcc	agtgtaaaaa	ggaagttgga	atgggagttg	gcgggcagtg	aacgagtgtg											1939	
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tggtagctca	gtgtgcatct	agagtgggac	tggggagggga	gctaagcttg	ggctgggctg											2059	
cttggggctt	ggcatagggg	ggaaagggct	accctggggc	tctgaccaca	ctgtagtatg											2119	
tgtggagggt	gccctcccg	ctccacaac	ttctgctata	acaataaact	gtagaggaat											2179	
ctgagtaccg	ttaaaaaaaa	aaaa														2203	

&lt;210&gt; 271

&lt;211&gt; 2622

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (255) .. (1817)

&lt;400&gt; 271

gtcagcctca	cgcgccggga	aggaaccggg	ccgaggcccc	gggctgccgg	cgcgccggcc	60	
cggcacgtcc	acaggctggg	tcgcgaggtg	gcgatcgctg	agaggcagga	gggccgaggc	120	



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gggcctggga ggcggcccg aggtggggcg ccgctggggc cggcccgcac gggcttcac 180
tgagggcgca cggcccgca ccgagcgtgc ggactggcct cccaagcgtg gggcgacaag 240
ctgccggagc tgca atg ggc cgc ggc tgg gga ttc ttg ttt ggc ctc ctg 290
      Met Gly Arg Gly Trp Gly Phe Leu Phe Gly Leu Leu
        1             5             10

ggc gcc gtg tgg ctg ctc agc tcg ggc cac gga gag gag cag ccc ccg 338
Gly Ala Val Trp Leu Leu Ser Ser Gly His Gly Glu Glu Gln Pro Pro
      15             20             25

gag aca gcg gca cag agg tgc ttc tgc cag gtt agt ggt tac ttg gat 386
Glu Thr Ala Ala Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp
      30             35             40

gat tgt acc tgt gat gtt gaa acc att gat aga ttt aat aac tac agg 434
Asp Cys Thr Cys Asp Val Glu Thr Ile Asp Arg Phe Asn Asn Tyr Arg
      45             50             55             60

ctt ttc cca aga cta caa aaa ctt ctt gaa agt gac tac ttt agg tat 482
Leu Phe Pro Arg Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg Tyr
      65             70             75

tac aag gta aac ctg aag agg ccg tgt cct ttc tgg aat gac atc agc 530
Tyr Lys Val Asn Leu Lys Arg Pro Cys Pro Phe Trp Asn Asp Ile Ser
      80             85             90

cag tgt gga aga agg gac tgt gct gtc aaa cca tgt caa tct gat gaa 578
Gln Cys Gly Arg Arg Asp Cys Ala Val Lys Pro Cys Gln Ser Asp Glu
      95             100             105

gtt cct gat gga att aaa tct gcg agc tac aag tat tct gaa gaa gcc 626
Val Pro Asp Gly Ile Lys Ser Ala Ser Tyr Lys Tyr Ser Glu Glu Ala
      110             115             120

aat aat ctc att gaa gaa tgt gaa caa gct gaa cga ctt gga gca gtg 674
Asn Asn Leu Ile Glu Glu Cys Glu Gln Ala Glu Arg Leu Gly Ala Val
      125             130             135             140

gat gaa tct ctg agt gag gaa aca cag aag gct gtt ctt cag tgg acc 722
Asp Glu Ser Leu Ser Glu Glu Thr Gln Lys Ala Val Leu Gln Trp Thr
      145             150             155

aag cat gat gat tct tca gat gga att aaa tct gcg agc tac aag tat 770
Lys His Asp Asp Ser Ser Asp Gly Ile Lys Ser Ala Ser Tyr Lys Tyr
      160             165             170

tct gaa gaa gcc aat aat ctc att gaa gaa tgt gaa caa gct gaa cga 818
Ser Glu Glu Ala Asn Asn Leu Ile Glu Glu Cys Glu Gln Ala Glu Arg
      175             180             185

ctt gga gca gtg gat gaa tct ctg agt gag gaa aca cag aag gct gtt 866
Leu Gly Ala Val Asp Glu Ser Leu Ser Glu Glu Thr Gln Lys Ala Val
      190             195             200

ctt cag tgg acc aag cat gat gat tct tca gat aac ttc tgt gaa gct 914
Leu Gln Trp Thr Lys His Asp Asp Ser Ser Asp Asn Phe Cys Glu Ala
      205             210             215             220

gat gac att cag tcc cct gaa gct gaa tat gta gat ttg ctt ctt aat 962
Asp Asp Ile Gln Ser Pro Glu Ala Glu Tyr Val Asp Leu Leu Leu Asn
      225             230             235

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cct gag cgc tac act ggt tac aag gga cca gat gct tgg aaa ata tgg	1010
Pro Glu Arg Tyr Thr Gly Tyr Lys Gly Pro Asp Ala Trp Lys Ile Trp	
240 245 250	
aat gtc atc tac gaa gaa aac tgt ttt aag cca cag aca att aaa aga	1058
Asn Val Ile Tyr Glu Glu Asn Cys Phe Lys Pro Gln Thr Ile Lys Arg	
255 260 265	
cct tta aat cct ttg gct tct ggt caa ggg aca agt gaa gag aac act	1106
Pro Leu Asn Pro Leu Ala Ser Gly Gln Gly Thr Ser Glu Glu Asn Thr	
270 275 280	
ttt tac agt tgg cta gaa ggt ctc tgt gta gaa aaa aga gca ttc tac	1154
Phe Tyr Ser Trp Leu Glu Gly Leu Cys Val Glu Lys Arg Ala Phe Tyr	
285 290 295 300	
aga ctt ata tct ggc cta cat gca agc att aat gtg cat ttg agt gca	1202
Arg Leu Ile Ser Gly Leu His Ala Ser Ile Asn Val His Leu Ser Ala	
305 310 315	
aga tat ctt tta caa gag acc tgg tta gaa aag aaa tgg gga cac aac	1250
Arg Tyr Leu Leu Gln Glu Thr Trp Leu Glu Lys Lys Trp Gly His Asn	
320 325 330	
att aca gaa ttt caa cag cga ttt gat gga att ttg act gaa gga gaa	1298
Ile Thr Glu Phe Gln Gln Arg Phe Asp Gly Ile Leu Thr Glu Gly Glu	
335 340 345	
ggt cca aga agg ctt aag aac ttg tat ttt ctc tac tta ata gaa cta	1346
Gly Pro Arg Arg Leu Lys Asn Leu Tyr Phe Leu Tyr Leu Ile Glu Leu	
350 355 360	
agg gct tta tcc aaa gtg tta cca ttc ttc gag cgc cca gat ttt caa	1394
Arg Ala Leu Ser Lys Val Leu Pro Phe Phe Glu Arg Pro Asp Phe Gln	
365 370 375 380	
ctc ttt act gga aat aaa att cag gat gag gaa aac aaa atg tta ctt	1442
Leu Phe Thr Gly Asn Lys Ile Gln Asp Glu Glu Asn Lys Met Leu Leu	
385 390 395	
ctg gaa ata ctt cat gaa atc aag tca ttt cct ttg cat ttt gat gag	1490
Leu Glu Ile Leu His Glu Ile Lys Ser Phe Pro Leu His Phe Asp Glu	
400 405 410	
aat tca ttt ttt gct ggg gat aaa aaa gaa gca cac aaa cta aag gag	1538
Asn Ser Phe Phe Ala Gly Asp Lys Lys Glu Ala His Lys Leu Lys Glu	
415 420 425	
gac ttt cga ctg cat ttt aga aat att tca aga att atg gat tgt gtt	1586
Asp Phe Arg Leu His Phe Arg Asn Ile Ser Arg Ile Met Asp Cys Val	
430 435 440	
ggt tgt ttt aaa tgt cgt ctg tgg gga aag ctt cag act cag ggt ttg	1634
Gly Cys Phe Lys Cys Arg Leu Trp Gly Lys Leu Gln Thr Gln Gly Leu	
445 450 455 460	
ggc act gct ctg aag atc tta ttt tct gag aaa ttg ata gca aat atg	1682
Gly Thr Ala Leu Lys Ile Leu Phe Ser Glu Lys Leu Ile Ala Asn Met	
465 470 475	
cca gaa agt gga cct agt tat gaa ttc cat cta acc aga caa gaa ata	1730
Pro Glu Ser Gly Pro Ser Tyr Glu Phe His Leu Thr Arg Gln Glu Ile	
480 485 490	

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gta tca tta ttc aac gca ttt gga aga att tct aca agt gtg aaa gaa      1778
Val Ser Leu Phe Asn Ala Phe Gly Arg Ile Ser Thr Ser Val Lys Glu
      495                      500                      505

tta gaa aac ttc agg aac ttg tta cag aat att cat taa agaaaacaag      1827
Leu Glu Asn Phe Arg Asn Leu Leu Gln Asn Ile His *
      510                      515                      520

ctgatatgtg cctgtttctg gacaatggag gcgaaagagt ggaatttcat tcaaaggcat      1887

aatagcaatg acagtcttaa gccaaacatt ttatataaag ttgcttttgt aaaggagaat      1947

tatattgttt taagtaaaca catttttaaa aattgtgtta agtctatgta taatactact      2007

gtgagtaaaa gtaatacttt aataatgtgg tacaaathtt aaagtttaat attgaataaa      2067

aggaggatta tcaaattcat atatgataaa agtgaatggt ctaagtctct caaactagcg      2127

ttttatgtaa taatatgtaa tataaataaa actatggtaa atgtgacaag catttaatag      2187

gaaaatgcta aggaggcctc ataaatgacc cataattacc aacgtagaat ttttcagtac      2247

atthaggggtt gctggattta gcaaataaaa ataaagattg cccagttaga tttgaatttc      2307

agataaacia ttagtthttt aatattttac atggaatatt tggaaaatac ttatactaaa      2367

aaattatttg tttgaaattc aaatttaact gggagtcttg tattttatct ggcaatccta      2427

aaatacattg gtatgaaaca aatcactttt agaagtatat tgctattttg attgggttgt      2487

ttttgtgtgt agaaacgtac aataacaact caaaggcaca ggagatttct aaacattgtg      2547

aaaagttgaa tagattatat atttattctc ataatacttt cactaatact aaataaaatt      2607

tggggaacac tttttt                                                    2622

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<210> 272
<211> 1461
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (179)..(802)

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<220>
<221> misc_feature
<222> (1)...(1461)
<223> n = a,t,c or g

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<400> 272
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cagcccttcc ccctccggct cccgcaccgc cggccgcctc ccctcgccct cctactctcc      120

cctccctgct ccttcgcttt ttctctctcc tctctcccg gccccggctg ccagcacc      178
atg tcc gca ggg gga gat ttt ggg aat cca ctg aga aaa ttc aag ttg      226
Met Ser Ala Gly Gly Asp Phe Gly Asn Pro Leu Arg Lys Phe Lys Leu
      1           5           10           15

gtg ttc ttg ggg gag cag agc gtc ggg aag acg tct ctg att acg agg      274

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Val	Phe	Leu	Gly	Glu	Gln	Ser	Val	Gly	Lys	Thr	Ser	Leu	Ile	Thr	Arg	
			20					25					30			
ttc	atg	tac	gac	agc	ttc	gac	aac	aca	tac	cag	gca	acc	att	ggg	att	322
Phe	Met	Tyr	Asp	Ser	Phe	Asp	Asn	Thr	Tyr	Gln	Ala	Thr	Ile	Gly	Ile	
		35					40					45				
gac	ttc	ttg	tca	aaa	acc	atg	tac	ttg	gag	gac	cgc	acg	gtg	cga	ctg	370
Asp	Phe	Leu	Ser	Lys	Thr	Met	Tyr	Leu	Glu	Asp	Arg	Thr	Val	Arg	Leu	
		50					55				60					
cag	ctc	tgg	gac	aca	gct	ggc	cag	gag	agg	ttc	cgc	agc	ctg	atc	ccc	418
Gln	Leu	Trp	Asp	Thr	Ala	Gly	Gln	Glu	Arg	Phe	Arg	Ser	Leu	Ile	Pro	
		65				70				75					80	
agc	tac	atc	cgg	gac	tcc	acg	gtg	gct	gtg	gtg	gtg	tac	gac	atc	aca	466
Ser	Tyr	Ile	Arg	Asp	Ser	Thr	Val	Ala	Val	Val	Val	Tyr	Asp	Ile	Thr	
				85					90					95		
aat	ctc	aac	tcc	ttc	caa	cag	acc	tct	aag	tgg	atc	gac	gac	gtc	agg	514
Asn	Leu	Asn	Ser	Phe	Gln	Gln	Thr	Ser	Lys	Trp	Ile	Asp	Asp	Val	Arg	
			100					105						110		
aca	gag	agg	ggc	agt	gat	gtt	atc	atc	atg	ctg	gtg	ggc	aac	aag	acg	562
Thr	Glu	Arg	Gly	Ser	Asp	Val	Ile	Ile	Met	Leu	Val	Gly	Asn	Lys	Thr	
			115				120					125				
gac	ctg	gct	gat	aag	agg	cag	ata	acc	atc	gag	gag	ggg	gag	cag	cgc	610
Asp	Leu	Ala	Asp	Lys	Arg	Gln	Ile	Thr	Ile	Glu	Glu	Gly	Glu	Gln	Arg	
			130			135						140				
gcc	aaa	gaa	ctg	agc	gtc	atg	ttc	att	gag	acc	agt	gcg	aag	act	ggc	658
Ala	Lys	Glu	Leu	Ser	Val	Met	Phe	Ile	Glu	Thr	Ser	Ala	Lys	Thr	Gly	
			145			150				155					160	
tac	aac	gtg	aag	cag	ctt	ttt	cga	cgt	gtg	gcg	tcg	gct	cta	ccc	gga	706
Tyr	Asn	Val	Lys	Gln	Leu	Phe	Arg	Arg	Val	Ala	Ser	Ala	Leu	Pro	Gly	
				165					170					175		
atg	gag	aat	gtc	cag	gag	aaa	agc	aaa	gaa	ggg	atg	att	gac	atc	aag	754
Met	Glu	Asn	Val	Gln	Glu	Lys	Ser	Lys	Glu	Gly	Met	Ile	Asp	Ile	Lys	
				180				185					190			
ctg	gac	aaa	ccc	cag	gag	ccc	ccg	gcc	agc	gag	ggc	ggc	tgc	tcc	tgc	802
Leu	Asp	Lys	Pro	Gln	Glu	Pro	Pro	Ala	Ser	Glu	Gly	Gly	Cys	Ser	Cys	
			195				200					205				
taatgcagag	ccgacctgtg	gcttcccatg	acactccttg	cttggtgtgt	tgcttcctat											862
tggttagctt	cctaaggagg	gaggaaccg	agttatcaag	atgggaggat	ttttcttttc											922
tctctgtctt	taggagtagg	gtgggatggg	gagggaggct	gggcatcagg	gatcacatca											982
ctcttaacgg	ctgttactta	aacaactatt	ttttggtttg	gttgtaatat	attgtacttt											1042
attaagattg	ccaaaaactg	ttaaaattta	aaaaaaattt	aatcatgtg	tatacaattt											1102
tttgccagat	aaaaatgtag	tcatttttat	ttgaaagatg	tgctttttgt	ttttgtatat											1162
ttgtaaaactt	atagagaacc	ttttccacac	acctcctcct	tcctgttctc	tttgaaccat											1222
tcatcacctc	tgcttctctc	ctatccccag	cccaataaat	taaaacaatt	aactgagcaa											1282
attaattagg	gcttcagtct	ggggggccat	ctggcncccc	ttcttctagg	ggcccctact											1342

ccagttttaa tcaaacattg ggttgaaca catcagcctc tggaaagggg aggctctgga 1402  
 cttcttgtct ttccatggcc agagtgggct gtcaacctcg tgtggagctg agaccaagg 1461

<210> 273  
 <211> 5910  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (194) .. (5365)

<400> 273  
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 ttttggacct tttttcattt ccatttctac cttgtatgcc tcaatttgct ggatttaagc 180  
 actgctgcac ttt atg aga gag aag gag caa gaa agg gaa gaa cag tta 229  
 Met Arg Glu Lys Glu Gln Glu Arg Glu Glu Gln Leu  
 1 5 10  
 atg gaa gac aag aaa agg aag aaa gag gat aaa aag aaa aaa gaa gcc 277  
 Met Glu Asp Lys Lys Arg Lys Lys Glu Asp Lys Lys Lys Lys Glu Ala  
 15 20 25  
 act cag aag gtc acg gaa caa aaa acc aaa gtg ccc gaa gtg acg aaa 325  
 Thr Gln Lys Val Thr Glu Gln Lys Thr Lys Val Pro Glu Val Thr Lys  
 30 35 40  
 cca agt tta agc caa cca acg gcc gcc agc cca att ggc agc tct cca 373  
 Pro Ser Leu Ser Gln Pro Thr Ala Ala Ser Pro Ile Gly Ser Ser Pro  
 45 50 55 60  
 tcg cca cca gtc aat ggt ggc aac aat gcc aaa agg gtg gca gtg ccg 421  
 Ser Pro Pro Val Asn Gly Gly Asn Asn Ala Lys Arg Val Ala Val Pro  
 65 70 75  
 aac gga caa ccg cca agc gcc gcc cgc tac atg cct cgg gag gtg ccg 469  
 Asn Gly Gln Pro Pro Ser Ala Ala Arg Tyr Met Pro Arg Glu Val Pro  
 80 85 90  
 ccg cga ttc cgt tgc cag cag gac cac aaa gtg tta cta aaa cgt ggg 517  
 Pro Arg Phe Arg Cys Gln Gln Asp His Lys Val Leu Leu Lys Arg Gly  
 95 100 105  
 cag ccc oct cca ccg tcc tgc atg ctc ctt ggg ggt ggg gca ggg cct 565  
 Gln Pro Pro Pro Pro Ser Cys Met Leu Leu Gly Gly Gly Ala Gly Pro  
 110 115 120  
 cct ccc tgc aca gca cct gga gca aac cca aac aac gca caa gtg aca 613  
 Pro Pro Cys Thr Ala Pro Gly Ala Asn Pro Asn Asn Ala Gln Val Thr  
 125 130 135 140  
 gga gcg ctg ctg cag agt gag agt ggg act gcg cca gac tca acc ctt 661  
 Gly Ala Leu Leu Gln Ser Glu Ser Gly Thr Ala Pro Asp Ser Thr Leu  
 145 150 155

gga ggt gct gct gct tca aat tat gca aat tcc act tgg ggc tcg gga	709
Gly Gly Ala Ala Ala Ser Asn Tyr Ala Asn Ser Thr Trp Gly Ser Gly	
160 165 170	
gcc tcc tcc aac aac ggc acc tcc ccc aac cca att cac atc tgg gac	757
Ala Ser Ser Asn Asn Gly Thr Ser Pro Asn Pro Ile His Ile Trp Asp	
175 180 185	
aag gtg att gta gac ggg tct gac atg gaa gag tgg cct tgt att gcc	805
Lys Val Ile Val Asp Gly Ser Asp Met Glu Glu Trp Pro Cys Ile Ala	
190 195 200	
agc aaa gac act gaa tct tct tcc gaa aac acc acc gat aac aac agt	853
Ser Lys Asp Thr Glu Ser Ser Ser Glu Asn Thr Thr Asp Asn Asn Ser	
205 210 215 220	
gcc tcg aac cct ggc tct gag aag agc act ctg cca gga agc acc act	901
Ala Ser Asn Pro Gly Ser Glu Lys Ser Thr Leu Pro Gly Ser Thr Thr	
225 230 235	
agt aac aaa gga aaa ggg agc cag tgc cag tct gca agt tct ggg aac	949
Ser Asn Lys Gly Lys Gly Ser Gln Cys Gln Ser Ala Ser Ser Gly Asn	
240 245 250	
gaa tgt aat ctt ggg gtc tgg aaa tct gac cct aag gct aaa tct gtt	997
Glu Cys Asn Leu Gly Val Trp Lys Ser Asp Pro Lys Ala Lys Ser Val	
255 260 265	
caa tct tcc aac tct act aca gag aac aac aat gga cta gga aat tgg	1045
Gln Ser Ser Asn Ser Thr Thr Glu Asn Asn Asn Gly Leu Gly Asn Trp	
270 275 280	
agg aat gtg agt ggt cag gat aga att gga cct ggc tct ggc ttc agc	1093
Arg Asn Val Ser Gly Gln Asp Arg Ile Gly Pro Gly Ser Gly Phe Ser	
285 290 295 300	
aac ttt aac cca aat agc aac cca tct gcc tgg cca gca ctg gtc caa	1141
Asn Phe Asn Pro Asn Ser Asn Pro Ser Ala Trp Pro Ala Leu Val Gln	
305 310 315	
gaa gga act tct agg aaa ggg gca ttg gaa aca gat aat agt aat tcc	1189
Glu Gly Thr Ser Arg Lys Gly Ala Leu Glu Thr Asp Asn Ser Asn Ser	
320 325 330	
agt gca cag gtt agc aca gta ggt cag aca tcc agg gaa cag cag tca	1237
Ser Ala Gln Val Ser Thr Val Gly Gln Thr Ser Arg Glu Gln Gln Ser	
335 340 345	
aag atg gaa aat gcg ggt gtt aat ttt gtt gtc tct ggc aga gaa cag	1285
Lys Met Glu Asn Ala Gly Val Asn Phe Val Val Ser Gly Arg Glu Gln	
350 355 360	
gct caa att cat aac act gat gga cca aaa aat gga aac act aac tcc	1333
Ala Gln Ile His Asn Thr Asp Gly Pro Lys Asn Gly Asn Thr Asn Ser	
365 370 375 380	
ttg aac tta agt tca cca aac ccc atg gag aat aag gga atg ccc ttt	1381
Leu Asn Leu Ser Ser Pro Asn Pro Met Glu Asn Lys Gly Met Pro Phe	
385 390 395	
gga atg ggc ttg ggg aac acc tcc agg agc act gat gcc cct tca caa	1429
Gly Met Gly Leu Gly Asn Thr Ser Arg Ser Thr Asp Ala Pro Ser Gln	
400 405 410	

agc act gga gat cga aag act ggg agt gtt gga tct tgg ggt gca gct	1477
Ser Thr Gly Asp Arg Lys Thr Gly Ser Val Gly Ser Trp Gly Ala Ala	
415 420 425	
agg ggg cct tct gga act gac aca gtc tct gga caa agc aat tct gga	1525
Arg Gly Pro Ser Gly Thr Asp Thr Val Ser Gly Gln Ser Asn Ser Gly	
430 435 440	
aac aat ggg aac aat gga aaa gag aga gag gac tcc tgg aaa gga gct	1573
Asn Asn Gly Asn Asn Gly Lys Glu Arg Glu Asp Ser Trp Lys Gly Ala	
445 450 455 460	
tct gtt cag aaa tca act ggg tca aaa aat gac tct tgg gac aac aat	1621
Ser Val Gln Lys Ser Thr Gly Ser Lys Asn Asp Ser Trp Asp Asn Asn	
465 470 475	
aac agg tct acg ggt ggg tcc tgg aac ttt ggc ccc cag gac tct aat	1669
Asn Arg Ser Thr Gly Gly Ser Trp Asn Phe Gly Pro Gln Asp Ser Asn	
480 485 490	
gac aac aaa tgg ggt gaa ggg aac aaa atg aca tct ggg gtc tct cag	1717
Asp Asn Lys Trp Gly Glu Gly Asn Lys Met Thr Ser Gly Val Ser Gln	
495 500 505	
gga gaa tgg aaa cag ccg act ggg tct gat gag ttg aaa att gga gaa	1765
Gly Glu Trp Lys Gln Pro Thr Gly Ser Asp Glu Leu Lys Ile Gly Glu	
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 Met Lys Trp  
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gtg tgg gcg ctc ttg ctg ttg gcg gcg ctg ggc agc ggc cgc gcg gag      165
Val Trp Ala Leu Leu Leu Leu Ala Ala Leu Gly Ser Gly Arg Ala Glu
      5                      10                      15

cgc gac tgc cga gtg agc agc ttc cga gtc aag gag aac ttc gac aag      213
Arg Asp Cys Arg Val Ser Ser Phe Arg Val Lys Glu Asn Phe Asp Lys
      20                      25                      30                      35

gct cgc ttc tct ggg acc tgg tac gcc atg gcc aag aag gac ccc gag      261
Ala Arg Phe Ser Gly Thr Trp Tyr Ala Met Ala Lys Lys Asp Pro Glu
                        40                      45                      50

ggc ctc ttt ctg cag gac aac atc gtc gcg gag ttc tcc gtg gac gag      309
Gly Leu Phe Leu Gln Asp Asn Ile Val Ala Glu Phe Ser Val Asp Glu
                        55                      60                      65

acc ggc cag atg agc gcc aca gcc aag ggc cga gtc cgt ctt ttg aat      357
Thr Gly Gln Met Ser Ala Thr Ala Lys Gly Arg Val Arg Leu Leu Asn
      70                      75                      80

aac tgg gac gtg tgc gca gac atg gtg ggc acc ttc aca gac acc gag      405
Asn Trp Asp Val Cys Ala Asp Met Val Gly Thr Phe Thr Asp Thr Glu
      85                      90                      95

gac cct gcc aag ttc aag atg aag tac tgg ggc gta gcc tcc ttt ctc      453
Asp Pro Ala Lys Phe Lys Met Lys Tyr Trp Gly Val Ala Ser Phe Leu
      100                      105                      110                      115

cag aaa gga aat gat gac cac tgg atc gtc gac aca gac tac gac acg      501
Gln Lys Gly Asn Asp Asp His Trp Ile Val Asp Thr Asp Tyr Asp Thr
                        120                      125                      130

tat gcc gtg cag tac tcc tgc cgc ctc ctg aac ctc gat ggc acc tgt      549
Tyr Ala Val Gln Tyr Ser Cys Arg Leu Leu Asn Leu Asp Gly Thr Cys
                        135                      140                      145

gct gac agc tac tcc ttc gtg ttt tcc cgg gac ccc aac ggc ctg ccc      597
Ala Asp Ser Tyr Ser Phe Val Phe Ser Arg Asp Pro Asn Gly Leu Pro
      150                      155                      160

cca gaa gcg cag aag att gta agg cag cgg cag gag gag ctg tgc ctg      645
Pro Glu Ala Gln Lys Ile Val Arg Gln Arg Gln Glu Glu Leu Cys Leu
      165                      170                      175

gcc agg cag tac agg ctg atc gtc cac aac ggt tac tgc gat ggc aga      693
Ala Arg Gln Tyr Arg Leu Ile Val His Asn Gly Tyr Cys Asp Gly Arg
      180                      185                      190                      195

tca gaa aga aac ctt ttg tag ca atatcaagaa tctagtttca tctgagaact      746
Ser Glu Arg Asn Leu Leu *
                        200

tctgattagc tctcagtcctt cagctctatt tatcttagga gtttaatttg cccttctctc      806

cccatcttcc ctcagttccc ataaaacctt cattacacat aaagatacac gtgggggtca      866

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taaactatag tcacccgtga aaaaaaaaaa      955

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 <213> Homo sapiens

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 <222> (463)..(1107)

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 gctagagaca gggagagcag agtaaaaccc tcaggctgct gaaatttcta ggctgttagg 180  
 aagcccctcg aattctgtga aaatgagggg ttcttaactc aactgagag cggaaggagg 240  
 cagacccttt tcataactcc ctcaagtgtg tgttaccttt ctttaccagc atggtaaaga 300  
 acaggacata tcccagcctc ggacatgtct gtatgatcca aggtacccaa agtcagacag 360  
 agtaaaactca agcctggcac tggctttctg ccgcttcattg tgctttggaa aaagcaggag 420  
 aagcaatagc agcaggagtc cccagcagct ggagccgcaa ga atg aac tgc aaa 474  
 Met Asn Cys Lys  
 1  
 gag gga act gac agc agc tgc ggc tgc agg ggc aac gac gag aag aag 522  
 Glu Gly Thr Asp Ser Ser Cys Gly Cys Arg Gly Asn Asp Glu Lys Lys  
 5 10 15 20  
 atg ttg aag tgt gtg gtg gtg ggg gac ggt gcc gtg ggg aaa acc tgc 570  
 Met Leu Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys  
 25 30 35  
 ctg ctg atg agc tac gcc aac gac gcc ttc cca gag gaa tac gtg ccc 618  
 Leu Leu Met Ser Tyr Ala Asn Asp Ala Phe Pro Glu Glu Tyr Val Pro  
 40 45 50  
 act gtg ttt gac cac tat gca gtt act gtg act gtg gga ggc aag caa 666  
 Thr Val Phe Asp His Tyr Ala Val Thr Val Thr Val Gly Gly Lys Gln  
 55 60 65  
 cac ttg ctc gga ctg tat gac acc gcg gga cag gag gac tac aac cag 714  
 His Leu Leu Gly Leu Tyr Asp Thr Ala Gly Gln Glu Asp Tyr Asn Gln  
 70 75 80  
 ctg agg cca ctc tcc tac ccc aac acg gat gtg ttt ttg atc tgc ttc 762  
 Leu Arg Pro Leu Ser Tyr Pro Asn Thr Asp Val Phe Leu Ile Cys Phe  
 85 90 95 100  
 tct gtc gta aac cct gcc tct tac cac aat gtc cag gag gaa tgg gtc 810  
 Ser Val Val Asn Pro Ala Ser Tyr His Asn Val Gln Glu Glu Trp Val  
 105 110 115  
 ccc gag ctc aag gac tgc atg cct cac gtg cct tat gtc ctc ata ggg 858  
 Pro Glu Leu Lys Asp Cys Met Pro His Val Pro Tyr Val Leu Ile Gly  
 120 125 130  
 acc cag att gat ctc cgt gat gac cca aaa acc ttg gcc cgt ttg ctg 906  
 Thr Gln Ile Asp Leu Arg Asp Asp Pro Lys Thr Leu Ala Arg Leu Leu  
 135 140 145  
 tat atg aaa gag aaa cct ctc act tac gag cat ggt gtg aag ctc gca 954



Tyr Met Lys Glu Lys Pro Leu Thr Tyr Glu His Gly Val Lys Leu Ala	
150 155 160	
aaa gcg atc gga gca cag tgc tac ttg gaa tgt tca gct ctg act cag	1002
Lys Ala Ile Gly Ala Gln Cys Tyr Leu Glu Cys Ser Ala Leu Thr Gln	
165 170 175 180	
aaa ggt ctc aaa gcg gtt ttt gat gaa gca atc ctc acc att ttc cac	1050
Lys Gly Leu Lys Ala Val Phe Asp Glu Ala Ile Leu Thr Ile Phe His	
185 190 195	
ccc aag aaa aag aag aaa cgc tgt tct gag ggt cac agc tgc tgt tca	1098
Pro Lys Lys Lys Lys Lys Arg Cys Ser Glu Gly His Ser Cys Cys Ser	
200 205 210	
att atc tga ggttgctc tgggacctgc ctccacccca tccagggatg agaatggcag	1154
Ile Ile *	
215	
ccaatctctg tggccaagct ccagccaaaa aggagggcac gaccagaaag gaactccctt	1214
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&lt;222&gt; (95) .. (766)

&lt;400&gt; 277

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                                         Met Gln Leu Lys Pro Met
                                         1           5

gag atc aac ccc gag atg ctg aac aaa gtg ctg tcc cgg ctg ggg gtc      160
Glu Ile Asn Pro Glu Met Leu Asn Lys Val Leu Ser Arg Leu Gly Val
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gcc ggc cag tgg cgc ttc gtg gac gtg ctg ggg ctg gaa gag gag tct      208
Ala Gly Gln Trp Arg Phe Val Asp Val Leu Gly Leu Glu Glu Glu Ser
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ctg ggc tcg gtg cca gcg cct gcc tgc gcg ctg ctg ctg ctg ttt ccc      256
Leu Gly Ser Val Pro Ala Pro Ala Cys Ala Leu Leu Leu Leu Phe Pro
                        40           45           50

ctc acg gcc cag cat gag aac ttc agg aaa aag cag att gaa gag ctg      304
Leu Thr Ala Gln His Glu Asn Phe Arg Lys Lys Gln Ile Glu Glu Leu
                        55           60           65           70

aag gga caa gaa gtt agt cct aaa gtg tac ttc atg aag cag acc att      352
Lys Gly Gln Glu Val Ser Pro Lys Val Tyr Phe Met Lys Gln Thr Ile
                        75           80           85

ggg aat tcc tgt ggc aca atc gga ctt att cac gca gtg gcc aat aat      400
Gly Asn Ser Cys Gly Thr Ile Gly Leu Ile His Ala Val Ala Asn Asn
                        90           95           100

caa gac aaa ctg gga ttt gag gat gga tca gtt ctg aaa cag ttt ctt      448
Gln Asp Lys Leu Gly Phe Glu Asp Gly Ser Val Leu Lys Gln Phe Leu
                        105           110           115

tct gaa aca gag aaa atg tcc cct gaa gcc aga gca aaa tgc ttt gaa      496
Ser Glu Thr Glu Lys Met Ser Pro Glu Ala Arg Ala Lys Cys Phe Glu
                        120           125           130

aag aat gag gcc ata cag gca gcc cat gat gcc gtg gca cag gaa ggc      544
Lys Asn Glu Ala Ile Gln Ala Ala His Asp Ala Val Ala Gln Glu Gly
                        135           140           145           150

caa tgt cgg gta gat gac aag gtg aat ttc cat ttt att ctg ttt aac      592
Gln Cys Arg Val Asp Asp Lys Val Asn Phe His Phe Ile Leu Phe Asn
                        155           160           165

aac gtg gat ggc cac ctc tat gaa ctt gat gga cga atg cct ttt ccg      640
Asn Val Asp Gly His Leu Tyr Glu Leu Asp Gly Arg Met Pro Phe Pro
                        170           175           180

gtg aac cat ggc gcc agt tca gag gac acc ctg ctg aag gac gct gcc      688
Val Asn His Gly Ala Ser Ser Glu Asp Thr Leu Leu Lys Asp Ala Ala
                        185           190           195

aag gtc tgc aga gaa ttc acc gag cgt gag caa gga gaa gtc cgc ttc      736
Lys Val Cys Arg Glu Phe Thr Glu Arg Glu Gln Gly Glu Val Arg Phe
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tct gcc gtg gct ctc tgc aag gca gcc taa t gctctgtggg agggactttg      787
Ser Ala Val Ala Leu Cys Lys Ala Ala *

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215

220

ctgatttccc ctcttcctt caacatgaaa atatataccc ccccatgcag tctaaaatgc 847  
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 caccaggca cttaaacaca agcagagtgc acagctgtcc actgggccaat tgtggtgtga 967  
 gcttcagatg gtgaagcatt ctccccagtg tatgtottgt atccgatata taacgcttta 1027  
 aatggctact ttggtttctg tctgtaagtt aagaccttgg atgtggttta attgtttgtc 1087  
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<220>  
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 <222> (1)..(2543)  
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 caggagtgcc tgggttagca gtcgcggagc catcccggcg tctgctgcca tgaccgactc 180  
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 gcggc atg ctc ccg cgg agg ctg ctg gcc gcc tgg ctg gcg ggg acg 407  
 Met Leu Pro Arg Arg Leu Leu Ala Ala Trp Leu Ala Gly Thr  
 1 5 10  
 cgg ggc ggg ggc ctg ctg gcg ctt ctg gcc aat cag tgc cgc ttc gtc 455  
 Arg Gly Gly Gly Leu Leu Ala Leu Leu Ala Asn Gln Cys Arg Phe Val  
 15 20 25 30  
 acg ggc ctg cgc gtg cgg cgc gcg cag cag atc gcg cag ctc tac ggc 503  
 Thr Gly Leu Arg Val Arg Arg Ala Gln Gln Ile Ala Gln Leu Tyr Gly  
 35 40 45  
 cgc ctc tac tcc gag agc tca cgc cgc gtt ctc ctc ggc cgc ctc tgg 551  
 Arg Leu Tyr Ser Glu Ser Ser Arg Arg Val Leu Leu Gly Arg Leu Trp  
 50 55 60  
 cgc cgg ctg cac ggc cgt cct ggc cat gcc tct gcc ttg atg gcg gcg 599  
 Arg Arg Leu His Gly Arg Pro Gly His Ala Ser Ala Leu Met Ala Ala

65	70	75	
tta gcc ggc gtc ttc gtt tgg gac gag gag agg atc cag gag gag gag Leu Ala Gly Val Phe Val Trp Asp Glu Glu Arg Ile Gln Glu Glu Glu 80 85 90			647
ttg cag aga tct att aat gag atg aag cgg ttg gaa gaa atg tca aat Leu Gln Arg Ser Ile Asn Glu Met Lys Arg Leu Glu Glu Met Ser Asn 95 100 105 110			695
atg ttt cag agc tct gga gtc cag cac cac cct cca gaa cca aaa gcc Met Phe Gln Ser Ser Gly Val Gln His His Pro Pro Glu Pro Lys Ala 115 120 125			743
caa aca gaa ggg aat gaa gat tca gag ggc aaa gag caa cgt tgg gaa Gln Thr Glu Gly Asn Glu Asp Ser Glu Gly Lys Glu Gln Arg Trp Glu 130 135 140			791
atg gtg atg gat aag aaa cac ttt aag ctg tgg cgg cgc cca att aca Met Val Met Asp Lys Lys His Phe Lys Leu Trp Arg Arg Pro Ile Thr 145 150 155			839
ggc acc cac ctt tac cag tac cga gtt ttt gga acc tac aca gat gtg Gly Thr His Leu Tyr Gln Tyr Arg Val Phe Gly Thr Tyr Thr Asp Val 160 165 170			887
aca cct cgg cag ttc ttc aat gtt cag ctg gac aca gag tat aga aaa Thr Pro Arg Gln Phe Phe Asn Val Gln Leu Asp Thr Glu Tyr Arg Lys 175 180 185 190			935
aaa tgg gat gcc ctg gta atc aag ctg gag gtg att gag agg gat gtg Lys Trp Asp Ala Leu Val Ile Lys Leu Glu Val Ile Glu Arg Asp Val 195 200 205			983
gtt agt ggt tcc gag gtt ctt cac tgg gta acc cat ttt cct tat cca Val Ser Gly Ser Glu Val Leu His Trp Val Thr His Phe Pro Tyr Pro 210 215 220			1031
atg tac tca cgg gat tat gtt tat gtt cgg cgg tat agt gtg gat cag Met Tyr Ser Arg Asp Tyr Val Tyr Val Arg Arg Tyr Ser Val Asp Gln 225 230 235			1079
gaa aac aac atg atg gtg ttg gtg tgg cgt gct gtg gag cat ccg agt Glu Asn Asn Met Met Val Leu Val Ser Arg Ala Val Glu His Pro Ser 240 245 250			1127
gtg cca gag tct cca gaa ttc gtc agg gtc aga tca tat gaa tcc caa Val Pro Glu Ser Pro Glu Phe Val Arg Val Arg Ser Tyr Glu Ser Gln 255 260 265 270			1175
atg gtt atc cgt ccc cac aag tca ttt gat gag aat ggc ttt gac tac Met Val Ile Arg Pro His Lys Ser Phe Asp Glu Asn Gly Phe Asp Tyr 275 280 285			1223
tta cta aca tac agt gac aat ccc caa acg gtg ttt cct cgc tac tgt Leu Leu Thr Tyr Ser Asp Asn Pro Gln Thr Val Phe Pro Arg Tyr Cys 290 295 300			1271
gtt agt tgg atg gtt tcc agt ggc atg cca gat ttc ctg gag aag ctg Val Ser Trp Met Val Ser Ser Gly Met Pro Asp Phe Leu Glu Lys Leu 305 310 315			1319
cac atg gcc act ctg aaa gcc aag aat atg gag att aaa gta aag gac His Met Ala Thr Leu Lys Ala Lys Asn Met Glu Ile Lys Val Lys Asp 320 325 330 335 340 345 350			1367

320	325	330	
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Tyr Ile Ser Ala Lys Pro Leu Glu Met Ser Ser Glu Ala Lys Ala Thr			
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agc cag tcc tct gag cga aag aac gag ggc agc tgt ggc cct gct cgg			1463
Ser Gln Ser Ser Glu Arg Lys Asn Glu Gly Ser Cys Gly Pro Ala Arg			
355	360	365	
att gag tat gct tga caggctttgg gataagaagg gacaagggtgc ttctagccct			1518
Ile Glu Tyr Ala *			
370			
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gaatttgtac aaagaaattt ccctccctgc ctgcacaata tcaccattg actcacctta			2178
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tcccc			2543

&lt;210&gt; 279

&lt;211&gt; 2190

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1570)

&lt;400&gt; 279

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	Met Ser Phe Arg Lys	
	1 5	
gtg gtc cgg cag agc aaa ttc cgg cat gtg ttc ggg cag ccg gtc aag		163
Val Val Arg Gln Ser Lys Phe Arg His Val Phe Gly Gln Pro Val Lys		
	10 15 20	
aac gac cag tgc tat gag gac att cgc gtg tcc cgt gtt acc tgg gac		211
Asn Asp Gln Cys Tyr Glu Asp Ile Arg Val Ser Arg Val Thr Trp Asp		
	25 30 35	
agc acc ttc tgc gcc gtc aac ccc aag ttc ctg gcg gtg att gtg gag		259
Ser Thr Phe Cys Ala Val Asn Pro Lys Phe Leu Ala Val Ile Val Glu		
	40 45 50	
gcc agt gga ggg ggt gcc ttt ctg gtg ctc ccc cta agc aag acg ggc		307
Ala Ser Gly Gly Gly Ala Phe Leu Val Leu Pro Leu Ser Lys Thr Gly		
	55 60 65	
cgc att gac aag gcc tac ccg acg gtg tgt ggg cac acg gga cct gtc		355
Arg Ile Asp Lys Ala Tyr Pro Thr Val Cys Gly His Thr Gly Pro Val		
	70 75 80 85	
ctg gac atc gac tgg tgt cct cac aac gac gaa gtc ata gcc agc ggc		403
Leu Asp Ile Asp Trp Cys Pro His Asn Asp Glu Val Ile Ala Ser Gly		
	90 95 100	
tcg gag gac tgc acg gtc atg gtg tgg cag atc cca gag aac ggg ctg		451
Ser Glu Asp Cys Thr Val Met Val Trp Gln Ile Pro Glu Asn Gly Leu		
	105 110 115	
acc tcc ccg ctg aca gag ccg gtg gtg gta ctg gag ggg cac acc aag		499
Thr Ser Pro Leu Thr Glu Pro Val Val Leu Glu Gly His Thr Lys		
	120 125 130	
cga gtg ggc atc atc gcc tgg cac ccc acg gcc cga aac gtg ctg ctc		547
Arg Val Gly Ile Ile Ala Trp His Pro Thr Ala Arg Asn Val Leu Leu		
	135 140 145	
agt gca ggc tgc gac aac gtg gta ctc atc tgg aat gtg ggc aca gcg		595
Ser Ala Gly Cys Asp Asn Val Val Leu Ile Trp Asn Val Gly Thr Ala		
	150 155 160 165	
gag gag ctg tac cgc ctg gac agc ctg cac cct gac ctc atc tac aat		643
Glu Glu Leu Tyr Arg Leu Asp Ser Leu His Pro Asp Leu Ile Tyr Asn		
	170 175 180	
gtc agc tgg aac cac aat ggc agc ctg ttt tgc tca gca tgc aag gac		691
Val Ser Trp Asn His Asn Gly Ser Leu Phe Cys Ser Ala Cys Lys Asp		
	185 190 195	
aag agc gtg cgc atc atc gac ccc cgt cgg ggc acc ctg gtg gca gag		739
Lys Ser Val Arg Ile Ile Asp Pro Arg Arg Gly Thr Leu Val Ala Glu		
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cgg gag aag gct cat gag ggg gcc cgg ccc atg cgg gcc atc ttc ctg		787
Arg Glu Lys Ala His Glu Gly Ala Arg Pro Met Arg Ala Ile Phe Leu		
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gca gat ggc aag gtg ttc acc aca ggc ttc agc cga atg agc gag cgg		835
Ala Asp Gly Lys Val Phe Thr Thr Gly Phe Ser Arg Met Ser Glu Arg		
	230 235 240 245	

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cag gaa ctg gac tgc agc aac ggg gcc ctg ctg ccc ttc tac gac ccc Gln Glu Leu Asp Ser Ser Asn Gly Ala Leu Leu Pro Phe Tyr Asp Pro 265 270 275	931
gac acc agt gtg gtc tac gtc tgc ggc aag ggt gac tcc agc atc cgg Asp Thr Ser Val Val Tyr Val Cys Gly Lys Gly Asp Ser Ser Ile Arg 280 285 290	979
tac ttt gag atc aca gag gag cct ccc tac atc cac ttc ctg aac acg Tyr Phe Glu Ile Thr Glu Glu Pro Pro Tyr Ile His Phe Leu Asn Thr 295 300 305	1027
ttc acc agc aag gag ccg cag cgg ggt atg ggc agc atg ccc aag cgg Phe Thr Ser Lys Glu Pro Gln Arg Gly Met Gly Ser Met Pro Lys Arg 310 315 320 325	1075
ggc ctg gag gtc agc aag tgc gag atc gcc cgg ttc tac aaa ctg cat Gly Leu Glu Val Ser Lys Cys Glu Ile Ala Arg Phe Tyr Lys Leu His 330 335 340	1123
gag cgc aag tgt gag ccc atc gtc atg act gtg cca aga aag tgc gac Glu Arg Lys Cys Glu Pro Ile Val Met Thr Val Pro Arg Lys Ser Asp 345 350 355	1171
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gcc acc ccc agc ggc agc ctg gcc aga gcc ggg gag gct ggg aag ctg Ala Thr Pro Ser Gly Ser Leu Ala Arg Ala Gly Glu Ala Gly Lys Leu 440 445 450	1459
gag gag gtg atg cag gag ctg cgg gcc ctg agg gcg ctg gtc aag gag Glu Glu Val Met Gln Glu Leu Arg Ala Leu Arg Ala Leu Val Lys Glu 455 460 465	1507
cag ggc gac cgc atc tgc cgc ctg gag gag cag ctg ggc cgc atg gag Gln Gly Asp Arg Ile Cys Arg Leu Glu Glu Gln Leu Gly Arg Met Glu 470 475 480 485	1555
aac ggg gat gcg tag ggccacagcc acacgccacc ttcattctcct ccgccgcccc Asn Gly Asp Ala * 490	1610

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<222> (104)..(673)

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Met Gly Thr Ala
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gga gcc atg cag ctg tgc tgg gtg atc ctg ggc ttc ctc ctg ttc cga 163
Gly Ala Met Gln Leu Cys Trp Val Ile Leu Gly Phe Leu Leu Phe Arg
5 10 15 20
ggc cac aac tcc cag ccc aca atg acc cag acc tct agc tct cag gga 211
Gly His Asn Ser Gln Pro Thr Met Thr Gln Thr Ser Ser Ser Gln Gly
25 30 35
ggc ctt ggc ggt cta agt ctg acc aca gag cca gtt tct tcc aac cca 259
Gly Leu Gly Gly Leu Ser Leu Thr Thr Glu Pro Val Ser Ser Asn Pro
40 45 50
gga tac atc cct tcc tca gag gct aac agg cca agc cat ctg tcc agc 307
Gly Tyr Ile Pro Ser Ser Glu Ala Asn Arg Pro Ser His Leu Ser Ser
55 60 65
act ggt acc cca gac aca ttt caa act gtt ccc ccc aat tca acc acc 355
Thr Gly Thr Pro Asp Thr Phe Gln Thr Val Pro Pro Asn Ser Thr Thr
70 75 80
atg agc ctg agc atg agg gaa gat gcg acc atc ctg ccc agc ccc acg 403
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**PCT/US01/04098**

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 Thr Gly Thr Pro Gly Ala Gly Val Pro Ser Ser Gly Arg Asp Gly Gly  
           70                                75                                80  
 aca agc aga gac aca ttt caa act gtt ccc ccc aat tca acc acc atg 403  
 Thr Ser Arg Asp Thr Phe Gln Thr Val Pro Pro Asn Ser Thr Thr Met  
           85                                90                                95                                100  
 agc ctg agc atg agg gaa gat gcg acc atc ctg ccc agc ccc acg tca 451  
 Ser Leu Ser Met Arg Glu Asp Ala Thr Ile Leu Pro Ser Pro Thr Ser  
                                 105                                110                                115  
 gag act gtg ctc act gtg gct gca ttt ggt gtt atc agc ttc att gtc 499  
 Glu Thr Val Leu Thr Val Ala Ala Phe Gly Val Ile Ser Phe Ile Val  
                                 120                                125                                130  
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 Ile Leu Val Val Val Val Ile Ile Leu Val Gly Val Val Ser Leu Arg  
                                 135                                140                                145  
 ttc aag tgt cgg aag agc aag gag tct gaa gat ccc cag aaa cct ggg 595  
 Phe Lys Cys Arg Lys Ser Lys Glu Ser Glu Asp Pro Gln Lys Pro Gly  
                                 150                                155                                160  
 agt tca ggg ctg tct gaa agc tgc tcc aca gcc aat gga gag aaa gac 643  
 Ser Ser Gly Leu Ser Glu Ser Cys Ser Thr Ala Asn Gly Glu Lys Asp  
                                 165                                170                                175                                180  
 agc atc acc ctt atc tcc atg aag aac atc aac atg aat aat ggc aaa 691  
 Ser Ile Thr Leu Ile Ser Met Lys Asn Ile Asn Met Asn Asn Gly Lys  
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 Gln Ser Leu Ser Ala Glu Lys Val Leu \*  
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Gly	Lys	His	Asp	Tyr	Asp	Asp	Ser	Ser	Glu	Glu	Gln	Ser	Ala	Glu	Asp		
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Ser	Tyr	Glu	Ala	Ser	Pro	Gly	Ser	Glu	Thr	Gln	Arg	Arg	Arg	Arg	Arg		
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cgg	cac	agg	cac	agc	ccc	acc	ggc	ccg	cca	ggc	ttc	ccc	cga	gac	ggc	1724	
Arg	His	Arg	His	Ser	Pro	Thr	Gly	Pro	Pro	Gly	Phe	Pro	Arg	Asp	Gly		
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Glu	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Lys	Ala	Ser	Asn	Ile	Val	Met		
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Leu	Arg	Met	Leu	Pro	Gln	Ala	Ala	Thr	Glu	Asp	Asp	Ile	Arg	Gly	Gln		
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Lys	Ser	Ser	Gly	Gln	Ser	Arg	Gly	Phe	Ala	Phe	Val	Glu	Phe	Ser	His		
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Ile	Asn	Glu	Asp	Trp	Leu	Cys	Asn	Lys	Cys	Gly	Val	Gln	Asn	Phe	Lys		
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cgc	cga	gag	aag	tgc	ttc	aaa	tgt	ggc	gtg	ccc	aag	tca	gag	gca	gag	2156	
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ggt	ggc	cgg	gag	ctg	agc	cag	ggc	ctg	ctt	ccc	ctg	ccg	cag	ccc	tac	2252	
Gly	Gly	Arg	Glu	Leu	Ser	Gln	Gly	Leu	Leu	Pro	Leu	Pro	Gln	Pro	Tyr		
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Pro	His	Ser	Thr	Met	Asp	Ser	Ile	Leu	Gly	Ala	Leu	Ala	Pro	Tyr	Ala		
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Val	Leu	Ser	Ser	Ser	Asn	Val	Arg	Val	Ile	Lys	Asp	Lys	Gln	Thr	Gln		
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cag	ctg	ctg	cag	atc	ctg	cag	gcc	ctg	cac	cca	cca	ctc	act	atc	gac	2540	
Gln	Leu	Leu	Gln	Ile	Leu	Gln	Ala	Leu	His	Pro	Pro	Leu	Thr	Ile	Asp		
			360					365					370				
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Gly	Lys	Thr	Ile	Asn	Val	Glu	Phe	Ala	Lys	Gly	Ser	Lys	Arg	Asp	Met		
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gcc	tcc	aat	gaa	ggc	agt	cgc	atc	agt	gct	gcc	tct	gtg	gcc	agc	act	2636	
Ala	Ser	Asn	Glu	Gly	Ser	Arg	Ile	Ser	Ala	Ala	Ser	Val	Ala	Ser	Thr		
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gcc	att	gct	gcg	gcc	cag	tgg	gcc	atc	tca	cag	gcc	tcc	caa	ggc	ggg	2684	
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	405				410					415					420		
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Glu	Gly	Thr	Trp	Ala	Thr	Ser	Glu	Glu	Pro	Pro	Val	Asp	Tyr	Ser	Tyr		
				425					430					435			
tac	caa	cag	gat	gag	ggc	tat	ggc	aac	agc	cag	ggc	aca	gag	tct	tcc	2780	
Tyr	Gln	Gln	Asp	Glu	Gly	Tyr	Gly	Asn	Ser	Gln	Gly	Thr	Glu	Ser	Ser		
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Leu	Tyr	Ala	His	Gly	Tyr	Leu	Lys	Gly	Thr	Lys	Gly	Pro	Gly	Ile	Thr		
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Pro	Gly	Ala	Asp	Ser	Val	Ser	Met	Gln	Ala	Phe	Ser	Arg	Pro	Gln	Pro		
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Val	Pro	Asp	Val	Ser	Thr	Tyr	Gln	Tyr	Asp	Glu	Thr	Ser	Gly	Tyr	Tyr	
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tat	gac	ccc	cag	acc	ggc	ctc	tac	tat	gac	ccc	aac	tcc	cag	tat	tac	3212
Tyr	Asp	Pro	Gln	Thr	Gly	Leu	Tyr	Tyr	Asp	Pro	Asn	Ser	Gln	Tyr	Tyr	
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Tyr	Asn	Ala	Gln	Ser	Gln	Gln	Tyr	Leu	Tyr	Trp	Asp	Gly	Glu	Arg	Arg	
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Thr	Tyr	Val	Pro	Ala	Leu	Glu	Gln	Ser	Ala	Asp	Gly	His	Lys	Glu	Thr	
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Gly	Ala	Pro	Ser	Lys	Glu	Gly	Lys	Glu	Lys	Lys	Glu	Lys	His	Lys	Thr	
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Lys	Thr	Ala	Gln	Gln	Ile	Ala	Lys	Asp	Met	Glu	Arg	Trp	Ala	Arg	Ser	
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Leu	Asn	Lys	Gln	Lys	Glu	Asn	Phe	Lys	Asn	Ser	Phe	Gln	Pro	Ile	Ser	
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tcc	ctg	cga	gat	gac	gag	agg	cgg	gag	tca	gcc	act	gca	gat	gct	ggc	3500
Ser	Leu	Arg	Asp	Asp	Glu	Arg	Arg	Glu	Ser	Ala	Thr	Ala	Asp	Ala	Gly	
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Tyr	Ala	Ile	Leu	Glu	Lys	Lys	Gly	Ala	Leu	Ala	Glu	Arg	Gln	His	Thr	
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Ser	Met	Asp	Leu	Pro	Lys	Leu	Ala	Ser	Asp	Asp	Arg	Pro	Ser	Pro	Pro	
	710					715					720					
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Arg	Gly	Leu	Val	Ala	Ala	Tyr	Ser	Gly	Glu	Ser	Asp	Ser	Glu	Glu	Glu	
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Gln	Glu	Arg	Gly	Gly	Pro	Glu	Arg	Glu	Glu	Lys	Leu	Thr	Asp	Trp	Gln	
				745					750					755		
aag	ctg	gcc	tgt	ctg	ctc	tgc	cga	cgc	cag	ttc	ccc	agc	aaa	gag	gcg	3740
Lys	Leu	Ala	Cys	Leu	Leu	Cys	Arg	Arg	Gln	Phe	Pro	Ser	Lys	Glu	Ala	
			760					765					770			
ctc	atc	cgg	cac	cag	cag	ctc	tca	ggg	ctc	cac	aag	caa	aac	ctt	gag	3788
Leu	Ile	Arg	His	Gln	Gln	Leu	Ser	Gly	Leu	His	Lys	Gln	Asn	Leu	Glu	
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Ile	His	Arg	Arg	Ala	His	Leu	Ser	Glu	Asn	Glu	Leu	Glu	Ala	Leu	Glu	
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aag	aat	gac	atg	gag	caa	atg	aag	tac	cgg	gac	cgt	gca	gct	gaa	cgc	3884

Lys Asn Asp Met Glu Gln Met Lys Tyr Arg Asp Arg Ala Ala Glu Arg  
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 Tyr Gly Gly Ile Ser Thr Ala Ser Val Asp Phe Glu Gln Pro Thr Arg  
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 Gly Trp Lys Glu Gly Ser Gly Leu Gly Arg Lys Lys Gln Gly Ile Val  
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 acc cac gcg tcc gct ccg agc ttc tta aac aca gcc ctt ggg cct acg 98  
 Thr His Ala Ser Ala Pro Ser Phe Leu Asn Thr Gly Leu Gly Pro Thr  
 15 20 25  
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 Ala Leu Gly Val Leu Gly Gly Ala Gly Ala Gly Leu Met Ser Asn Pro  
 30 35 40

tcc ccc cag gtt cca gag gaa gaa gcc tcc aca tct gtc tgc cgg ccc	194
Ser Pro Gln Val Pro Glu Glu Glu Ala Ser Thr Ser Val Cys Arg Pro	
45 50 55	
aag agt tcc atg gcc tcc act tcc cgc cgc caa cgc cga gaa cgt cgc	242
Lys Ser Ser Met Ala Ser Thr Ser Arg Arg Gln Arg Arg Glu Arg Arg	
60 65 70 75	
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Phe Arg Arg Tyr Leu Ser Ala Gly Arg Leu Val Arg Ala Gln Ala Leu	
80 85 90	
ctc cag cga cac cca ggc ctc gat gta gat gct ggg cag ccc cca cca	338
Leu Gln Arg His Pro Gly Leu Asp Val Asp Ala Gly Gln Pro Pro Pro	
95 100 105	
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Leu His Arg Ala Cys Ala Arg His Asp Ala Pro Ala Leu Cys Leu Leu	
110 115 120	
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Leu Arg Leu Gly Ala Asp Pro Ala His Gln Asp Arg His Gly Asp Thr	
125 130 135	
gca ctg cat gct gct gcc cgc cag ggc cca gat gcc tac acc gat ttc	482
Ala Leu His Ala Ala Ala Arg Gln Gly Pro Asp Ala Tyr Thr Asp Phe	
140 145 150 155	
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Phe Leu Pro Leu Leu Ser Arg Cys Pro Ser Ala Met Gly Ile Lys Asn	
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aag gat ggg gag acc cct ggc caa att ttg ggc tgg gga ccc ccc tgg	578
Lys Asp Gly Glu Thr Pro Gly Gln Ile Leu Gly Trp Gly Pro Pro Trp	
175 180 185	
gat tct gct gaa gag gag gaa gaa gat gat gcc tcc aag gag cgg gaa	626
Asp Ser Ala Glu Glu Glu Glu Glu Asp Asp Ala Ser Lys Glu Arg Glu	
190 195 200	
tgg aga cag aag ctc cag ggt gag ctg gag gac gag tgg cag gaa gtc	674
Trp Arg Gln Lys Leu Gln Gly Glu Leu Glu Asp Glu Trp Gln Glu Val	
205 210 215	
atg ggg agg ttt gaa ggt gat gcc tcc cat gaa acc cag gaa cct gag	722
Met Gly Arg Phe Glu Gly Asp Ala Ser His Glu Thr Gln Glu Pro Glu	
220 225 230 235	
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Ser Phe Ser Ala Trp Ser Asp Arg Leu Ala Arg Glu His Ala Gln Lys	
240 245 250	
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Cys Gln Gln Gln Arg Glu Ala Glu Gly Ser Cys Arg Pro Pro Arg	
255 260 265	
gct gag ggc tcc agc cag agc tgg cga cag cag gag gag gag cag cgg	866
Ala Glu Gly Ser Ser Gln Ser Trp Arg Gln Gln Glu Glu Glu Gln Arg	
270 275 280	
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Leu Phe Arg Glu Arg Ala Arg Ala Lys Glu Glu Glu Leu Arg Glu Ser	
285 290 295	



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cga gcc agg agg gcg cag gag gct cta ggg gac cga gaa ccc aag cca      962
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acc agg gcc ggg ccc agg gaa gag cac ccc aga gga gcg ggg agg ggc      1010
Thr Arg Ala Gly Pro Arg Glu Glu His Pro Arg Gly Ala Gly Arg Gly
320                               325                               330

agc ctc tgg cga ttt ggt gat gtg ccc tgg ccc tgc cct ggg gga ggg      1058
Ser Leu Trp Arg Phe Gly Asp Val Pro Trp Pro Cys Pro Gly Gly Gly
335                               340                               345

gac cca gag gcc atg gct gca gcc ctg gtg gcc agg ggc ccc cct ttg      1106
Asp Pro Glu Ala Met Ala Ala Leu Val Ala Arg Gly Pro Pro Leu
350                               355                               360

gag gaa cag ggg gct ctg agg agg tac ttg agg gtc cag cag gtc cgc      1154
Glu Glu Gln Gly Ala Leu Arg Arg Tyr Leu Arg Val Gln Gln Val Arg
365                               370                               375

tgg cac cct gac cgc ttc ctg cag cga ttc cga agc cag att gag acc      1202
Trp His Pro Asp Arg Phe Leu Gln Arg Phe Arg Ser Gln Ile Glu Thr
380                               385                               390                               395

tgg gag ctg ggc cgt gtg atg gga gca gtg aca gcc ctt tct cag gcc      1250
Trp Glu Leu Gly Arg Val Met Gly Ala Val Thr Ala Leu Ser Gln Ala
400                               405                               410

ctg aat cgc cat gca gag gcc ctc aag tgacc ctagggaaga agcaagaaac      1302
Leu Asn Arg His Ala Glu Ala Leu Lys
415                               420

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<213> Homo sapiens

<220>
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<222> (1884)..(1910)

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aatacattaa aataaataca aagaaaaaat tctcccagca aatactagat tcaatccaa      180

caatacagac acagtcttaa aaaatcagtt atttttttat ttgcatagaa ccaaaggaaa      240

gacttaaaat tccaacatac atcctacgag gcttacaatt taattacaaa tccaattttg      300

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&lt;221&gt; CDS

&lt;222&gt; (4062) .. (4073)

&lt;400&gt; 285

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cagaaactcc ggccgttgta ttgatggga ctttaagagaa atagaagcct ctatataagg 180  
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<213> Homo sapiens

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aacagtccca aaatccctca gcatgcccag ccctcagggg agttcctact tgtttatgaa 420
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gatacattga ccctggacac tgaatattcc tttctgatgg aggagaagaa cccatccaaa 720
gcaaacttgc ttgcagaata ggcagcaacc attggataag ccactttccc agccagagag 780
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ctaggaaagg acc atg cag cta gag atc aaa gtg gcc ctg aac ttc atc		289
Met Gln Leu Glu Ile Lys Val Ala Leu Asn Phe Ile		
1 5 10		
atc tcc tac ttg tac aac aag ctg ccc cgg cgc cgg gca gac ctg ttt		337
Ile Ser Tyr Leu Tyr Asn Lys Leu Pro Arg Arg Arg Ala Asp Leu Phe		
15 20 25		
ggg gag gag cta gag cgg ctt ttg aaa aag aaa tat gaa ggc cac tgg		385
Gly Glu Glu Leu Glu Arg Leu Leu Lys Lys Lys Tyr Glu Gly His Trp		
30 35 40		
tac cct gag aag cca ctg aaa ggc tct ggc ttc cgc tgt gtt cac att		433
Tyr Pro Glu Lys Pro Leu Lys Gly Ser Gly Phe Arg Cys Val His Ile		
45 50 55 60		
ggg gag atg gtg gac ccc gtg gtg gag ctg gcc gcc aag cgg agt ggc		481
Gly Glu Met Val Asp Pro Val Val Glu Leu Ala Ala Lys Arg Ser Gly		
65 70 75		

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Leu Ala Val Glu Asp Val Arg Ala Asn Val Pro Glu Glu Leu Ser Val	
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Trp Ile Asp Pro Phe Glu Val Ser Tyr Gln Ile Gly Glu Lys Gly Ala	
95 100 105	
gtg aaa gtg ctg tac ctg gat gac agt gag ggt tgc ggt gcc cca gag	625
Val Lys Val Leu Tyr Leu Asp Asp Ser Glu Gly Cys Gly Ala Pro Glu	
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ctg gac aag gag atc aag agc agc ttc aac cct gac gcc cag gtg ttc	673
Leu Asp Lys Glu Ile Lys Ser Ser Phe Asn Pro Asp Ala Gln Val Phe	
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Val Pro Ile Gly Ser Gln Asp Ser Ser Leu Ser Asn Ser Pro Ser Pro	
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Ser Phe Gly Gln Ser Pro Ser Pro Thr Phe Ile Pro Arg Ser Ala Gln	
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Pro Ile Thr Phe Thr Thr Ala Ser Phe Ala Ala Thr Lys Phe Gly Ser	
175 180 185	
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Thr Lys Met Lys Lys Gly Gly Gly Ala Ala Ser Gly Gly Gly Val Ala	
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Arg Ser Pro Thr Asn Ser Leu Leu Lys His Lys Ser Leu Ser Leu Ser	
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Met His Ser Leu Asn Phe Ile Thr Ala Asn Pro Ala Pro Gln Ser Gln	
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ctc tca ccc aat gcc aag gag ttc gtg tac aac ggt ggt ggc tca ccc	1057
Leu Ser Pro Asn Ala Lys Glu Phe Val Tyr Asn Gly Gly Gly Ser Pro	
255 260 265	
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Ser Leu Phe Phe Asp Ala Ala Asp Gly Arg Ala Ala Ala Pro Gln Ala	
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Trp Pro Arg Tyr Leu Glu Val Val Pro Thr Ala Ser Ser Trp Arg Arg	
305 310 315	
cac ccc ttt gtg gaa ggc ctc agc tac aac ctg aac acc atg cag tat	1249
His Pro Phe Val Glu Gly Leu Ser Tyr Asn Leu Asn Thr Met Gln Tyr	
320 325 330	

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 aacagcatca tcagcatc atg cta tta caa tcc caa acc atg ggg gtt tct 231  
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 His Ser Phe Thr Pro Lys Gly Ile Thr Ile Pro Gln Arg Glu Lys Pro  
                           15                                  20                                  25  
 gga cac atg tac caa aac gaa gat tac ctg cag aac ggg ctg cca aca 327  
 Gly His Met Tyr Gln Asn Glu Asp Tyr Leu Gln Asn Gly Leu Pro Thr  
                           30                                  35                                  40  
 gaa acc acc gtt ctt ggg act gtc cag atc ctg tgt tgc cta ttg att 375  
 Glu Thr Thr Val Leu Gly Thr Val Gln Ile Leu Cys Cys Leu Leu Ile  
                           45                                  50                                  55  
 tca agt ctg ggg gcc atc ttg gtt ttt gct ccc tac ccc tcc cac ttc 423  
 Ser Ser Leu Gly Ala Ile Leu Val Phe Ala Pro Tyr Pro Ser His Phe  
                           60                                  65                                  70                                  75  
 aat cca gca att tcc acc act ttg atg tct ggg tac cca ttt tta gga 471  
 Asn Pro Ala Ile Ser Thr Thr Leu Met Ser Gly Tyr Pro Phe Leu Gly  
                           80                                  85                                  90  
 gct ctg tgt ttt ggc att act gga tcc ctc tca att atc tct gga aaa 519  
 Ala Leu Cys Phe Gly Ile Thr Gly Ser Leu Ser Ile Ile Ser Gly Lys  
                           95                                  100                                  105  
 caa tca act aag ccc ttt gac ctg agc agc ttg acc tca aat gca gtg 567  
 Gln Ser Thr Lys Pro Phe Asp Leu Ser Ser Leu Thr Ser Asn Ala Val  
                           110                                  115                                  120  
 agt tct gtt act gca gga gca ggc ctc ttc ctc ctt gct gac agc atg 615  
 Ser Ser Val Thr Ala Gly Ala Gly Leu Phe Leu Leu Ala Asp Ser Met  
                           125                                  130                                  135  
 gta gcc ctg agg act gcc tct caa cat tgt ggc tca gaa atg gat tat 663  
 Val Ala Leu Arg Thr Ala Ser Gln His Cys Gly Ser Glu Met Asp Tyr  
                           140                                  145                                  150                                  155



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cta tcc tca ttg cct tat tcg gag tac tat tat cca ata tat gaa atc      711
Leu Ser Ser Leu Pro Tyr Ser Glu Tyr Tyr Tyr Pro Ile Tyr Glu Ile
                160                      165                      170

aaa gat tgt ctc ctg acc agt gtc agt tta aca ggt gtc cta gtg gtg      759
Lys Asp Cys Leu Leu Thr Ser Val Ser Leu Thr Gly Val Leu Val Val
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atg ctc atc ttc act gtg ctg gag ctc tta tta gct gca tac agt tct      807
Met Leu Ile Phe Thr Val Leu Glu Leu Leu Leu Ala Ala Tyr Ser Ser
                190                      195                      200

gtc ttt tgg tgg aaa cag ctc tac tcc aac aac cct ggg agt tca ttt      855
Val Phe Trp Trp Lys Gln Leu Tyr Ser Asn Asn Pro Gly Ser Ser Phe
                205                      210                      215

tcc tcg acc cag tca caa gat cat atc caa cag gtc aaa aag agt tct      903
Ser Ser Thr Gln Ser Gln Asp His Ile Gln Gln Val Lys Lys Ser Ser
                220                      225                      230                      235

tca cgg tct tgg ata taa gtaact cttggcctca gaggaaggaa aagcaactca      957
Ser Arg Ser Trp Ile *
                240

acactcatgg tcaagtgtga ttagactttc ctgaaatctc tgccatttta gatactgtga 1017

aacaaactaa aaaaaaaaaa                                         1036

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<210> 289  
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 <212> DNA  
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<220>  
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 <222> (169)..(456)

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attggggagat ctacagctaa gacgccagga acccctggaa gcctagaa atg gag aac      177
                               Met Glu Asn
                               1

ctg aag tct gga gtg tat cct ctc aag gaa gca agt gga tgc cct ggg      225
Leu Lys Ser Gly Val Tyr Pro Leu Lys Glu Ala Ser Gly Cys Pro Gly
                5                      10                      15

gct gac agg aat ctt ctg gtg tac tct ttt tat gaa aag ggg cca ttg      273
Ala Asp Arg Asn Leu Leu Val Tyr Ser Phe Tyr Glu Lys Gly Pro Leu
                20                      25                      30                      35

aca ttt agg gat gtg gcc ata gaa ttt tct ctg gag gag tgg caa tgc      321
Thr Phe Arg Asp Val Ala Ile Glu Phe Ser Leu Glu Glu Trp Gln Cys
                40                      45                      50

ctg gac act gct cag cag gat ttg tat aga aaa gtg atg tta gag aac      369
Leu Asp Thr Ala Gln Gln Asp Leu Tyr Arg Lys Val Met Leu Glu Asn

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55						60						65						
tac	aga	aac	ctg	gtc	ttc	ttg	ggg	gag	aat	aac	ttt	aat	aca	aaa	tcc	417		
Tyr	Arg	Asn	Leu	Val	Phe	Leu	Gly	Glu	Asn	Asn	Phe	Asn	Thr	Lys	Ser			
			70				75				80							
ctt	ata	tac	cct	aaa	gtt	ttc	att	tct	ctg	ttt	tca	tag	aataat	tttt	466			
Leu	Ile	Tyr	Pro	Lys	Val	Phe	Ile	Ser	Leu	Phe	Ser	*						
			85				90				95							
ggtaatttat	gctttgcata	agt	gagtttc	tgatgcctgt	tttaaagaaa	tcttgaagaa	526											
ctgtccgtgt	ggaaaaaaat	ttcttcagga	tgttttatct	tggcctgatc	tttttacatt	586												
tctgagccgg	tctgtatcct	tcactctaca	gtagtggtaa	tttcagaaat	ttagtagtat	646												
aaaatatgt	tgtccatatg	ttaaaatcta	tatgccacca	ctaatttttt	atccatgaat	706												
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ctgtcattaa	atagtatttt	gggataaatt	ttctagaata	ttctattaca	tcctctttac	826												
taagcatggg	actaggtagg	taattagaga	atatgagcaa	gattcatggt	at ttat tttt	886												
aataaagcag	gtattgctgt	ctctaagcca	gatctgggtca	cctgtctgga	gcaaggaaaa	946												
gatccctgga	atatgaaggg	acacagtacg	gtagtcaaac	cccaggtag	gtgagagtga	1006												
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<210> 290
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<213> Homo sapiens
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<220>
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<222> (221) .. (904)
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cagtagccgc tgaggggatt gcagataacc gcttcccgca cggggaaagt ctacctgccc	180
tgccactttc tgctcgccgt cagcgccgga gctcgccagc	235
	atg tct gtg gta ccg
	Met Ser Val Val Pro
	1 5
ccc aat cgc tgc cag acc ggc tgg ccc cgg ggg gtc act cag ttc ggc	283
Pro Asn Arg Ser Gln Thr Gly Trp Pro Arg Gly Val Thr Gln Phe Gly	
	10 15 20
aac aag tac atc cag cag acg aag ccc ctc acc ctg gag cgc acc atc	331
Asn Lys Tyr Ile Gln Gln Thr Lys Pro Leu Thr Leu Glu Arg Thr Ile	
	25 30 35
aac ctg tac cct ctt acc aat tat act ttt ggt aca aaa gag ccc ctc	379
Asn Leu Tyr Pro Leu Thr Asn Tyr Thr Phe Gly Thr Lys Glu Pro Leu	
	40 45 50

tac gag aag gac agc tct gtt gca gcc aga ttt cag cgc atg agg gaa Tyr Glu Lys Asp Ser Ser Val Ala Ala Arg Phe Gln Arg Met Arg Glu 55 60 65	427
gaa ttt gat aaa att gga atg agg agg act gta gaa ggg gtt ctg att Glu Phe Asp Lys Ile Gly Met Arg Arg Thr Val Glu Gly Val Leu Ile 70 75 80 85	475
gta cat gag cac cgg cta ccc cat gtg tta ctg ctg cag ctg gga aca. Val His Glu His Arg Leu Pro His Val Leu Leu Leu Gln Leu Gly Thr 90 95 100	523
act ttc ttc aaa cta cct ggt ggt gaa ctt aac cca gga gaa gat gaa Thr Phe Phe Lys Leu Pro Gly Gly Glu Leu Asn Pro Gly Glu Asp Glu 105 110 115	571
gtt gaa gga cta aaa cgc tta atg aca gag ata ctg ggt cgt cag gat Val Glu Gly Leu Lys Arg Leu Met Thr Glu Ile Leu Gly Arg Gln Asp 120 125 130	619
gga gtt ttg caa gac tgg gtc att gac gat tgc att ggt aac tgg tgg Gly Val Leu Gln Asp Trp Val Ile Asp Asp Cys Ile Gly Asn Trp Trp 135 140 145	667
aga cca aat ttt gaa cct cct cag tat cca tat att cct gca cat att Arg Pro Asn Phe Glu Pro Pro Gln Tyr Pro Tyr Ile Pro Ala His Ile 150 155 160 165	715
aca aag cct aag gaa cat aag aag ttg ttt ctg gtt cag ctt caa gaa Thr Lys Pro Lys Glu His Lys Lys Leu Phe Leu Val Gln Leu Gln Glu 170 175 180	763
aaa gcc ttg ttt gca gtc cct aaa aat tac aag ctg gta gct gca cca Lys Ala Leu Phe Ala Val Pro Lys Asn Tyr Lys Leu Val Ala Ala Pro 185 190 195	811
ttg ttt gaa ttg tat gac aat gca cca gga tat gga ccc atc att tct Leu Phe Glu Leu Tyr Asp Asn Ala Pro Gly Tyr Gly Pro Ile Ile Ser 200 205 210	859
agt ctc cct cag ctg ttg agc agg ttc aat ttt att tac aac tga att Ser Leu Pro Gln Leu Leu Ser Arg Phe Asn Phe Ile Tyr Asn * 215 220 225	907
cctgcgcagt ggagaagtaa aagaagccgc ttgtctctgt gagcacagct atatacagtg	967
tagaataaat gtggtagaaa agtttttttg gttttatctc ttttgcgatc cctaaattgc	1027
cacctttcta ttgtttgaat agtaaaatta atatgaagaa ctagatagtg gtgtaaaaca	1087
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atttttgtga tgaagagctt ccattacttc tgaaaactat atttatctga gtgagtccea	1387
ggtgcaactc ctaaatgaat tgtgttgacag agaactccca gtataattca ctgaccagta	1447
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ggacgcagct gacgcccgtt tattagctct cgctgcgtcg ccccggtcca gaagctccgt	180
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gagagaaagt cagatgcccc ttttaaactc cctcttcaaa actcatctcc tgggtgactg	300
agttaataga gtggatacaa ccttgctgaa gatgaagaat atacaatatt gaggatattt	360
ttttcttttt ttttttcaag tcttgatttg tggcttacct caagttacca tttttcagtc	420
aagtctgttt gtttgcttct tcagaa atg ttt ttt aca atc tca aga aaa aat	473
Met Phe Phe Thr Ile Ser Arg Lys Asn	
1 5	
atg tcc cag aaa ttg agt tta ctg ttg ctt gta ttt gga ctc att tgg	521
Met Ser Gln Lys Leu Ser Leu Leu Leu Val Phe Gly Leu Ile Trp	
10 15 20 25	
gga ttg atg tta ctg cac tat act ttt caa caa cca aga cat caa agc	569
Gly Leu Met Leu Leu His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser	
30 35 40	
agt gtc aag tta cgt gag caa ata cta gac tta agc aaa aga tat gtt	617
Ser Val Lys Leu Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val	
45 50 55	
aaa gct cta gca gag gaa aat aag aac aca gtg gat gtc gag aac ggt	665
Lys Ala Leu Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly	
60 65 70	

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gct tct atg gca gga tat gcg gat ctg aaa aga aca att gct gtc ctt      713
Ala Ser Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu
   75                               80                               85

ctg gat gac att ttg caa cga ttg gtg aag ctg gag aac aaa gtt gac      761
Leu Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp
   90                               95                               100                               105

tat att gtt gtg aat ggc tca gca gcc aac acc acc aat ggt act agt      809
Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr Ser
                110                               115                               120

ggg aat ttg gtg cca gta acc aca aat aaa aga acg aat gtc tcg ggc      857
Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val Ser Gly
                125                               130                               135

agt atc aga tag cag ttgaaaatca ccttgtgctg ctccatccac tgtggattat      912
Ser Ile Arg *
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aagctctaca cattttcaaa aaaaaaa      999

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<210> 292  
 <211> 1975  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (91)..(1488)

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                                         Met Asp Gly Arg Met Met Arg
                                         1                               5

agc atg agg ctg aga gag gag gag tca ccc gga ccc agc cac aca gcg      159
Ser Met Arg Leu Arg Glu Glu Glu Ser Pro Gly Pro Ser His Thr Ala
   10                               15                               20

tcc tgc ctc tgc ggc tct gcc ccc tgc atc ctg tgc agc tgc tgc ccc      207
Ser Cys Leu Cys Gly Ser Ala Pro Cys Ile Leu Cys Ser Cys Cys Pro
   25                               30                               35

gcc agc cgc aac tcc acc gtg agc cgc ctc atc ttc acg ttc ttc ctc      255
Ala Ser Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe Leu
   40                               45                               50                               55

ttc ctg ggg gtg ctg gtg tcc atc att atg ctg agc ccg ggc gtg gag      303
Phe Leu Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly Val Glu
                60                               65                               70

agt cag ctc tac aag ctg ccc tgg gtg tgt gag gag ggg gcc ggg atc      351
Ser Gln Leu Tyr Lys Leu Pro Trp Val Cys Glu Glu Gly Ala Gly Ile
                75                               80                               85

ccc acc gtc ctg cag ggc cac atc gac tgt ggc tcc ctg ctt ggc tac      399

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Pro	Thr	Val	Leu	Gln	Gly	His	Ile	Asp	Cys	Gly	Ser	Leu	Leu	Gly	Tyr	
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cgc	gct	gtc	tac	cgc	atg	tgc	ttc	gcc	acg	gcg	gcc	ttc	ttc	ttc	ttt	447
Arg	Ala	Val	Tyr	Arg	Met	Cys	Phe	Ala	Thr	Ala	Ala	Phe	Phe	Phe	Phe	
	105					110					115					
ttc	acc	ctg	ctc	atg	ctc	tgc	gtg	agc	agc	agc	cgg	gac	ccc	cgg	gct	495
Phe	Thr	Leu	Leu	Met	Leu	Cys	Val	Ser	Ser	Ser	Arg	Asp	Pro	Arg	Ala	
120					125					130					135	
gcc	atc	cag	aat	ggg	ttt	tgg	ttc	ttt	aag	ttc	ctg	atc	ctg	gtg	ggc	543
Ala	Ile	Gln	Asn	Gly	Phe	Trp	Phe	Phe	Lys	Phe	Leu	Ile	Leu	Val	Gly	
			140						145					150		
ctc	acc	gtg	ggg	gcc	ttc	tac	att	cct	gac	ggc	tcc	ttc	acc	aac	atc	591
Leu	Thr	Val	Gly	Ala	Phe	Tyr	Ile	Pro	Asp	Gly	Ser	Phe	Thr	Asn	Ile	
			155					160					165			
tgg	ttc	tac	ttc	ggc	gtc	gtg	ggc	tcc	ttc	ctc	ttc	atc	ctc	atc	cag	639
Trp	Phe	Tyr	Phe	Gly	Val	Val	Gly	Ser	Phe	Leu	Phe	Ile	Leu	Ile	Gln	
	170						175					180				
ctg	gtg	ctg	ctc	atc	gac	ttt	gcg	cac	tcc	tgg	aac	cag	cgg	tgg	ctg	687
Leu	Val	Leu	Leu	Ile	Asp	Phe	Ala	His	Ser	Trp	Asn	Gln	Arg	Trp	Leu	
	185					190					195					
ggc	aag	gcc	gag	gag	tgc	gat	tcc	cgt	gcc	tgg	tac	gca	ggc	ctc	ttc	735
Gly	Lys	Ala	Glu	Glu	Cys	Asp	Ser	Arg	Ala	Trp	Tyr	Ala	Gly	Leu	Phe	
200					205					210				215		
ttc	ttc	act	ctc	ctc	ttc	tac	ttg	ctg	tcg	atc	gcg	gcc	gtg	gcg	ctg	783
Phe	Phe	Thr	Leu	Leu	Phe	Tyr	Leu	Leu	Ser	Ile	Ala	Ala	Val	Ala	Leu	
			220						225				230			
atg	ttc	atg	tac	tac	act	gag	ccc	agc	ggc	tgc	cac	gag	ggc	aag	gtc	831
Met	Phe	Met	Tyr	Tyr	Thr	Glu	Pro	Ser	Gly	Cys	His	Glu	Gly	Lys	Val	
			235					240					245			
ttc	atc	agc	ctc	aac	ctc	acc	ttc	tgt	gtc	tgc	gtg	tcc	atc	gct	gct	879
Phe	Ile	Ser	Leu	Asn	Leu	Thr	Phe	Cys	Val	Cys	Val	Ser	Ile	Ala	Ala	
	250						255					260				
gtc	ctg	ccc	aag	gtc	cag	gac	gcc	cag	ccc	aac	tcg	ggg	ctg	ctg	cag	927
Val	Leu	Pro	Lys	Val	Gln	Asp	Ala	Gln	Pro	Asn	Ser	Gly	Leu	Leu	Gln	
	265					270					275					
gcc	tcg	gtc	atc	acc	ctc	tac	acc	atg	ttt	gtc	acc	tgg	tca	gcc	cta	975
Ala	Ser	Val	Ile	Thr	Leu	Tyr	Thr	Met	Phe	Val	Thr	Trp	Ser	Ala	Leu	
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Ser	Ser	Ile	Pro	Glu	Gln	Lys	Cys	Asn	Pro	His	Leu	Pro	Thr	Gln	Leu	
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ggc	aac	gag	aca	gtt	gtg	gca	ggc	ccc	gag	ggc	tat	gag	acc	cag	tgg	1071
Gly	Asn	Glu	Thr	Val	Val	Ala	Gly	Pro	Glu	Gly	Tyr	Glu	Thr	Gln	Trp	
			315					320					325			
tgg	gat	gcc	ccg	agc	att	gtg	ggc	ctc	atc	atc	ttc	ctc	ctg	tgc	acc	1119
Trp	Asp	Ala	Pro	Ser	Ile	Val	Gly	Leu	Ile	Ile	Phe	Leu	Leu	Cys	Thr	
	330						335					340				
ctc	ttc	atc	agt	ctg	cgc	tcc	tca	gac	cac	cgg	cag	gtg	aac	agc	ctg	1167

Leu	Phe	Ile	Ser	Leu	Arg	Ser	Ser	Asp	His	Arg	Gln	Val	Asn	Ser	Leu	
345						350					355					
atg	cag	acc	gag	gag	tgc	cca	cct	atg	cta	gac	gcc	aca	cag	cag	cag	1215
Met	Gln	Thr	Glu	Glu	Cys	Pro	Pro	Met	Leu	Asp	Ala	Thr	Gln	Gln	Gln	
360					365				370					375		
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Gln	Gln	Gln	Val	Ala	Ala	Cys	Glu	Gly	Arg	Ala	Phe	Asp	Asn	Glu	Gln	
				380					385					390		
gac	ggc	gtc	acc	tac	agc	tac	tcc	ttc	ttc	cac	ttc	tgc	ctg	gtg	ctg	1311
Asp	Gly	Val	Thr	Tyr	Ser	Tyr	Ser	Phe	Phe	His	Phe	Cys	Leu	Val	Leu	
			395					400					405			
gcc	tca	ctg	cac	gtc	atg	atg	acg	ctc	acc	aac	tgg	tac	aag	ccc	ggc	1359
Ala	Ser	Leu	His	Val	Met	Met	Thr	Leu	Thr	Asn	Trp	Tyr	Lys	Pro	Gly	
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Glu	Thr	Arg	Lys	Met	Ile	Ser	Thr	Trp	Thr	Ala	Val	Trp	Val	Lys	Ile	
	425					430					435					
tgt	gcc	agc	tgg	gca	ggg	ctg	ctc	ctc	tac	ctg	tgg	acc	ctg	gta	gcc	1455
Cys	Ala	Ser	Trp	Ala	Gly	Leu	Leu	Leu	Tyr	Leu	Trp	Thr	Leu	Val	Ala	
440					445				450					455		
cca	ctc	ctc	ctg	cgc	aac	cgc	gac	ttc	agc	tga	ggcagcct	cacagcctgc				1506
Pro	Leu	Leu	Leu	Arg	Asn	Arg	Asp	Phe	Ser	*						
				460					465							
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&lt;210&gt; 293

&lt;211&gt; 2389

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (136)..(1347)

&lt;400&gt; 293

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Met Phe Val Ala Ser Glu Arg Lys Met Arg Ala His	
1 5 10	
cag gtg ctc acc ttc ctc ctg ctc ttc gtg atc acc tcg gtg gcc tct	219
Gln Val Leu Thr Phe Leu Leu Leu Phe Val Ile Thr Ser Val Ala Ser	
15 20 25	
gaa aac gcc agc aca tcc cga ggc tgt ggg ctg gac ctc ctc cct cag	267
Glu Asn Ala Ser Thr Ser Arg Gly Cys Gly Leu Asp Leu Leu Pro Gln	
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Tyr Val Ser Leu Cys Asp Leu Asp Ala Ile Trp Gly Ile Val Val Glu	
45 50 55 60	
gcg gtg gcc ggg gcg ggc gcc ctg atc aca ctg ctc ctg atg ctc atc	363
Ala Val Ala Gly Ala Gly Ala Leu Ile Thr Leu Leu Leu Met Leu Ile	
65 70 75	
ctc ctg gtg cgg ctg ccc ttc atc aag gag aag gag aag aag agc cct	411
Leu Leu Val Arg Leu Pro Phe Ile Lys Glu Lys Glu Lys Lys Ser Pro	
80 85 90	
gtg ggc ctc cac ttt ctg ttc ctc ctg ggg acc ctg ggc ctc ttt ggg	459
Val Gly Leu His Phe Leu Phe Leu Leu Gly Thr Leu Gly Leu Phe Gly	
95 100 105	
ctg acg ttt gcc ttc atc atc cag gag gac gag acc atc tgc tct gtc	507
Leu Thr Phe Ala Phe Ile Ile Gln Glu Asp Glu Thr Ile Cys Ser Val	
110 115 120	
cgc cgc ttc ctc tgg ggc gtc ctc ttt gcg ctc tgc ttc tcc tgc ctg	555
Arg Arg Phe Leu Trp Gly Val Leu Phe Ala Leu Cys Phe Ser Cys Leu	
125 130 135 140	
ctg agc cag gca tgg cgc gtg cgg agg ctg gtg cgg cat ggc acg ggc	603
Leu Ser Gln Ala Trp Arg Val Arg Arg Leu Val Arg His Gly Thr Gly	
145 150 155	
ccc gcg ggc tgg cag ctg gtg ggc ctg gcg ctg tgc ctg atg ctg gtg	651
Pro Ala Gly Trp Gln Leu Val Gly Leu Ala Leu Cys Leu Met Leu Val	
160 165 170	
caa gtc atc atc gct gtg gag tgg ctg gtg ctc acc gtg ctg cgt gac	699
Gln Val Ile Ile Ala Val Glu Trp Leu Val Leu Thr Val Leu Arg Asp	
175 180 185	
aca agg cca gcc tgc gcc tac gag ccc atg gac ttt gtg atg gcc ctc	747
Thr Arg Pro Ala Cys Ala Tyr Glu Pro Met Asp Phe Val Met Ala Leu	
190 195 200	
atc tac gac atg gta ctg ctt gtg gtc acc ctg ggg ctg gcc ctc ttc	795
Ile Tyr Asp Met Val Leu Leu Val Val Thr Leu Gly Leu Ala Leu Phe	
205 210 215 220	
act ctg tgc ggc aag ttc aag agg tgg aag ctg aac ggg gcc ttc ctc	843
Thr Leu Cys Gly Lys Phe Lys Arg Trp Lys Leu Asn Gly Ala Phe Leu	
225 230 235	
ctc atc aca gcc ttc ctc tct gtg ctc atc tgg gtg gcc tgg atg acc	891
Leu Ile Thr Ala Phe Leu Ser Val Leu Ile Trp Val Ala Trp Met Thr	
240 245 250	



atg tac ctc ttc ggc aat gtc aag ctg cag cag ggg gat gcc tgg aac	939
Met Tyr Leu Phe Gly Asn Val Lys Leu Gln Gln Gly Asp Ala Trp Asn	
255 260 265	
gac ccc acc ttg gcc atc acg ctg gcg gcc agc ggc tgg gtc ttc gtc	987
Asp Pro Thr Leu Ala Ile Thr Leu Ala Ala Ser Gly Trp Val Phe Val	
270 275 280	
atc ttc cac gcc atc cct gag atc cac tgc acc ctt ctg cca gcc ctg	1035
Ile Phe His Ala Ile Pro Glu Ile His Cys Thr Leu Leu Pro Ala Leu	
285 290 295 300	
cag gag aac acg ccc aac tac ttc gac acg tgc cag ccc agg atg cgg	1083
Gln Glu Asn Thr Pro Asn Tyr Phe Asp Thr Ser Gln Pro Arg Met Arg	
305 310 315	
gag acg gcc ttc gag gag gac gtg cag ctg ccg cgg gcc tat atg gag	1131
Glu Thr Ala Phe Glu Glu Asp Val Gln Leu Pro Arg Ala Tyr Met Glu	
320 325 330	
aac aag gcc ttc tcc atg gat gaa cac aat gca gct ctc cga aca gca	1179
Asn Lys Ala Phe Ser Met Asp Glu His Asn Ala Ala Leu Arg Thr Ala	
335 340 345	
gga ttt ccc aac ggc agc ttg gga aaa aga ccc agt ggc agc ttg ggg	1227
Gly Phe Pro Asn Gly Ser Leu Gly Lys Arg Pro Ser Gly Ser Leu Gly	
350 355 360	
aaa aga ccc agc gct ccg ttt aga agc aac gtg tat cag cca act gag	1275
Lys Arg Pro Ser Ala Pro Phe Arg Ser Asn Val Tyr Gln Pro Thr Glu	
365 370 375 380	
atg gcc gtc gtg ctc aac ggt ggg acc atc cca act gct ccg cca agt	1323
Met Ala Val Val Leu Asn Gly Gly Thr Ile Pro Thr Ala Pro Pro Ser	
385 390 395	
cac aca gga aga cac ctt tgg tga aagactttaa gttccagaga atcagaattt	1377
His Thr Gly Arg His Leu Trp *	
400	
ctcttaccga ttgacctccc tggctgtgtc tttcttgagg gagaaatcgg taacagttgc	1437
cgaaccaggc cgcctcacag ccaggaaatt tggaaatcct agccaagggg atttcgtgta	1497
aatgtgaaca ctgacgaact gaaaagctaa caccgactgc ccgcccctcc cctgccacac	1557
acacagacac gtaataccag accaacctca atccccgcaa actaaagcaa agctaattgc	1617
aaatagtatt aggcctactg gaaaatgtgg ctgggaagac tgtttcatcc tctgggggta	1677
gaacagaacc aaattcacag ctgggtgggcc agactgggtg tggttggagg tggggggctc	1737
ccactcttat cacctctccc cagcaagtgc tggaccccag gtagcctctt ggagatgacc	1797
gttgcgttga ggacaaatgg ggactttgcc accggcttgc ctgggtggtt gcacatttca	1857
gggggggtcag gagagttaag gaggttgtgg gtgggattcc aaggtgaggg ccaactgaat	1917
cgtgggggtga gctttatagc cagtagaggt ggagggaacc tggcatgtgc caaagaagag	1977
gccctctggg tgatgaagtg accatcacat ttggaaagt atcaaccact gttccttcta	2037
tggggctctt gctctagtgt ctatggtgag aacacaggcc ccgccccttc cctttagtag	2097

ccatagaaat attctggcctt ggggcagcag tcccttcttc ccttgatcat ctgcacctgt	2157
tcctacactt acgggtgtat ctccaaatcc tctcccaatt ttattccctt attcatttca	2217
agagctccaa tggggtctcc agctgaaagc cccctccggg aggcagggtg gaaggcaggc	2277
accacggcag gttttccgcg atgatgtcac ctagcagggc ttcaggggtt cccactagga	2337
tgcagagatg acctctcgct gcctcacaag cagtgcaccc tcgggtcctt tc	2389

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<210> 294
<211> 1239
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (153) .. (572)
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gggagcttgttttgcgccagcggctgctgctgccactgctgtgctgtgggggc caggtcgccca	120
ggcaaaaagc cctcccacgt ttgaggggag tc atg agc cgt ttc ctg aat gtg Met Ser Arg Phe Leu Asn Val	173
15	5
tta aga agt tgg ctg gtt atg gtg tcc atc ata gcc atg ggg aac acg	221
Leu Arg Ser Trp Leu Val Met Val Ser Ile Ile Ala Met Gly Asn Thr	
101520	
ctg cag agc ttc cga gac cac act ttt ctc tat gaa aag ctc tac act	269
Leu Gln Ser Phe Arg Asp His Thr Phe Leu Tyr Glu Lys Leu Tyr Thr	
253035	
ggc aag cca aac ctt gtg aat ggc ctc caa gct cgg acc ttt ggg atc	317
Gly Lys Pro Asn Leu Val Asn Gly Leu Gln Ala Arg Thr Phe Gly Ile	
40455055	
tgg acg ctg ctc tca tca gtg att cgc tgc ctc tgt gcc att gac att	365
Trp Thr Leu Leu Ser Ser Val Ile Arg Cys Leu Cys Ala Ile Asp Ile	
606570	
cac aac aag acg ctc tat cac atc aca ctc tgg acc ttc ctc ctt gcc	413
His Asn Lys Thr Leu Tyr His Ile Thr Leu Trp Thr Phe Leu Leu Ala	
758085	
ctg ggg cat ttc ctc tct gag ttg ttt gtc tat gga act gca gct cc	461
Leu Gly His Phe Leu Ser Glu Leu Phe Val Tyr Gly Thr Ala Ala Pro	
9095100	
acg att ggc gtc ctg gca ccc ctg atg gtg gca agt ttc tcc atc ctg	509
Thr Ile Gly Val Leu Ala Pro Leu Met Val Ala Ser Phe Ser Ile Leu	
105110115	
ggt atg ctg gtc ggg ctc cgg tat cta gaa gta gaa cca gta tcc aga	557
Gly Met Leu Val Gly Leu Arg Tyr Leu Glu Val Glu Pro Val Ser Arg	
120125130135	
cag aaq aag aga aac tqaggccagc attatcacct ccaggacctt ctcgttttcc	612

Gln Lys Lys Arg Asn  
140

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accttgGCCA tcttcttCct tcgtcgtctc tcctctttaa tttcttttct attccatcat    672
ctgcccctttt attcaactttt agcctctttt ttttaattttt aaaattttaaa gatatgcata    732
ctgaaaagta tataacatgt acgtacaatt taaagaataa ttttaaagtg aatactacgt    792
aactccatcc aagtaagaa attgccagct tctcggaagc ccactgtgtc tccttcccct    852
acctgcaacc tcttccaggc tcccttttcc agccttcccc tttttccctt ttattttcat    912
gccttgattt gacttgtgtg gtgggaacat gtgaactatg aaacttaaac ctgctgcccA    972
cccagagcag ctgtgaccaa gggctgcctc aaggggttgt ccacgcaggt tgggctcctc   1032
tctgtgtgtg gacccaagac tctgaacctt ccaagggaca ggcagttctt ctaagaaggg   1092
ctcccctgtg tgtgagcaag accacagctc tccttctatc tacagatgca tgagggttgg   1152
aagagtctgg gctgttttta gaccttctgg tcagctgtat ttgtgtaacA acttttgtaa   1212
taaatagaaa aaccctcaaa aaaaaaa                                1239

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<210> 295  
<211> 1962  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (448)..(1179)

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<400> 295
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gcggcagcgg tggtgccggg gcagcggcgg cggcggttag ggcgcagggc gcgctgccat   120
gggcctggcc gggctgcagg cgggaagatg tccaagccct gcgcggtgga ggcggcgggc   180
gcggcggttg cagcgacggc cccggggccg gagatggttg agcggagggg cccggggagg   240
ccccgcaccg acggggagaa cgtatttacc gggcagtcaa agatctattc ctacatgagc   300
ccgaacaaat gctctggaat gcgtttcccc cttcaggaag agaactcagt tacacatcac   360
gaagtcaaat gccaggggaa accattagcc ggaatctaca ggaaacgaga agagaaaaga   420
aatgctggga acgcagtacg gagcgcc      atg aag tcc gag gaa cag aag atc    471
                                Met Lys Ser Glu Glu Gln Lys Ile
                                1                                5

aaa gac gcc agg aaa ggt ccc ctg gta cct ttt cca aac caa aaa tct    519
Lys Asp Ala Arg Lys Gly Pro Leu Val Pro Phe Pro Asn Gln Lys Ser
    10                                15                                20

gaa gca gca gaa cct cca aaa act cca ccc tca tct tgt gat tcc acc    567
Glu Ala Ala Glu Pro Pro Lys Thr Pro Pro Ser Ser Cys Asp Ser Thr
    25                                30                                35                                40

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aat gca gcc atc gcc aag caa gcc ctg aaa aag ccc atc aag ggc aaa	615
Asn Ala Ala Ile Ala Lys Gln Ala Leu Lys Lys Pro Ile Lys Gly Lys	
45 50 55	
cag gcc ccc cga aaa aaa gct caa gga aaa acg caa cag aat cgc aaa	663
Gln Ala Pro Arg Lys Lys Ala Gln Gly Lys Thr Gln Gln Asn Arg Lys	
60 65 70	
ctt acg gat ttc tac cct gtc cga agg agc tcc agg aag agc aaa gcc	711
Leu Thr Asp Phe Tyr Pro Val Arg Arg Ser Ser Arg Lys Ser Lys Ala	
75 80 85	
gag ctg cag tct gaa gaa agg aaa aga ata gat gaa ttg att gaa agt	759
Glu Leu Gln Ser Glu Glu Arg Lys Arg Ile Asp Glu Leu Ile Glu Ser	
90 95 100	
ggg aag gaa gaa gga atg aag att gac ctc atc gat ggc aaa ggc agg	807
Gly Lys Glu Glu Gly Met Lys Ile Asp Leu Ile Asp Gly Lys Gly Arg	
105 110 115 120	
ggt gtg att gcc acc aag cag ttc tcc cgg ggt gac ttt gtg gtg gaa	855
Gly Val Ile Ala Thr Lys Gln Phe Ser Arg Gly Asp Phe Val Val Glu	
125 130 135	
tac cac ggg gac ctc atc gag atc acc gac gcc aag aaa cgg gag gct	903
Tyr His Gly Asp Leu Ile Glu Ile Thr Asp Ala Lys Lys Arg Glu Ala	
140 145 150	
ctg tac gca cag gac cct tcc acg ggc tgc tac atg tac tat ttt cag	951
Leu Tyr Ala Gln Asp Pro Ser Thr Gly Cys Tyr Met Tyr Tyr Phe Gln	
155 160 165	
tat ctg agc aaa acc tac tgc gtg gat gca act aga gag aca aat cgc	999
Tyr Leu Ser Lys Thr Tyr Cys Val Asp Ala Thr Arg Glu Thr Asn Arg	
170 175 180	
cta gga aga ctg atc aat cac agc aaa tgt ggg aac tgc caa acc aaa	1047
Leu Gly Arg Leu Ile Asn His Ser Lys Cys Gly Asn Cys Gln Thr Lys	
185 190 195 200	
ctg cac gac atc gac ggc gta cct cac ctc atc ctc atc gcc tcc cga	1095
Leu His Asp Ile Asp Gly Val Pro His Leu Ile Leu Ile Ala Ser Arg	
205 210 215	
gac atc gcg gct ggg gag gag ctc ctg tat gac tat ggg gac cgc agc	1143
Asp Ile Ala Ala Gly Glu Glu Leu Leu Tyr Asp Tyr Gly Asp Arg Ser	
220 225 230	
aag gct tcc att gaa gcc cac ccg tgg ctg aag cat taac cgggtggccc	1193
Lys Ala Ser Ile Glu Ala His Pro Trp Leu Lys His	
235 240	
cgtgccctcc ccgccccact ttcccttctt caaaggacaa agtgccctca aagggaattg	1253
aatttttttt ttacacactt aatcttagcg gattacttca gatgttttta aaaagtatat	1313
taagatgcct ttctactgta gtattttaat atctgttaca ggtttccaag gtggacttga	1373
acagatggcc ttatattacc aaaactttta tattctagtt gtttttgtac tttttttgca	1433
tacaagccga acgtttgtgc ttcccgtgca tgcagtcaaa gactcagcac aggttttaga	1493
ggaaaatagtc aaacatgaac taggaagcca ggtgagtctc ctttctccag tggaagagcc	1553

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gggaccttcc cctgcacccc ccgacatcca gggacgggggt gtgaggaaga cgctgcctcc 1613
caatggcctg gacgggatgt ttccaagctc ttgttccctt aacgtctcaa caggcgctca 1673
ctgaagtgta tgaatatttt ttaaaaaggt ttttgcagta agctagtctt cccctctgct 1733
ttctcgaaag cttactgagc cctgggcccc aagcacgggc cgggcataga ttctctcttc 1793
cacaagctgc cgcttttctg ggcacettga agcatcaggg cgtgaaatca aactagatgt 1853
gggcagggag aggggttgcct acctgccctg ctggggcagg gtttcctgaa actgggttaa 1913
ttctttatag aaatgtgaac actgaattta ttttaaaaaa aaaaaaaaaa 1962

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<210> 296
<211> 1446
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (106)..(894)

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<220>
<221> misc_feature
<222> (1)...(1446)
<223> n = a,t,c or g

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<400> 296
ctgcgtgtgg taccgaccnn nnatccccggg tcgacgattt cgtgttccga actcaaagga 60

accagtgcc gggccacagc cgggtcacgt ggccggcggc ccccc atg acg tgc 114
                                     Met Thr Cys
                                     1

tgg ctg cgg ggc gtc acg gcg acg ttc ggg cga cct gcc gag tgg cca 162
Trp Leu Arg Gly Val Thr Ala Thr Phe Gly Arg Pro Ala Glu Trp Pro
      5              10              15

ggc tac ctc agt cac ctg tgt ggt cgc agt gct gcc atg gac ctg gga 210
Gly Tyr Leu Ser His Leu Cys Gly Arg Ser Ala Ala Met Asp Leu Gly
      20              25              30              35

ccc atg cgc aag agt tac cgc ggg gac cga gag gca ttt gag gag act 258
Pro Met Arg Lys Ser Tyr Arg Gly Asp Arg Glu Ala Phe Glu Glu Thr
              40              45              50

cat ctg acc tcc ctt gac cca gtg aaa cag ttt gct gcc tgg ttt gag 306
His Leu Thr Ser Leu Asp Pro Val Lys Gln Phe Ala Ala Trp Phe Glu
              55              60              65

gag gct gtt cag tgt cct gac ata ggg gaa gcc aat gcc atg tgt ctg 354
Glu Ala Val Gln Cys Pro Asp Ile Gly Glu Ala Asn Ala Met Cys Leu
              70              75              80

gct acc tgc acc aga gat gga aaa ccc tct gct cgc atg ttg ctg ctg 402
Ala Thr Cys Thr Arg Asp Gly Lys Pro Ser Ala Arg Met Leu Leu Leu
      85              90              95

aag ggc ttc ggg aaa gat ggc ttc cgc ttc ttc act aac ttc gag agt 450
Lys Gly Phe Gly Lys Asp Gly Phe Arg Phe Phe Thr Asn Phe Glu Ser

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100	105	110	115	
cga aaa gga aaa gag ctg gac tct aat ccc ttt gct tcc ctt gtc ttc				498
Arg Lys Gly Lys Glu Leu Asp Ser Asn Pro Phe Ala Ser Leu Val Phe				
	120	125	130	
tac tgg gag cca ctt aac cgt cag gtg cgt gtg gaa ggc cct gtg aag				546
Tyr Trp Glu Pro Leu Asn Arg Gln Val Arg Val Glu Gly Pro Val Lys				
	135	140	145	
aaa ctg cct gag gag gag gct gaa gtt gct act ttc cac ttc ccc ggc				594
Lys Leu Pro Glu Glu Glu Ala Glu Val Ala Thr Phe His Phe Pro Gly				
	150	155	160	
ccc aag agc agc cag att ggg gct gtg gtc agc cac cag agt tct gtg				642
Pro Lys Ser Ser Gln Ile Gly Ala Val Val Ser His Gln Ser Ser Val				
	165	170	175	
atc cct gat cgg gag tat ctg aga aag aaa aat gag gaa ctg gaa cag				690
Ile Pro Asp Arg Glu Tyr Leu Arg Lys Lys Asn Glu Glu Leu Glu Gln				
	180	185	190	195
ctc tac cag gat caa gag gtg ccc aag cca aaa tcc tgg ggt ggc tat				738
Leu Tyr Gln Asp Gln Glu Val Pro Lys Pro Lys Ser Trp Gly Gly Tyr				
	200	205	210	
gtc ctg tac cct cag gtg atg gag ttc tgg caa ggt caa acc aac cgc				786
Val Leu Tyr Pro Gln Val Met Glu Phe Trp Gln Gly Gln Thr Asn Arg				
	215	220	225	
ctg cat gac cgg ata gtc ttt cgg cgg ggc cta ccc aca gga gat tcc				834
Leu His Asp Arg Ile Val Phe Arg Arg Gly Leu Pro Thr Gly Asp Ser				
	230	235	240	
cct ttg ggg ccc atg acc cac cgc ggg gag gaa gac tgg ctc tat gag				882
Pro Leu Gly Pro Met Thr His Arg Gly Glu Glu Asp Trp Leu Tyr Glu				
	245	250	255	
aga ctt gca cct taa ctctgggacc tgctggccca gaggaggagct agggctaggt				937
Arg Leu Ala Pro				
	260			
gtcaagagag ggtgtgggat tgggaccag gcccttcttt cttaaactcaa ccatttccc				997
tccttaccac ttattctcag gactcttcag agctaattcct ctaagttctc tgtactcagt				1057
tggttctcag ttagctgggc aagtggagtg taatggtggc gtagagaatc acaaattggaa				1117
aataattcca taattatttt tttagccttg cctatgattg attaggatag ctccctctag				1177
gggtagcagc cgggtgtgact ccttttctgg tgacagacag ggccccagca gccctgtctg				1237
ttaccatgtg agtcatactg gccaaagctt agtcctagca tatgcacctg agccaacctg				1297
gccaatcaga ttgttttgtc aataatttga aatttgaact cggagagatc cagaaccttg				1357
ggagtcatta aagccaagtc attcatagca gccaggaaac aataggaacc aacagcctct				1417
gcctgctgct attgcaattc ccaggatct				1446

<211> 1783  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (78)..(1214)

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<400> 297
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gcgagtcctgg totcaaa  atg gag gta aaa ccg ccg ccc ggt cgc ccc cag      110
      Met Glu Val Lys Pro Pro Pro Gly Arg Pro Gln
              1              5              10

ccc gac tcc ggc cgt cgc cgt cgc cgc cgg ggg gag gag ggc cat gat      158
Pro Asp Ser Gly Arg Arg Arg Arg Arg Arg Gly Glu Glu Gly His Asp
              15              20              25

cca aag gaa cca gag cag ttg aga aaa ctg ttt att ggt ggt ctg agc      206
Pro Lys Glu Pro Glu Gln Leu Arg Lys Leu Phe Ile Gly Gly Leu Ser
              30              35              40

ttt gaa act aca gat gat agt tta cga gaa cat ttt gag aaa tgg ggc      254
Phe Glu Thr Thr Asp Asp Ser Leu Arg Glu His Phe Glu Lys Trp Gly
              45              50              55

aca ctc aca gat tgt gtg gta atg aga gac ccc caa aca aaa cgt tcc      302
Thr Leu Thr Asp Cys Val Val Met Arg Asp Pro Gln Thr Lys Arg Ser
              60              65              70              75

agg ggc ttt ggt ttt gtg act tat tct tgt gtt gaa gag gtg gat gca      350
Arg Gly Phe Gly Phe Val Thr Tyr Ser Cys Val Glu Glu Val Asp Ala
              80              85              90

gca atg tgt gct cga cca cac aag gtt gat ggg cgt gta gtg gaa cca      398
Ala Met Cys Ala Arg Pro His Lys Val Asp Gly Arg Val Val Glu Pro
              95              100              105

aag aga gct gtt tct aga gag gat tct gta aag cct ggt gcc cat cta      446
Lys Arg Ala Val Ser Arg Glu Asp Ser Val Lys Pro Gly Ala His Leu
              110              115              120

aca gtg aag aaa att ttt gtt ggt ggt att aaa gaa gat aca gaa gaa      494
Thr Val Lys Lys Ile Phe Val Gly Gly Ile Lys Glu Asp Thr Glu Glu
              125              130              135

tat aat ttg aga gac tac ttt gaa aag tat ggc aag att gaa acc ata      542
Tyr Asn Leu Arg Asp Tyr Phe Glu Lys Tyr Gly Lys Ile Glu Thr Ile
              140              145              150              155

gaa gtt atg gaa gac agg cag agt gga aaa aag aga gga ttt gct ttt      590
Glu Val Met Glu Asp Arg Gln Ser Gly Lys Lys Arg Gly Phe Ala Phe
              160              165              170

gta act ttt gat gat cat gat aca gtt gat aaa att gtt gtt cag aaa      638
Val Thr Phe Asp Asp His Asp Thr Val Asp Lys Ile Val Val Gln Lys
              175              180              185

tac cac act att aat ggg cat aac tgt gaa gtg aaa aag gcc ctt gct      686
Tyr His Thr Ile Asn Gly His Asn Cys Glu Val Lys Lys Ala Leu Ala
              190              195              200

aaa caa gtg atg cag ccg gct gga tca cag agg ggt cgt gga ggt gga      734

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Lys	Gln	Val	Met	Gln	Pro	Ala	Gly	Ser	Gln	Arg	Gly	Arg	Gly	Gly	Gly	
205						210					215					
tct	ggc	aat	tgt	atg	ggt	cac	aga	gga	aac	ttt	gga	ggt	ggt	gga	ggt	782
Ser	Gly	Asn	Cys	Met	Gly	His	Arg	Gly	Asn	Phe	Gly	Gly	Gly	Gly	Gly	
220					225				230					235		
aat	ttt	ggc	cgt	gat	gga	aac	ttt	ggt	gga	aga	gga	ggc	tat	ggt	ggt	830
Asn	Phe	Gly	Arg	Asp	Gly	Asn	Phe	Gly	Gly	Arg	Gly	Gly	Tyr	Gly	Gly	
			240					245					250			
gga	ggt	ggt	ggc	agc	aga	ggt	agt	tat	gga	gga	ggt	gat	ggt	gga	tat	878
Gly	Gly	Gly	Gly	Ser	Arg	Gly	Ser	Tyr	Gly	Gly	Gly	Asp	Gly	Gly	Tyr	
			255				260					265				
aat	gga	ttt	gga	ggt	gat	ggt	ggc	aac	tat	ggc	ggt	ggt	cct	ggt	tat	926
Asn	Gly	Phe	Gly	Gly	Asp	Gly	Gly	Asn	Tyr	Gly	Gly	Gly	Pro	Gly	Tyr	
	270					275						280				
agt	agt	aga	ggg	ggc	tat	ggt	ggt	ggt	gga	cca	gga	tat	gga	aac	caa	974
Ser	Ser	Arg	Gly	Gly	Tyr	Gly	Gly	Gly	Gly	Pro	Gly	Tyr	Gly	Asn	Gln	
	285					290					295					
ggt	ggt	gga	tat	ggt	gga	ggt	gga	gga	tat	gat	ggt	tac	aat	gaa	gga	1022
Gly	Gly	Gly	Tyr	Gly	Gly	Gly	Gly	Gly	Tyr	Asp	Gly	Tyr	Asn	Glu	Gly	
300				305					310				315			
gga	aat	ttt	ggc	ggt	ggt	aac	tat	ggt	ggt	ggt	ggg	aac	tat	aat	gat	1070
Gly	Asn	Phe	Gly	Gly	Gly	Asn	Tyr	Gly	Gly	Gly	Gly	Asn	Tyr	Asn	Asp	
			320					325					330			
ttt	gga	aat	tat	agt	gga	caa	cag	caa	tca	aat	tat	gga	ccc	atg	aaa	1118
Phe	Gly	Asn	Tyr	Ser	Gly	Gln	Gln	Gln	Ser	Asn	Tyr	Gly	Pro	Met	Lys	
		335					340						345			
ggg	ggc	agt	ttt	ggt	gga	aga	agc	tcg	ggc	agt	ccc	tat	ggt	ggt	ggt	1166
Gly	Gly	Ser	Phe	Gly	Gly	Arg	Ser	Ser	Gly	Ser	Pro	Tyr	Gly	Gly	Gly	
	350					355					360					
tat	gga	tct	ggt	ggt	gga	agt	ggt	gga	tat	ggt	agc	aga	agg	ttc	taa	1214
Tyr	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Tyr	Gly	Ser	Arg	Arg	Phe	*	
	365					370				375						
aaacagcaga aaagggtac agttcttagc aggagagaga gcgaggagtt gtcaggaaag																1274
ctgcaggtta ctttgagaca gtctgtcccaa atgcattaga ggaactgtaa aaatctgcca																1334
cagaaggaac gatgatccat agtcagaaaa gttactgcag cttaaacagg aaacccttct																1394
tggttcaggac tgtcatagcc acagtttgca aaaagtgagc ctattgatta atgcaatgta																1454
gtgtcaatta gatgtacatt cctgaggtct tttatctggt gtagctttgt ctttttcttt																1514
ttcttttcat tacatcaggt atattgccct gtaaattgtg gtagtggtac caggaataaa																1574
aaattaagga atttttaact tttcaatatt tgtgtagttc agtttttcta catttttagta																1634
cagaaacttt aacaaaatgc agtttcgaag gtgtttccct gtgagttaac aagtaaagaa																1694
gatcattggt aattactatt ttgtatgaat tttgctaaag ttaactgtaa agaaacacct																1754
gctgacttgc agtttaaggg gaatctatt																1783



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 <213> Homo sapiens

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 Met Ala Ala Leu Arg Asp Ala Glu Ile Gln Lys  
 1 5 10  
 gac gtg cag acc tac tac ggg cag gtg ctg aag aga tcg gca gac ctc 158  
 Asp Val Gln Thr Tyr Tyr Gly Gln Val Leu Lys Arg Ser Ala Asp Leu  
 15 20 25  
 cag acc aac ggc tgt gtc acc aca gcc agg ccg gtc ccc aag cac atc 206  
 Gln Thr Asn Gly Cys Val Thr Thr Ala Arg Pro Val Pro Lys His Ile  
 30 35 40  
 cggtgaa gcc ttg caa aat gta cac gaa gaa gta gcc cta aga tat tat 254  
 Arg Glu Ala Leu Gln Asn Val His Glu Glu Val Ala Leu Arg Tyr Tyr  
 45 50 55  
 ggc tgt ggt ctg gtg atc cct gag cat cta gaa aac tgc tgg att ttg 302  
 Gly Cys Gly Leu Val Ile Pro Glu His Leu Glu Asn Cys Trp Ile Leu  
 60 65 70 75  
 gat ctg ggt agt gga agt ggc aga gat tgc tat gta ctt agc cag ctg 350  
 Asp Leu Gly Ser Gly Ser Gly Arg Asp Cys Tyr Val Leu Ser Gln Leu  
 80 85 90  
 gtt ggt gaa aaa gga cac gtg act gga ata gac atg acc aaa ggc cag 398  
 Val Gly Glu Lys Gly His Val Thr Gly Ile Asp Met Thr Lys Gly Gln  
 95 100 105  
 gtg gaa gtg gct gaa aag tat ctt gac tat cac atg gaa aaa tat ggc 446  
 Val Glu Val Ala Glu Lys Tyr Leu Asp Tyr His Met Glu Lys Tyr Gly  
 110 115 120  
 ttc cag gca tct aat gtg act ttt att cat ggc tac att gag aag ttg 494  
 Phe Gln Ala Ser Asn Val Thr Phe Ile His Gly Tyr Ile Glu Lys Leu  
 125 130 135  
 gga gag gct gga atc aag aat gag agc cat gat att gtt gta tca aac 542  
 Gly Glu Ala Gly Ile Lys Asn Glu Ser His Asp Ile Val Val Ser Asn  
 140 145 150 155  
 tgt gtt att aac ctt gtg cct gat aaa caa caa gtg ctt cag gag gca 590  
 Cys Val Ile Asn Leu Val Pro Asp Lys Gln Gln Val Leu Gln Glu Ala  
 160 165 170  
 tat cgg gtg ctg aag cat ggt ggg gag tta tat ttc agt gac gtc tat 638  
 Tyr Arg Val Leu Lys His Gly Gly Glu Leu Tyr Phe Ser Asp Val Tyr  
 175 180 185  
 acg agc ctt gaa ctg cca gaa gaa atc agg aca cac aaa gtt tta tgg 686  
 Thr Ser Leu Glu Leu Pro Glu Glu Ile Arg Thr His Lys Val Leu Trp

190	195	200	
ggt gag tgt ctg ggt ggt gct tta tac tgg aag gaa ctt gct gtc ctt			734
Gly Glu Cys Leu Gly Gly Ala Leu Tyr Trp Lys Glu Leu Ala Val Leu			
205	210	215	
gct caa aaa att ggg ttc tgc cct cca cgt ttg gtc act gcc aat ctc			782
Ala Gln Lys Ile Gly Phe Cys Pro Pro Arg Leu Val Thr Ala Asn Leu			
220	225	230	235
att aca att caa aac aag gaa ctg gaa aga gtt atc ggt gac tgt cgt			830
Ile Thr Ile Gln Asn Lys Glu Leu Glu Arg Val Ile Gly Asp Cys Arg			
	240	245	250
ttt gtt tct gca aca ttt cgc ctc ttc aaa cac tct aag aca gga cca			878
Phe Val Ser Ala Thr Phe Arg Leu Phe Lys His Ser Lys Thr Gly Pro			
	255	260	265
acc aag aga tgc caa gtt att tac aat gga gga att aca gga cat gaa			926
Thr Lys Arg Cys Gln Val Ile Tyr Asn Gly Gly Ile Thr Gly His Glu			
	270	275	280
aaa gaa cta atg ttt gat gcc aat ttt aca ttt aag gaa ggt gaa att			974
Lys Glu Leu Met Phe Asp Ala Asn Phe Thr Phe Lys Glu Gly Glu Ile			
	285	290	295
gtt gaa gtg gat gaa gaa aca gca gct atc ttg aag aat tca aga ttt			1022
Val Glu Val Asp Glu Glu Thr Ala Ala Ile Leu Lys Asn Ser Arg Phe			
300	305	310	315
gct caa gat ttt ctg atc aga cca att gga gag aag ttg cca aca tct			1070
Ala Gln Asp Phe Leu Ile Arg Pro Ile Gly Glu Lys Leu Pro Thr Ser			
	320	325	330
gga ggc tgt tct gct ttg gag tta aag gat ata atc aca cat cca ttt			1118
Gly Gly Cys Ser Ala Leu Glu Leu Lys Asp Ile Ile Thr His Pro Phe			
	335	340	345
aag ctt gca gaa aag ttt gac cct atg aat tcc aca cga gcc cct gat			1166
Lys Leu Ala Glu Lys Phe Asp Pro Met Asn Ser Thr Arg Ala Pro Asp			
	350	355	360
gct tct taa ggctgct gtgtatcaaa aaatagctgc tgaagccatt gcctaccag			1222
Ala Ser *			
365			
tgaccactca agtgtgcggg aaagcacctc ctgagtatga acccagtttc ccccttaccg			1282
gcagctgtac aacgcaaacg caccatccct tgagcgcggc cataaacgaa ttattttctcc			1342
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 <212> DNA  
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tcgcaggccg aggagac atg gct gca ctt cgt gac gct gag ata cag aag 110  
Met Ala Ala Leu Arg Asp Ala Glu Ile Gln Lys  
1 5 10

gac gtg cag acc tac tac ggg cag gtg ctg aag aga tcg gca gac ctc 158  
Asp Val Gln Thr Tyr Tyr Gly Gln Val Leu Lys Arg Ser Ala Asp Leu  
15 20 25

cag acc aac ggc tgt gtc acc aca gcc agg ccg gtc ccc aag cac atc 206  
Gln Thr Asn Gly Cys Val Thr Thr Ala Arg Pro Val Pro Lys His Ile  
30 35 40

cgg gaa gcc ttg caa aat gta cac gaa gaa gta gcc cta aga tat tat 254  
Arg Glu Ala Leu Gln Asn Val His Glu Glu Val Ala Leu Arg Tyr Tyr  
45 50 55

ggc tgt ggt ctg gtg atc cct gag cat cta gaa aac tgc tgg att ttg 302  
Gly Cys Gly Leu Val Ile Pro Glu His Leu Glu Asn Cys Trp Ile Leu  
60 65 70 75

gat ctg ggt agt gga agt ggc aga gat tgc tat gta ctt agc cag ctg 350  
Asp Leu Gly Ser Gly Ser Gly Arg Asp Cys Tyr Val Leu Ser Gln Leu  
80 85 90

gtt ggt gaa aaa gga cac gtg act gga ata gac atg acc aaa ggc cag 398  
Val Gly Glu Lys Gly His Val Thr Gly Ile Asp Met Thr Lys Gly Gln  
95 100 105

gtg gaa gtg gct gaa aag tat ctt gac tat cac atg gaa aaa tat ggc 446  
Val Glu Val Ala Glu Lys Tyr Leu Asp Tyr His Met Glu Lys Tyr Gly  
110 115 120

ttc cag gca tct aat gtg act ttt att cat ggc tac att gag aag ttg 494  
Phe Gln Ala Ser Asn Val Thr Phe Ile His Gly Tyr Ile Glu Lys Leu  
125 130 135

gga gag gct gga atc aag aat gag agc cat gat att gtt gta tca aac 542  
Gly Glu Ala Gly Ile Lys Asn Glu Ser His Asp Ile Val Val Ser Asn  
140 145 150 155

tgt gtt att aac ctt gtg cct gat aaa caa caa gtg ctt cag gag gca 590  
Cys Val Ile Asn Leu Val Pro Asp Lys Gln Gln Val Leu Gln Glu Ala  
160 165 170

tat cgg gtg ctg aag gtt gca aaa ggt agt aaa tcc gag gtg aca gtt 638  
Tyr Arg Val Leu Lys Val Ala Lys Gly Ser Lys Ser Glu Val Thr Val  
175 180 185

gtc act gaa tgt gtt aag cat ggt ggg gag tta tat ttc agt gac gtc 686  
Val Thr Glu Cys Val Lys His Gly Gly Glu Leu Tyr Phe Ser Asp Val  
190 195 200

tat acg agc ctt gaa ctg cca gaa gaa atc agg aca cac aaa gtt tta 734  
Tyr Thr Ser Leu Glu Leu Pro Glu Glu Ile Arg Thr His Lys Val Leu  
205 210 215

tgg ggt gag tgt ctg ggt ggt gct tta tac tgg aag gaa ctt gct gtc 782  
Trp Gly Glu Cys Leu Gly Gly Ala Leu Tyr Trp Lys Glu Leu Ala Val  
220 225 230 235

ctt gct caa aaa att ggg ttc tgc cct cca cgt ttg gtc act gcc aat 830

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Leu Ala Gln Lys Ile Gly Phe Cys Pro Pro Arg Leu Val Thr Ala Asn
      240 .                245                250

ctc att aca att caa aac aag gaa ctg gaa aga gtt atc ggt gac tgt      878
Leu Ile Thr Ile Gln Asn Lys Glu Leu Glu Arg Val Ile Gly Asp Cys
      255                260                265

cgt ttt gtt tct gca aca ttt cgc ctc ttc aaa cac tct aag aca gga      926
Arg Phe Val Ser Ala Thr Phe Arg Leu Phe Lys His Ser Lys Thr Gly
      270                275                280

cca acc aag aga tgc caa gtt att tac aat gga gga att aca gga cat      974
Pro Thr Lys Arg Cys Gln Val Ile Tyr Asn Gly Gly Ile Thr Gly His
      285                290                295

gaa aaa gaa cta atg ttt gat gcc aat ttt aca ttt aag gaa ggt gaa      1022
Glu Lys Glu Leu Met Phe Asp Ala Asn Phe Thr Phe Lys Glu Gly Glu
      300                305                310                315

att gtt gaa gtg gat gaa gaa aca gca gct atc ttg aag aat tca aga      1070
Ile Val Glu Val Asp Glu Glu Thr Ala Ala Ile Leu Lys Asn Ser Arg
      320                325                330

ttt gct caa gat ttt ctg atc aga cca att gga gag aag ttg cca aca      1118
Phe Ala Gln Asp Phe Leu Ile Arg Pro Ile Gly Glu Lys Leu Pro Thr
      335                340                345

tct gga ggc tgt tct gct ttg gag tta aag gat ata atc aca cat cca      1166
Ser Gly Gly Cys Ser Ala Leu Glu Leu Lys Asp Ile Ile Thr His Pro
      350                355                360

ttt aag ctt gca gaa aag ttt gac cct atg aat tcc aca cga gcc cct      1214
Phe Lys Leu Ala Glu Lys Phe Asp Pro Met Asn Ser Thr Arg Ala Pro
      365                370                375

gat gct tct taa ggc tgctgtgtat caaaaaatag ctgctgaagc cattgcctac      1269
Asp Ala Ser *
      380

cacgtgacca ctcaagtgtg cgggaaagca cctcctgagt atgaacccag tttccccctt      1329

accggcagct gtacaacgca aacgcacccat cccttgagcg cggccataaa cgaattatct      1389

ctcctaggcg tgtgttagtg atgcacagga attacttg      1427

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<210> 300
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<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (1)..(627)

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Lys Leu Val Arg Leu Gln Val Pro Val Arg Asn Ser Arg Val Asp Pro
  1              5              10              15

cgc gtc cgc ctg ggt tcg aac acg gca ccc gca ctg cgc gtc atg gtg      96
Arg Val Arg Leu Gly Ser Asn Thr Ala Pro Ala Leu Arg Val Met Val

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20	25	30	
cag gcc tgg tat atg gac gac gcc ccg ggc gac ccg cgg caa ccc cac Gln Ala Trp Tyr Met Asp Asp Ala Pro Gly Asp Pro Arg Gln Pro His 35 40 45			144
cgc ccc gac ccc ggc cgc cca gtg ggc ctg gag cag ctg cgg cgg ctc Arg Pro Asp Pro Gly Arg Pro Val Gly Leu Glu Gln Leu Arg Arg Leu 50 55 60			192
ggg gtg ctc tac tgg aag ctg gat gct gac aaa tat gag aat gat cca Gly Val Leu Tyr Trp Lys Leu Asp Ala Asp Lys Tyr Glu Asn Asp Pro 65 70 75 80			240
gaa tta gaa aag atc cga aga gag agg aac tac tcc tgg atg gac atc Glu Leu Glu Lys Ile Arg Arg Glu Arg Asn Tyr Ser Trp Met Asp Ile 85 90 95			288
ata acc ata tgc aaa gat aaa cta cca aat tat gaa gaa aag att aag Ile Thr Ile Cys Lys Asp Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys 100 105 110			336
atg ttc tac gag gag cat ttg cac ttg gac gat gag atc cgc tac atc Met Phe Tyr Glu Glu His Leu His Leu Asp Asp Glu Ile Arg Tyr Ile 115 120 125			384
ctg gat ggc agt ggg tac ttc gat gtg agg gac aag gag gac cag tgg Leu Asp Gly Ser Gly Tyr Phe Asp Val Arg Asp Lys Glu Asp Gln Trp 130 135 140			432
atc cgg atc ttc atg gag aag gga gac atg gtg acg ctc ccc gcg ggg Ile Arg Ile Phe Met Glu Lys Gly Asp Met Val Thr Leu Pro Ala Gly 145 150 155 160			480
atc tat cac cgc ttc acg gtg gac gag aag aac tac acg aag gcc atg Ile Tyr His Arg Phe Thr Val Asp Glu Lys Asn Tyr Thr Lys Ala Met 165 170 175			528
cgg ctg ttt gtg gga gaa ccg gtg tgg aca gcg tac aac cgg ccc gct Arg Leu Phe Val Gly Glu Pro Val Trp Thr Ala Tyr Asn Arg Pro Ala 180 185 190			576
gac cat ttt gaa gcc cgc ggg cag tac gtg aaa ttt ctg gca cag acc Asp His Phe Glu Ala Arg Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr 195 200 205			624
gcc tagc agtgctgcct gggaactaac acgcgcctcg taaaggtccc caatgtaatg Ala			681
actgagcaga aaatcaatca ctttctcttt gcttttagag gatagccttg aggctagggt			741
atctttcctt tgtaagatta ttgatcaga atattttgta atgaaaggat ctagaaagca			801
acttggaagt gtaaagagtc accttcattt tctgtaactc aatcaagact ggtgggtcca			861
tggcctgtg ttagttcatg cattcagttg agtcccaaat gaaagtttca tctcccga			921
tgcagttcct tagatgcccc tctggacgtg atgccgcgcc tgccatgtaa gaagtgcaa			981
tctagataa cacagctagc cagatagaag acactttttt ctccaaaatg atgccttggg			1041
gtggggagtg gtagggggaa gagctcccca ccctaagggg cacacactga gttgcttatg			1101

ccacttcctt gttcaaaata aagtaactgc cttaatctta tactcatggc ttggagttac 1161  
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 cttctataat tgttcttata gataagtaat ttatatatga gctgtgtag tattttttca 1281  
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 cataaatttt ctactcaaca attccgagat aggattatgc ctagtgtgac atatcacaga 1401  
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 cccaccggtg gtgtgatgat gccatatacc gcagggttg cttctgtcaa gtgtgactct 1641  
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 tgggcatt 1709

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 <212> DNA  
 <213> Homo sapiens

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 ggaaaaggcg ctccgctc atg ggg atc cag acg agc ccc gtc ctg ctg gcc 170  
 Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala  
 1 5 10  
 tcc ctg ggg gtg ggg ctg gtc act ctg ctc ggc ctg gct gtg ggc tcc 218  
 Ser Leu Gly Val Gly Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser  
 15 20 25  
 tac ttg gtt cgg agg tcc cgc cgg cct cag gtc act ctc ctg gac ccc 266  
 Tyr Leu Val Arg Arg Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro  
 30 35 40  
 aat gaa aag tac ctg cta cga ctg cta gac aag acg act gtg agc cac 314  
 Asn Glu Lys Tyr Leu Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His  
 45 50 55  
 aac acc aag agg ttc cgc ttt gcc ctg ccc acc gcc cac cac act ctg 362  
 Asn Thr Lys Arg Phe Arg Phe Ala Leu Pro Thr Ala His His Thr Leu  
 60 65 70 75  
 ggg ctg cct gtg ggc aaa cat atc tac ctc tcc acc cga att gat ggc 410  
 Gly Leu Pro Val Gly Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly  
 80 85 90  
 agc ctg gtc atc agg cca tac act cct gtc acc agt gat gag gat caa 458

Ser	Leu	Val	Ile	Arg	Pro	Tyr	Thr	Pro	Val	Thr	Ser	Asp	Glu	Asp	Gln	
			95					100					105			
ggc	tat	gtg	gat	ctt	gtc	atc	aag	gtc	tac	ctg	aag	ggg	gtg	cac	ccc	506
Gly	Tyr	Val	Asp	Leu	Val	Ile	Lys	Val	Tyr	Leu	Lys	Gly	Val	His	Pro	
		110					115					120				
aaa	ttt	cct	gag	gga	ggg	aag	atg	tct	cag	tac	ctg	gat	agc	ctg	aag	554
Lys	Phe	Pro	Glu	Gly	Gly	Lys	Met	Ser	Gln	Tyr	Leu	Asp	Ser	Leu	Lys	
		125				130					135					
gtt	ggg	gat	gtg	gtg	gag	ttt	cgg	ggg	cca	agc	ggg	ttg	ctc	act	tac	602
Val	Gly	Asp	Val	Val	Glu	Phe	Arg	Gly	Pro	Ser	Gly	Leu	Leu	Thr	Tyr	
140					145				150					155		
act	gga	aaa	ggg	cat	ttt	aac	att	cag	ccc	aac	aag	aaa	tct	cca	cca	650
Thr	Gly	Lys	Gly	His	Phe	Asn	Ile	Gln	Pro	Asn	Lys	Lys	Ser	Pro	Pro	
				160				165					170			
gaa	ccc	cga	gtg	gcg	aag	aaa	ctg	gga	atg	att	gcc	ggc	ggg	aca	gga	698
Glu	Pro	Arg	Val	Ala	Lys	Lys	Leu	Gly	Met	Ile	Ala	Gly	Gly	Thr	Gly	
			175				180						185			
atc	acc	cca	atg	cta	cag	ctg	atc	cgg	gcc	atc	ctg	aaa	gtc	cct	gaa	746
Ile	Thr	Pro	Met	Leu	Gln	Leu	Ile	Arg	Ala	Ile	Leu	Lys	Val	Pro	Glu	
		190				195					200					
gat	cca	acc	cag	tgc	ttt	ctg	ctt	ttt	gcc	aac	cag	aca	gaa	aag	gat	794
Asp	Pro	Thr	Gln	Cys	Phe	Leu	Leu	Phe	Ala	Asn	Gln	Thr	Glu	Lys	Asp	
		205				210					215					
atc	atc	ttg	cgg	gag	gac	tta	gag	gaa	ctg	cag	gcc	cgc	tat	ccc	aat	842
Ile	Ile	Leu	Arg	Glu	Asp	Leu	Glu	Glu	Leu	Gln	Ala	Arg	Tyr	Pro	Asn	
220				225					230				235			
cgc	ttt	aag	ctc	tgg	ttc	act	ctg	gat	cat	ccc	cca	aaa	gat	tgg	gcc	890
Arg	Phe	Lys	Leu	Trp	Phe	Thr	Leu	Asp	His	Pro	Pro	Lys	Asp	Trp	Ala	
			240					245					250			
tac	agc	aag	ggc	ttt	gtg	act	gcc	gac	atg	atc	cgg	gaa	cac	ctg	ccc	938
Tyr	Ser	Lys	Gly	Phe	Val	Thr	Ala	Asp	Met	Ile	Arg	Glu	His	Leu	Pro	
			255				260					265				
gct	cca	ggg	gat	gat	gtg	ctg	gta	ctg	ctt	tgt	ggg	cca	ccc	cca	atg	986
Ala	Pro	Gly	Asp	Asp	Val	Leu	Val	Leu	Leu	Cys	Gly	Pro	Pro	Pro	Met	
		270				275						280				
gtg	cag	ctg	gcc	tgc	cat	ccc	aac	ttg	gac	aaa	ctg	ggc	tac	tca	caa	1034
Val	Gln	Leu	Ala	Cys	His	Pro	Asn	Leu	Asp	Lys	Leu	Gly	Tyr	Ser	Gln	
		285				290					295					
aag	atg	cga	ttc	acc	tac	tga	gc	atcctccagc	ttccctgggtg	ctgttcgctg						1087
Lys	Met	Arg	Phe	Thr	Tyr	*										
300				305												
cagttgttcc	ccatcagttac	tcaagcacta	taagccttag	attcctttcc	tcagagtttc											1147
aggtttttttc	agttacatct	agagctgaaa	tctggatagt	acctgcagga	acaatatctc											1207
tgtagccatg	gaagagggcc	aaggctcagt	cactccttgg	atggcctcct	aaatctcccc											1267
gtggcaacag	gtccaggaga	ggcccatgga	gcagtctctt	ccatggagta	agaaggaagg											1327
gagcatgtac	gcttggtcca	agattggcta	gttccttgat	agcatcttac	tctcaccttc											1387

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aacctatgag caaatctgta tgtgtgagta taagttgagc atagcatact tccagaggtg 1507
gtcttatgga gatggcaaga aaggaggaaa tgatttcttc agatctcaaa ggagtctgaa 1567
atatcatatt tctgtgtgtg tctctctcag ccctgcccc ggctagaggg aaacagctac 1627
tgataatcga aaactgctgt ttgtggcagg aacccctggc tgtgcaaata aatggggctg 1687
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<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (127)..(1110)

```

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<220>
<221> misc_feature
<222> (1)...(1635)
<223> n = a,t,c or g

```

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<400> 302
atttggccct cgaggccaag aattcggcac gaggttacgc acgtcctgat tctcctggag 60
tctccagccc gcccagtggc cgcagtcacc caggtccaga ggcggcggta tcacaggctc 120
tccgac atg tct atg ctg gct gaa cgt cgg cgg aag cag aag tgg gct 168
      Met Ser Met Leu Ala Glu Arg Arg Arg Lys Gln Lys Trp Ala
        1             5             10

gtg gat cct cag aac act gcc tgg agt aat gac gat tcc aag ttt ggc 216
Val Asp Pro Gln Asn Thr Ala Trp Ser Asn Asp Asp Ser Lys Phe Gly
  15             20             25             30

cag cgg atg cta gag aag atg ggg tgg tct aaa gga aag ggt tta ggg 264
Gln Arg Met Leu Glu Lys Met Gly Trp Ser Lys Gly Lys Gly Leu Gly
      35             40             45

gct cag gag caa gga gcc aca gat cat att aaa gtt caa gtg aaa aat 312
Ala Gln Glu Gln Gly Ala Thr Asp His Ile Lys Val Gln Val Lys Asn
      50             55             60

aac cac ctg gga ctc gga gct acc atc aat aat gaa gac aac tgg att 360
Asn His Leu Gly Leu Gly Ala Thr Ile Asn Asn Glu Asp Asn Trp Ile
      65             70             75

gcc cat cag gat gat ttt aac cag ctt ctg gcc gaa ctg aac act tgc 408
Ala His Gln Asp Asp Phe Asn Gln Leu Leu Ala Glu Leu Asn Thr Cys
      80             85             90

cat ggg cag gaa acc aca gat tcc tcg gac aag aag gaa aag aaa tct 456
His Gly Gln Glu Thr Thr Asp Ser Ser Asp Lys Lys Glu Lys Lys Ser
      95             100             105             110

ttt agc ctt gag gaa aag tcc aaa atc tcc aaa aac cgt gtt cac tat 504

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Phe	Ser	Leu	Glu	Glu	Lys	Ser	Lys	Ile	Ser	Lys	Asn	Arg	Val	His	Tyr	
				115					120					125		
atg	aaa	ttc	aca	aaa	ggg	aag	gat	ctg	tca	tct	cgg	agc	aaa	aca	gat	552
Met	Lys	Phe	Thr	Lys	Gly	Lys	Asp	Leu	Ser	Ser	Arg	Ser	Lys	Thr	Asp	
			130					135					140			
ctt	gac	tgc	att	ttt	ggg	aaa	aga	cag	agt	aag	aag	act	ccc	gag	ggc	600
Leu	Asp	Cys	Ile	Phe	Gly	Lys	Arg	Gln	Ser	Lys	Lys	Thr	Pro	Glu	Gly	
			145				150					155				
gat	gcc	agt	ccc	tcc	act	cca	gag	gag	aac	gaa	acc	acg	aca	acc	agc	648
Asp	Ala	Ser	Pro	Ser	Thr	Pro	Glu	Glu	Asn	Glu	Thr	Thr	Thr	Thr	Ser	
	160					165					170					
gcc	ttc	acc	atc	cag	gag	tac	ttt	gcc	aag	cgg	atg	gca	gca	ctg	aag	696
Ala	Phe	Thr	Ile	Gln	Glu	Tyr	Phe	Ala	Lys	Arg	Met	Ala	Ala	Leu	Lys	
175				180					185					190		
aac	aag	ccc	cag	gtt	cca	gtt	cca	ggg	tct	gac	att	tct	gag	acg	cag	744
Asn	Lys	Pro	Gln	Val	Pro	Val	Pro	Gly	Ser	Asp	Ile	Ser	Glu	Thr	Gln	
			195					200					205			
gtg	gaa	cgt	aaa	agg	ggg	aag	aaa	aga	aat	aaa	gag	gcc	aca	ggt	aaa	792
Val	Glu	Arg	Lys	Arg	Gly	Lys	Lys	Arg	Asn	Lys	Glu	Ala	Thr	Gly	Lys	
			210				215					220				
gat	gtg	gaa	agt	tac	ctc	cag	cct	aag	gcc	aag	agg	cac	acg	gag	gga	840
Asp	Val	Glu	Ser	Tyr	Leu	Gln	Pro	Lys	Ala	Lys	Arg	His	Thr	Glu	Gly	
			225			230						235				
aag	ccc	gag	agg	gcc	gag	gcc	cag	gag	cga	gtg	gcc	aag	aag	aag	agc	888
Lys	Pro	Glu	Arg	Ala	Glu	Ala	Gln	Glu	Arg	Val	Ala	Lys	Lys	Lys	Ser	
	240					245					250					
gcg	cca	gca	gaa	gag	cag	ctc	aga	ggc	ccc	tgc	tgg	gac	cag	agt	tcc	936
Ala	Pro	Ala	Glu	Glu	Gln	Leu	Arg	Gly	Pro	Cys	Trp	Asp	Gln	Ser	Ser	
255					260				265					270		
aag	gcc	tct	gct	cag	gat	gca	ggg	gac	cat	gtg	cag	ccg	cct	gag	ggc	984
Lys	Ala	Ser	Ala	Gln	Asp	Ala	Gly	Asp	His	Val	Gln	Pro	Pro	Glu	Gly	
			275					280						285		
cgg	gac	ttc	acc	ctg	aag	ccc	aaa	aag	agg	aga	ggg	aag	aaa	aag	ctg	1032
Arg	Asp	Phe	Thr	Leu	Lys	Pro	Lys	Lys	Arg	Arg	Gly	Lys	Lys	Lys	Leu	
			290				295					300				
caa	aaa	cca	gta	gag	ata	gca	gag	gac	gct	aca	cta	gaa	gaa	acg	cta	1080
Gln	Lys	Pro	Val	Glu	Ile	Ala	Glu	Asp	Ala	Thr	Leu	Glu	Glu	Thr	Leu	
			305			310						315				
gtg	aaa	aag	aag	aag	aag	aaa	gat	tcc	aaa	t	gaatccttcc	cagccggggc				1131
Val	Lys	Lys	Lys	Lys	Lys	Lys	Asp	Ser	Lys							
	320					325										
cttccgacca	ctcagctgtc	agggcactgc	gggggcagac	acctctggcc	tgaagtcaca											1191
gcagagttca	ccccagagcg	cctgggcgca	tcttgtggca	tgcccatggg	ctgccgagtc											1251
ctgccctctc	gccacatttc	ccccaagtta	cattcccagg	aggacctttt	taatgttctc											1311
aatcgtggct	ctcagacaca	aataaatttt	tttgtaaact	ctgagccctt	cagcaagaga											1371
gtttaattat	aatcattaca	aatacatgca	ttcatgtaag	tgtgcacacg	tgtgtgtgca											1431

tgtgcgcac tgtgtgtgtg tgtgtgtgtc actatctccg tttgctctcg gttcccttca 1491  
 ataacaatga atggtgcttt cttctgaaag actcagccta attaaaggat taagaggcaa 1551  
 tagcttggat tcagaatgtt ctttttgttc tataatnnnc ctgtattgcg cccgctcgag 1611  
 agtatcccag catacgtgcg cgta 1635

<210> 303  
 <211> 566  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (110) .. (361)

<400> 303  
 tgcgagactc ggccggcgct gttgagggag tccggccgag actgtggtag tttttatacc 60  
 ttcccgcgag gacgccggcg ctgccaacgg aaggcgggc tctgctgcc atg aag 115  
 Met Lys  
 1  
 gtg aag att aag tgc tgg aac ggc gtg gcc act tgg ctc tgg gtg gcc 163  
 Val Lys Ile Lys Cys Trp Asn Gly Val Ala Thr Trp Leu Trp Val Ala  
 5 10 15  
 aac gat gag aac tgt ggc atc tgc agg atg gca ttt aac gga tgc tgc 211  
 Asn Asp Glu Asn Cys Gly Ile Cys Arg Met Ala Phe Asn Gly Cys Cys  
 20 25 30  
 cct gac tgc aag gtg ccc ggc gac gac tgc ccg ctg gtg tgg ggc cag 259  
 Pro Asp Cys Lys Val Pro Gly Asp Asp Cys Pro Leu Val Trp Gly Gln  
 35 40 45 50  
 tgc tcc cac tgc ttc cac atg cat tgc atc ctc aag tgg ctg cac gca 307  
 Cys Ser His Cys Phe His Met His Cys Ile Leu Lys Trp Leu His Ala  
 55 60 65  
 cag cag gtg cag cag cac tgc ccc atg tgc cgc cag gaa tgg aag ttc 355  
 Gln Gln Val Gln Gln His Cys Pro Met Cys Arg Gln Glu Trp Lys Phe  
 70 75 80  
 aag gag tgaggccga cctggctctc gctggagggg catcctgaga ctcttctc 411  
 Lys Glu  
 atgctggcgc cgatggctgc tggggacagc gccctgagc tgcaacaagg tggaaacaag 471  
 ggctggagct gcgtttgttt tgccatcact atgttgacac ttttatccaa taagtgaaaa 531  
 ctcattaaac tactcaaatac ttgaaaaaaaa aaaaa 566

<210> 304  
 <211> 2172  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (415) .. (669)

&lt;400&gt; 304

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actatagaat acaagctact tggtcttttt gcaggatccc atcgataagc ttgcttggtc      60
ttttggccga agcggcctac ggctgcgaga agacgacaga aggggtacggc tgcgagaaga      120
cgacagaagg gtacggctgc gagaagacga cagaagggtta cggctgcgag aagacgacag      180
aagggtacgg ctgcgagaag acgacagaag ggtacggctg cgagaagacg acagaagggt      240
acggctgcga gaagacgaca gaagggtacg gctgcgagaa gacgacagaa gggtagggct      300
gcgagaagac gacagaaggg tacggctgcg agaagacgac agaaggggac actagaggaa      360
gtcgtgctac ccccgcgag tggtcgtgtg ttctggattc attccggcac cacc  atg      417
                                     Met
                                     1

tcg aag gtt tcc ttt aag atc acg ctg acg tcg gac cca cgg ctg cgg      465
Ser Lys Val Ser Phe Lys Ile Thr Leu Thr Ser Asp Pro Arg Leu Pro
          5                      10                      15

tac aaa gta ctc agt gtt cct gaa agt aca cct ttc aca gca gtc tta      513
Tyr Lys Val Leu Ser Val Pro Glu Ser Thr Pro Phe Thr Ala Val Leu
          20                      25                      30

aag ttt gca gca gaa gaa ttt aaa gtt cct gct gca aca agt gca att      561
Lys Phe Ala Ala Glu Glu Phe Lys Val Pro Ala Ala Thr Ser Ala Ile
          35                      40                      45

att acc aat gat gga ata gga ata aat cct gca cag act gct gga aat      609
Ile Thr Asn Asp Gly Ile Gly Ile Asn Pro Ala Gln Thr Ala Gly Asn
          50                      55                      60                      65

gtt ttt cta aaa cat ggt tca gaa ctg cgg att att cct aga gat cgt      657
Val Phe Leu Lys His Gly Ser Glu Leu Arg Ile Ile Pro Arg Asp Arg
          70                      75                      80

gtt gga agt tgt taa tatctgctac ttggaacata cgattgcctt tcagaataaa      712
Val Gly Ser Cys
          85

tattggtatt ttttggtggt gtaaaattga aatcaggcat ttaacatact atgaaaacac      772
caggagtcaa tgattaatga aaggtagctc atctgtccct ttttggtgtc catactcttc      832
ctatgaagag ggaatgcgta tgaattaagg ctactactgt cacagaagat catagtcttt      892
gatgctacct cacaacacaa acaggtagtt cgttgggggc aaatgaatta gccaaactggt      952
aactggaagc ttttgataat tttttttttt agaacaattt ggaacattaa aatttactga      1012
atcgatatata ttcattctgag ataaaaatat aaaaagaatt atggaccctg gatggcaatt      1072
tgcttgatag catctgattt gcagactcat aatttgattt ttaattaaat atataggtta      1132
tgatgaagtg aatagacata tcagtgaaca gttaactata ttaaattttt atcatttact      1192
ttttttaaga ttcagacctc agttatataa atttcagttt aatatcaacc aaaaaattaa      1252

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aattttaatc taacccttat gtgtataaat tgggtgtccca taccagcttt taatggtgga 1312
cctatagaat ccagtacttt taatggtggg aatttacagt agaagcatcc tttgctgagt 1372
tatacattcc tttatcaatc tcttttgata caacatttaa aacaagtagc ttcaagaaac 1432
cactggtggt ttgaggatag tattttctaaa tagcattcag gaacagagta ttattgcaca 1492
gatctgaaga tcaaaaaaaaa gctcaaggaa atacagatcg gaagtgtgta tgagttatat 1552
ttattgaaaa cccaactttt aaggaagtgc taagatcagt caccatgtg aataagaagc 1612
caggaaagga aagatgggga agcccagatc accaggcttc tattaaggag gaaagcaaca 1672
gaggaaacag tgaaggggaa cagaaggggg tagcaaagtg ttacagaaaa gcggactgga 1732
tagacaaaac tgcagaaggt gtatgttggg gagaactgaa agggaaaaca aaatacttga 1792
catagtctta agtagaagaa ggcagttaga gaaaacaaag tatctactgg ccttgtcaac 1852
atacagactt caaaataccc cttatgagaa tccaaagaat gatgtgtgta agggaagatt 1912
ttatttgccc ttccggaaga aatcagtatc tatgcaaac ttgaaagacg aaatcaaagc 1972
ccattaatga ttcagaatca gtgcttgacc tctgtattc tgaatggtga actctggaag 2032
cagggattgt gtctggctct ttttagagct ggaaatgtag tggctttcat taaatacttg 2092
ctgtaaagtc tttctaagac caattattat cttagcatgt ttcagtatct tctctatcat 2152
aggccctaag ttcattgggg 2172

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<210> 305
<211> 1509
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (69)..(1214)

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<400> 305
aacctgcaaa atctttacat acacagaaga acagacagtt cttcaatgaa ccagaagaaa 60
atttctgg atg gtc atg gtt gtt cgg aat cct ata att gaa aaa cag agt 110
      Met Val Met Val Val Arg Asn Pro Ile Ile Glu Lys Gln Ser
      1             5             10
aaa gat gga aaa cca gtt att gaa tat caa gag gag gag ttg ttg gac 158
Lys Asp Gly Lys Pro Val Ile Glu Tyr Gln Glu Glu Leu Leu Asp
15             20             25             30
aag gtt tat agc tcg gtg ctg cgg cag tgc tac agc atg tac aag ctt 206
Lys Val Tyr Ser Ser Val Leu Arg Gln Cys Tyr Ser Met Tyr Lys Leu
35             40             45
ttt aat ggt aca ttt ctg aaa gcc atg gaa gac gga ggc gtc aag ctt 254
Phe Asn Gly Thr Phe Leu Lys Ala Met Glu Asp Gly Gly Val Lys Leu
50             55             60

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ctg aaa gaa aga tta gag aaa ttc ttc cat cgg tat ttg caa acg cta Leu Lys Glu Arg Leu Glu Lys Phe Phe His Arg Tyr Leu Gln Thr Leu 65 70 75	302
cat ttg cag tca tgt gac cta ctt gac att ttt ggt gga atc agc ttc His Leu Gln Ser Cys Asp Leu Leu Asp Ile Phe Gly Gly Ile Ser Phe 80 85 90	350
ttc ccg ttg gat aaa atg act tat ttg aaa atc cag tcc ttt att aat Phe Pro Leu Asp Lys Met Thr Tyr Leu Lys Ile Gln Ser Phe Ile Asn 95 100 105 110	398
aga atg gag gaa agc ctg aat ata gtc aaa tac act gct ttt ctc tat Arg Met Glu Glu Ser Leu Asn Ile Val Lys Tyr Thr Ala Phe Leu Tyr 115 120 125	446
aac gat cag ctt atc tgg agt gga tta gaa caa gat gac atg aga att Asn Asp Gln Leu Ile Trp Ser Gly Leu Glu Gln Asp Asp Met Arg Ile 130 135 140	494
tta tac aaa tac ctt acc acc tcc ctt ttc cca agg cac atc gaa cct Leu Tyr Lys Tyr Leu Thr Thr Ser Leu Phe Pro Arg His Ile Glu Pro 145 150 155	542
gag tta gca gga agg gat tct cca ata aga gca gaa atg cca gga aat Glu Leu Ala Gly Arg Asp Ser Pro Ile Arg Ala Glu Met Pro Gly Asn 160 165 170	590
ctt caa cac tat gga aga ttt ctt acc gga ccc ttg aac ctc aat gat Leu Gln His Tyr Gly Arg Phe Leu Thr Gly Pro Leu Asn Leu Asn Asp 175 180 185 190	638
cca gat gca aaa tgc aga ttc ccc aaa att ttt gta aat aca gat gac Pro Asp Ala Lys Cys Arg Phe Pro Lys Ile Phe Val Asn Thr Asp Asp 195 200 205	686
act tat gaa gag ctc cat tta atc gtt tat aag gcc atg agt gcg gct Thr Tyr Glu Glu Leu His Leu Ile Val Tyr Lys Ala Met Ser Ala Ala 210 215 220	734
gtg tgc ttt atg atc gac gcc tct gtc cac cca acg ttg gat ttt tgc Val Cys Phe Met Ile Asp Ala Ser Val His Pro Thr Leu Asp Phe Cys 225 230 235	782
cga aga ctg gac agc atc gtt ggg ccc cag ctc aca gtg ctg gcc tct Arg Arg Leu Asp Ser Ile Val Gly Pro Gln Leu Thr Val Leu Ala Ser 240 245 250	830
gac atc tgt gaa cag ttt aac atc aac aag agg atg tcc ggg tct gag Asp Ile Cys Glu Gln Phe Asn Ile Asn Lys Arg Met Ser Gly Ser Glu 255 260 265 270	878
aaa gaa ccc cag ttt aag ttt atc tac ttc aac cac atg aat ctc gcc Lys Glu Pro Gln Phe Lys Phe Ile Tyr Phe Asn His Met Asn Leu Ala 275 280 285	926
gag aag agc aca gtt cac atg agg aaa acg ccc agc gtg tgc ctc act Glu Lys Ser Thr Val His Met Arg Lys Thr Pro Ser Val Ser Leu Thr 290 295 300	974
tcc gtg cac ccg gat tta atg aag att ctc ggt gac atc aac agt gac Ser Val His Pro Asp Leu Met Lys Ile Leu Gly Asp Ile Asn Ser Asp 305 310 315	1022

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ttt acc aga gtg gat gaa gat gag gag atc att gtg aag gcc atg agt      1070
Phe Thr Arg Val Asp Glu Asp Glu Glu Ile Ile Val Lys Ala Met Ser
    320                      325                      330

gat tac tgg gtt gtt gga aag aag tct gat cgg cgg gag ctc tat gtt      1118
Asp Tyr Trp Val Val Gly Lys Lys Ser Asp Arg Arg Glu Leu Tyr Val
    335                      340                      345                      350

att ttg aat caa aaa aat gca aac ctg att gaa gta aat gaa gag gtc      1166
Ile Leu Asn Gln Lys Asn Ala Asn Leu Ile Glu Val Asn Glu Glu Val
    355                      360                      365

aag aaa ctt tgt gca aca cag ttc aac aac atc ttc ttc ttg gat tga      1214
Lys Lys Leu Cys Ala Thr Gln Phe Asn Asn Ile Phe Phe Leu Asp *
    370                      375                      380

cggatgacgg ctcactgaga gcatacttaa aaaacactct gcaaacattt ggtcacatgc      1274

aagttagtagg tcatatgacg gactgcattc aggacaaggg taaagcaata cttgctttga      1334

agaatcacat ttcgactcgg tctgctgacg tgagggttttt agatttttaa tatttatgtg      1394

gaattaatta aaggtagttg gctatatcgc tatcatttca ttcttttgac attatgtgaa      1454

tattttactg gaaaataaga ctaataaatt gttaaaagtt tttaaaaaaa aaaaa      1509

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&lt;210&gt; 306

&lt;211&gt; 1919

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (198)..(1622)

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1919)

&lt;223&gt; n = a,t,c or g

&lt;400&gt; 306

```

gagtcnnan gnnngnnnnnt tttgaaaccg tcctgatagc tttacgcctg cggtagccgc      60

ccggaattcc cgggtcgacg atttcgtcgt gtggtgagge ctacagaagc ggccttcagc      120

tggaccttgg tctccccgcc ggacttcgag ggtgtcatcg ccgccctgt tgggggtgag      180

cgccgcgcgg ctgcagc   atg cct cac agg aag aaa aag ccc ttt ata gag      230
                Met Pro His Arg Lys Lys Lys Pro Phe Ile Glu
                  1                5                10

aag aag aaa gct gtg tct ttt cac ttg gtc cac cgg agc caa cga gat      278
Lys Lys Lys Ala Val Ser Phe His Leu Val His Arg Ser Gln Arg Asp
    15                      20                      25

cct tta gca gca gat gag agt gca ccc cag agg gtt cta ttg ccc aca      326
Pro Leu Ala Ala Asp Glu Ser Ala Pro Gln Arg Val Leu Leu Pro Thr
    30                      35                      40

caa aaa ata gac aat gaa gaa agg cga gca gaa cag agg aag tat gga      374
Gln Lys Ile Asp Asn Glu Glu Arg Arg Ala Glu Gln Arg Lys Tyr Gly

```

45	50	55	
gtg ttc ttt gat gac gac tat gac tac ctg cag cac ctg aag gaa cca			422
Val Phe Phe Asp Asp Asp Tyr Asp Tyr Leu Gln His Leu Lys Glu Pro			
60	65	70	75
tct ggg cct tca gag ctt att ccc tca agt acc ttc agt gca cac aac			470
Ser Gly Pro Ser Glu Leu Ile Pro Ser Ser Thr Phe Ser Ala His Asn			
	80	85	90
agg aga gag gag aaa gaa gaa acg cta gta att cca agc act gga att			518
Arg Arg Glu Glu Lys Glu Glu Thr Leu Val Ile Pro Ser Thr Gly Ile			
	95	100	105
aag ttg cct tca tca gtg ttt gct tca gag ttt gag gaa gat gtt gga			566
Lys Leu Pro Ser Ser Val Phe Ala Ser Glu Phe Glu Glu Asp Val Gly			
	110	115	120
ttg tta aat aaa gca gct cca gtt tca gga cct cga ctg gat ttt gat			614
Leu Leu Asn Lys Ala Ala Pro Val Ser Gly Pro Arg Leu Asp Phe Asp			
	125	130	135
cct gac att gtt gca gct ctt gat gat gat ttt gac ttt gat gat cca			662
Pro Asp Ile Val Ala Ala Leu Asp Asp Asp Phe Asp Phe Asp Asp Pro			
140	145	150	155
gat aat ctg ctt gag gat gac ttt att ctt cag gcc aat aag gca aca			710
Asp Asn Leu Leu Glu Asp Asp Phe Ile Leu Gln Ala Asn Lys Ala Thr			
	160	165	170
gga gag gaa gag gga atg gat ata cag aaa tct gag aat gaa gat gac			758
Gly Glu Glu Glu Gly Met Asp Ile Gln Lys Ser Glu Asn Glu Asp Asp			
	175	180	185
agc gag tgg gaa gat gtg gat gat gag aag gga gat agc aat gat gac			806
Ser Glu Trp Glu Asp Val Asp Asp Glu Lys Gly Asp Ser Asn Asp Asp			
	190	195	200
tat gac tct gca ggc cta ttg tca gat gaa gac tgt atg tct gtg ccc			854
Tyr Asp Ser Ala Gly Leu Leu Ser Asp Glu Asp Cys Met Ser Val Pro			
	205	210	215
gga aaa act cac aga gct ata gca gat cac ttg ttc tgg agt gag gaa			902
Gly Lys Thr His Arg Ala Ile Ala Asp His Leu Phe Trp Ser Glu Glu			
	220	225	230
aca aag agt cgc ttc acg gag tat tcg atg act tcc tca gtc atg agg			950
Thr Lys Ser Arg Phe Thr Glu Tyr Ser Met Thr Ser Ser Val Met Arg			
	240	245	250
aga aat gaa cag ctg acc cta cat gat gag agg ttt gag aag ttt tat			998
Arg Asn Glu Gln Leu Thr Leu His Asp Glu Arg Phe Glu Lys Phe Tyr			
	255	260	265
gag caa tat gat gat gat gaa att gga gct ctg gat aat gca gaa ttg			1046
Glu Gln Tyr Asp Asp Asp Glu Ile Gly Ala Leu Asp Asn Ala Glu Leu			
	270	275	280
gaa ggt tct att caa gtg gac agc aat cgc tta cag gaa gtt ttg aat			1094
Glu Gly Ser Ile Gln Val Asp Ser Asn Arg Leu Gln Glu Val Leu Asn			
	285	290	295
gac tac tat aaa gag aag gca gag aat tgt gta aaa ttg aat acc ctt			1142
Asp Tyr Tyr Lys Glu Lys Ala Glu Asn Cys Val Lys Leu Asn Thr Leu			

300	305	310	315	
gaa ccc ttg gag gat	caa gac ctg cca atg aat	gag ctt gat gag tct		1190
Glu Pro Leu Glu Asp	Gln Asp Leu Pro Met	Asn Glu Leu Asp Glu Ser		
	320	325	330	
gag gag gaa gaa atg att act gta gtc ctt gaa gaa gcc aaa gag aag				1238
Glu Glu Glu Glu Met Ile Thr Val Val Leu Glu Glu Ala Lys Glu Lys				
	335	340	345	
tgg gat tgt gaa tct att tgt agt aca tac tca aat tta tat aac cat				1286
Trp Asp Cys Glu Ser Ile Cys Ser Thr Tyr Ser Asn Leu Tyr Asn His				
	350	355	360	
cca cag ctt atc aag tat caa cca aag ccc aaa caa att cga ata tct				1334
Pro Gln Leu Ile Lys Tyr Gln Pro Lys Pro Lys Gln Ile Arg Ile Ser				
	365	370	375	
tct aaa aca gga ata cct ctc aat gtc tta cca aag aaa gga ctc aca				1382
Ser Lys Thr Gly Ile Pro Leu Asn Val Leu Pro Lys Lys Gly Leu Thr				
	380	385	390	395
gca aag caa act gaa aga ata cag atg att aat ggc agt gat ctt cct				1430
Ala Lys Gln Thr Glu Arg Ile Gln Met Ile Asn Gly Ser Asp Leu Pro				
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aaa gta tca act cag cca cgt tct aaa aat gaa agc aaa gaa gat aaa				1478
Lys Val Ser Thr Gln Pro Arg Ser Lys Asn Glu Ser Lys Glu Asp Lys				
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Arg Ala Arg Lys Gln Ala Ile Lys Glu Glu Arg Lys Glu Arg Arg Val				
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Glu Lys Lys Ala Asn Lys Leu Ala Phe Lys Leu Glu Lys Arg Arg Gln				
	445	450	455	
gaa aaa gag ctg ctg aac ttg aag aag aat gtt gag ggt cta aag cta				1622
Glu Lys Glu Leu Leu Asn Leu Lys Lys Asn Val Glu Gly Leu Lys Leu				
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tagacagtgg agcatacagg gcaaggcact ttattagggg ctcctcatct ttgggttattg				1682
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gtaatacttt aatttttaat attataagct tacatttgct ctgaagtaaa tgacttcatg				1862
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&lt;210&gt; 307

&lt;211&gt; 2138

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (224)..(1180)



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aat gat aca caa att tca gaa ttt ctt ctt ctg gga ttt tca caa gaa Asn Asp Thr Gln Ile Ser Glu Phe Leu Leu Leu Gly Phe Ser Gln Glu 5 10 15 20	283
cct gga ctg caa ccc ttc ctc ttt ggg ctg ttc ctg tcc atg tac ctg Pro Gly Leu Gln Pro Phe Leu Phe Gly Leu Phe Leu Ser Met Tyr Leu 25 30 35	331
gtc act gtg ctc ggg aac ctg ctc atc atc ctg gcc aca atc tca gac Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Thr Ile Ser Asp 40 45 50	379
tcc cac ctc cac acc ccc atg tac ttc ttc ctc tcc aac ctg tcc ttt Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe 55 60 65	427
gct gac att tgt gtt act tcc acc acc att cca aaa atg ctg atg aac Ala Asp Ile Cys Val Thr Ser Thr Thr Ile Pro Lys Met Leu Met Asn 70 75 80	475
atc cag aca cag aac aaa gtc atc acc tac ata gcc tgc ctc atg cag Ile Gln Thr Gln Asn Lys Val Ile Thr Tyr Ile Ala Cys Leu Met Gln 85 90 95 100	523
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gtg atg gcc tat gac cgg ttt gtg gcc atc tgt cac ccc ctg cac tac Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His Tyr 120 125 130	619
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ggg atc ctt tac tct tac tct aag ata att tct tcc ata cat gca atc	907

Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Ile Ser Ser Ile His Ala Ile	
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Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser His	
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Leu Ser Val Val Ser Leu Phe Tyr Gly Ala Ile Leu Gly Val Tyr Leu	
245 250 255 260	
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Ser Ser Ala Ala Thr Arg Asn Ser His Ser Ser Ala Thr Ala Ser Val	
265 270 275	
atg tac act gtg gtc acc ccc atg ctg aac ccc ttt atc tat agt ctg	1099
Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu	
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Arg Asn Lys Asp Ile Lys Arg Ala Leu Gly Ile His Leu Leu Trp Gly	
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Thr Met Lys Gly Gln Phe Phe Lys Lys Cys Pro	
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&lt;210&gt; 308

&lt;211&gt; 7445

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<213> Homo sapiens

<220>  
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gggtgactga acatgggaca ccaaagccct ttcgaaagtt tgacagtgtg gcttttggag      180
aaagtcaaag tgaggatgaa caatttgaaa atgacttaga gacagacca cccaactggc      240
agcagcttgt tagtcgagaa gtgttactgg gactaaaacc ttgtgaaatc aaaagacagg      300
aagtgattaa tgaattgttc tacactgaaa gagctcatgt tcgaacactg aaggttcttg      360
atcaagtgtt ctatcagcga gtatccagag aaggaattct gtcacctca gagctacgga      420
aaattttttc aaacttgga gatattcttc aacttcatat tggattgaat gaacaa      476
atg aag gct gtt cga aag aga aat gag acc tct gtt atc gat cag att      524
Met Lys Ala Val Arg Lys Arg Asn Glu Thr Ser Val Ile Asp Gln Ile
  1             5             10            15

ggg gaa gat ttg ctg aca tgg ttc agc gga cca gga gag gag aaa ttg      572
Gly Glu Asp Leu Leu Thr Trp Phe Ser Gly Pro Gly Glu Glu Lys Leu
      20             25             30

aaa cat gct gct gct acc ttt tgc agt aac caa cct ttc gcc ctg gaa      620
Lys His Ala Ala Ala Thr Phe Cys Ser Asn Gln Pro Phe Ala Leu Glu
      35             40             45

atg atc aaa tct cgt cag aaa aag gat tct cga ttt cag act ttt gtg      668
Met Ile Lys Ser Arg Gln Lys Lys Asp Ser Arg Phe Gln Thr Phe Val
      50             55             60

caa gat gct gaa agt aat cca ctg tgt cgt cgt ctt caa ctg aag gat      716
Gln Asp Ala Glu Ser Asn Pro Leu Cys Arg Arg Leu Gln Leu Lys Asp
      65             70             75             80

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Ile Ile Pro Thr Gln Met Gln Arg Leu Thr Lys Tyr Pro Leu Leu Leu
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gat aat att gcc aaa tac aca gaa tgg cca aca gaa agg gag aag gtg      812
Asp Asn Ile Ala Lys Tyr Thr Glu Trp Pro Thr Glu Arg Glu Lys Val
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aag aaa gct gca gat cac tgt cgt cag atc tta aat tat gta aat cag      860
Lys Lys Ala Ala Asp His Cys Arg Gln Ile Leu Asn Tyr Val Asn Gln
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gct gtc aag gag gca gaa aac aag cag cgc cta gaa gat tat cag cgt      908
Ala Val Lys Glu Ala Glu Asn Lys Gln Arg Leu Glu Asp Tyr Gln Arg
      130            135            140

cgc ctt gat acc tcc agc ctg aag ttg tca gag tac cca aat gtt gaa      956
Arg Leu Asp Thr Ser Ser Leu Lys Leu Ser Glu Tyr Pro Asn Val Glu
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gag ctc agg aat ttg gat tta aca aaa agg aag atg att cat gaa ggg      1004

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Pro	Leu	Val	Trp	Lys	Val	Asn	Arg	Asp	Lys	Thr	Ile	Asp	Leu	Tyr	Thr		
			180					185					190				
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Leu	Leu	Leu	Glu	Asp	Ile	Leu	Val	Leu	Leu	Gln	Lys	Gln	Asp	Asp	Arg		
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Leu	Val	Leu	Arg	Cys	His	Ser	Lys	Ile	Leu	Ala	Ser	Thr	Ala	Asp	Ser		
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Lys	His	Thr	Phe	Ser	Pro	Val	Ile	Lys	Leu	Ser	Thr	Val	Leu	Val	Arg		
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Thr	Val	Trp	Gln	Asp	Leu	Ile	Cys	Arg	Met	Ala	Ala	Ser	Val	Lys	Glu		
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Asp	Asn	Asp	Glu	Glu	Asp	Pro	Ser	Lys	Leu	Lys	Glu	Glu	Gln	His	Gly		
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Ile	Ser	Val	Thr	Gly	Leu	Gln	Ser	Pro	Asp	Arg	Asp	Leu	Gly	Leu	Glu		
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Ser	Thr	Leu	Ile	Ser	Ser	Lys	Pro	Gln	Ser	His	Ser	Leu	Ser	Thr	Ser		
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caacttggat ctttagacct catctataaa ttgaaattat atttttaagt cataagccaa 4392  
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 caacagcatt ttagctcaga aggctcgtt actttgggca tttgctgtat tttggttttg 7092  
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 tacatatctg gtggaacaaa gaaatacctg taccattccc acttgctctt tgatagccac 7392  
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 gga gat gcc cag ccc aac ccc gat aag tac ctc gaa ggg gcc gca ggt 99  
 Gly Asp Ala Gln Pro Asn Pro Asp Lys Tyr Leu Glu Gly Ala Ala Gly  
 10 15 20  
 cag cag ccc act gcc cct gat aaa agc aaa gag acc aac aaa aca gat 147  
 Gln Gln Pro Thr Ala Pro Asp Lys Ser Lys Glu Thr Asn Lys Thr Asp



25	30	35	
aac act gag gca cct gta acc aag att gaa ctt ctg ccg tcc tac tcc Asn Thr Glu Ala Pro Val Thr Lys Ile Glu Leu Leu Pro Ser Tyr Ser 40 45 50 55			195
acg gct aca ctg ata gat gag ccc act gag gtg gat gac ccc tgg aac Thr Ala Thr Leu Ile Asp Glu Pro Thr Glu Val Asp Asp Pro Trp Asn 60 65 70			243
cta ccc act ctt cag gac tcg ggg atc aag tgg tca gag aga gac acc Leu Pro Thr Leu Gln Asp Ser Gly Ile Lys Trp Ser Glu Arg Asp Thr 75 80 85			291
aaa ggg aag att ctc tgt ttc ttc caa ggg att ggg aga ttg att tta Lys Gly Lys Ile Leu Cys Phe Phe Gln Gly Ile Gly Arg Leu Ile Leu 90 95 100			339
ctt ctc gga ttt ctc tac ttt ttc gtg tgc tcc ctg gat att ctt agt Leu Leu Gly Phe Leu Tyr Phe Phe Val Cys Ser Leu Asp Ile Leu Ser 105 110 115			387
agc gcc ttc cag ctg gtt gga gga aaa atg gca gga cag ttc ttc agc Ser Ala Phe Gln Leu Val Gly Gly Lys Met Ala Gly Gln Phe Phe Ser 120 125 130 135			435
aac agc tct att atg tcc aac cct ttg ttg ggg ctg gtg atc ggg gtg Asn Ser Ser Ile Met Ser Asn Pro Leu Leu Gly Leu Val Ile Gly Val 140 145 150			483
ctg gtg acc gtc ttg gtg cag agc tcc agc acc tca acg tcc atc gtt Leu Val Thr Val Leu Val Gln Ser Ser Ser Thr Ser Thr Ser Ile Val 155 160 165			531
gtc agc atg gtg tcc tct tca ttg ctc act gtt cgg gct gcc atc ccc Val Ser Met Val Ser Ser Ser Leu Leu Thr Val Arg Ala Ala Ile Pro 170 175 180			579
att atc atg ggg gcc aac att gga acg tca atc acc aac act att gtt Ile Ile Met Gly Ala Asn Ile Gly Thr Ser Ile Thr Asn Thr Ile Val 185 190 195			627
gcg ctc atg cag gtg gga gat cgg agt gag ttc aga aga gct ttt gca Ala Leu Met Gln Val Gly Asp Arg Ser Glu Phe Arg Arg Ala Phe Ala 200 205 210 215			675
gga gcc act gtc cat gac ttc ttc aac tgg ctg tcc gtg ttg gtg ctc Gly Ala Thr Val His Asp Phe Phe Asn Trp Leu Ser Val Leu Val Leu 220 225 230			723
ttg ccc gtg gag gtg gcc acc cat tac ctc gag atc ata acc cag ctt Leu Pro Val Glu Val Ala Thr His Tyr Leu Glu Ile Ile Thr Gln Leu 235 240 245			771
ata gtg gag agc ttc cac ttc aag aat gga gaa gat gcc cca gat ctt Ile Val Glu Ser Phe His Phe Lys Asn Gly Glu Asp Ala Pro Asp Leu 250 255 260			819
ctg aaa gtc atc act aag ccc ttc aca aag ctc att gtc cag ctg gat Leu Lys Val Ile Thr Lys Pro Phe Thr Lys Leu Ile Val Gln Leu Asp 265 270 275			867
aaa aaa gtt atc agc caa att gca atg aac gat gaa aaa gcg aaa aac Lys Lys Val Ile Ser Gln Ile Ala Met Asn Asp Glu Lys Ala Lys Asn			915

280	285	290	295	
aag agt ctt gtc aag att tgg tgc aaa act ttt acc aac aag acc cag Lys Ser Leu Val Lys Ile Trp Cys Lys Thr Phe Thr Asn Lys Thr Gln 300 305 310				963
att aac gtc act gtt ccc tcg act gct aac tgc acc tcc cct tcc ctc Ile Asn Val Thr Val Pro Ser Thr Ala Asn Cys Thr Ser Pro Ser Leu 315 320 325				1011
tgt tgg acg gat ggc atc caa aac tgg acc atg aag aat gtg acc tac Cys Trp Thr Asp Gly Ile Gln Asn Trp Thr Met Lys Asn Val Thr Tyr 330 335 340				1059
aag gag aac atc gcc aaa tgc cag cat atc ttt gtg aat ttc cac ctc Lys Glu Asn Ile Ala Lys Cys Gln His Ile Phe Val Asn Phe His Leu 345 350 355				1107
ccg gat ctt gct gtg ggc acc atc ttg ctc ata ctc tcc ctg ctg gtc Pro Asp Leu Ala Val Gly Thr Ile Leu Leu Ile Leu Ser Leu Leu Val 360 365 370 375				1155
ctc tgt ggt tgc ctg atc atg att gtc aag atc ctg ggc tct gtg ctc Leu Cys Gly Cys Leu Ile Met Ile Val Lys Ile Leu Gly Ser Val Leu 380 385 390				1203
aag ggg cag gtc gcc act gtc atc aag aag acc atc aac act gat ttc Lys Gly Gln Val Ala Thr Val Ile Lys Lys Thr Ile Asn Thr Asp Phe 395 400 405				1251
ccc ttt ccc ttt gca tgg ttg act ggc tac ctg gcc atc ctc gtc ggg Pro Phe Pro Phe Ala Trp Leu Thr Gly Tyr Leu Ala Ile Leu Val Gly 410 415 420				1299
gca ggc atg acc ttc atc gta cag agc agc tct gtg ttc acg tcg gcc Ala Gly Met Thr Phe Ile Val Gln Ser Ser Ser Val Phe Thr Ser Ala 425 430 435				1347
ttg acc ccc ctg att gga atc ggc gtg ata acc att gag agg gct tat Leu Thr Pro Leu Ile Gly Ile Gly Val Ile Thr Ile Glu Arg Ala Tyr 440 445 450 455				1395
cca ctc acg ctg ggc tcc aac atc ggc acc acc acc acc gcc atc ctg Pro Leu Thr Leu Gly Ser Asn Ile Gly Thr Thr Thr Thr Ala Ile Leu 460 465 470				1443
gcc gcc tta gcc agc cct ggc aat gca ttg agg agt tca ctc cag atc Ala Ala Leu Ala Ser Pro Gly Asn Ala Leu Arg Ser Ser Leu Gln Ile 475 480 485				1491
gcc ctg tgc cac ttt ttc ttc aac atc tcc ggc atc ttg ctg tgg tac Ala Leu Cys His Phe Phe Phe Asn Ile Ser Gly Ile Leu Leu Trp Tyr 490 495 500				1539
ccg atc ccg ttc act cgc ctg ccc atc cgc atg gcc aag ggg ctg gcc Pro Ile Pro Phe Thr Arg Leu Pro Ile Arg Met Ala Lys Gly Leu Gly 505 510 515				1587
aac atc tct gcc aag tat cgc tgg ttc gcc gtc ttc tac ctg atc atc Asn Ile Ser Ala Lys Tyr Arg Trp Phe Ala Val Phe Tyr Leu Ile Ile 520 525 530 535				1635
ttc ttc ttc ctg atc ccg ctg acg gtg ttt ggc ctc tcg ctg gcc gcc Phe Phe Phe Leu Ile Pro Leu Thr Val Phe Gly Leu Ser Leu Ala Gly 540 545 550 555				1683

540	545	550	
tgg cgg gtg ctg gtt ggt gtc ggg gtt ccc gtc gtc ttc atc atc atc			1731
Trp Arg Val Leu Val Gly Val Gly Val Pro Val Val Phe Ile Ile Ile			
555	560	565	
ctg gta ctg tgc ctc cga ctc ctg cag tct cgc tgc cca cgc gtc ctg			1779
Leu Val Leu Cys Leu Arg Leu Leu Gln Ser Arg Cys Pro Arg Val Leu			
570	575	580	
ccg aag aaa ctc cag aac tgg aac ttc ctg ccg ctg tgg atg cgc tcg			1827
Pro Lys Lys Leu Gln Asn Trp Asn Phe Leu Pro Leu Trp Met Arg Ser			
585	590	595	
ctg aag ccc tgg gat gcc gtc gtc tcc aag ttc acc ggc tgc ttc cag			1875
Leu Lys Pro Trp Asp Ala Val Val Ser Lys Phe Thr Gly Cys Phe Gln			
600	605	610	615
atg cgc tgc tgc tgc tgc tgc cgc gtg tgc tgc cgc gcg tgc tgc ttg			1923
Met Arg Cys Cys Cys Cys Cys Arg Val Cys Cys Arg Ala Cys Cys Leu			
620	625	630	
ctg tgt ggc tgc ccc aag tgc tgc cgc tgc agc aag tgc tgc gag gac			1971
Leu Cys Gly Cys Pro Lys Cys Cys Arg Cys Ser Lys Cys Cys Glu Asp			
635	640	645	
ttg gag gag gcg cag gag ggg cag gat gtc cct gtc aag gct cct gag			2019
Leu Glu Glu Ala Gln Glu Gly Gln Asp Val Pro Val Lys Ala Pro Glu			
650	655	660	
acc ttt gat aac ata acc att agc aga gag gct cag ggt gag gtc cct			2067
Thr Phe Asp Asn Ile Thr Ile Ser Arg Glu Ala Gln Gly Glu Val Pro			
665	670	675	
gcc tcg gac tca aag acc gaa tgc acg gcc ttg taggggac gccccagatt			2118
Ala Ser Asp Ser Lys Thr Glu Cys Thr Ala Leu			
680	685	690	
gtcaggggatt gggggatggt ccttgagttt tgcattctct cctccctccc acttctgcac			2178
cctttcacca cctcgaggag atttgctccc cattagcgaa tgaaattgat gcagtcctac			2238
ctaactcgat tcccttttggc ttggtgggta ggctgcagg gcactttttat tccaacccct			2298
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tagcctggac	ctgccggccc	tccctccagg	acogaggggc	tcccaaggga	aactcaggcg		180									
tgtgctggtc	cca	atg	tca	gtg	aaa	ccc	agc	tgg	ggg	cct	ggc	ccc	tcg		229	
		Met	Ser	Val	Lys	Pro	Ser	Trp	Gly	Pro	Gly	Pro	Ser			
		1					5				10					
gag	ggg	gtc	acc	gca	gtg	cct	acc	agt	gac	ctt	gga	gag	atc	cac	aac	277
Glu	Gly	Val	Thr	Ala	Val	Pro	Thr	Ser	Asp	Leu	Gly	Glu	Ile	His	Asn	
		15					20				25					
tgg	acc	gag	ctg	ctt	gac	ctc	ttc	aac	cac	act	ttg	tct	gag	tgc	cac	325
Trp	Thr	Glu	Leu	Leu	Asp	Leu	Phe	Asn	His	Thr	Leu	Ser	Glu	Cys	His	
		30				35					40					
gtg	gag	ctc	agc	cag	agc	acc	aag	cgc	gtg	gtc	ctc	ttt	gcc	ctc	tac	373
Val	Glu	Leu	Ser	Gln	Ser	Thr	Lys	Arg	Val	Val	Leu	Phe	Ala	Leu	Tyr	
		45				50				55					60	
ctg	gcc	atg	ttt	gtg	gtt	ggg	ctg	gtg	gag	aac	ctc	ctg	gtg	ata	tgc	421
Leu	Ala	Met	Phe	Val	Val	Gly	Leu	Val	Glu	Asn	Leu	Leu	Val	Ile	Cys	
				65					70					75		
gtc	aac	tgg	cgc	ggc	tca	ggc	cgg	gca	ggg	ctg	atg	aac	ctc	tac	atc	469
Val	Asn	Trp	Arg	Gly	Ser	Gly	Arg	Ala	Gly	Leu	Met	Asn	Leu	Tyr	Ile	
			80					85					90			
ctc	aac	atg	gcc	atc	gcg	gac	ctg	ggc	att	gtc	ctg	tct	ctg	ccc	gtg	517
Leu	Asn	Met	Ala	Ile	Ala	Asp	Leu	Gly	Ile	Val	Leu	Ser	Leu	Pro	Val	
		95					100					105				
tgg	atg	ctg	gag	gtc	acg	ctg	gac	tac	acc	tgg	ctc	tgg	ggc	agc	ttc	565
Trp	Met	Leu	Glu	Val	Thr	Leu	Asp	Tyr	Thr	Trp	Leu	Trp	Gly	Ser	Phe	
		110				115					120					
tcc	tgc	cgc	ttc	act	cac	tac	ttc	tac	ttt	gtc	aac	atg	tat	agc	agc	613
Ser	Cys	Arg	Phe	Thr	His	Tyr	Phe	Tyr	Phe	Val	Asn	Met	Tyr	Ser	Ser	
					130					135					140	
atc	ttc	ttc	ctg	gtg	tgc	ctc	agt	gtc	gac	cgc	tat	gtc	acc	ctc	acc	661
Ile	Phe	Phe	Leu	Val	Cys	Leu	Ser	Val	Asp	Arg	Tyr	Val	Thr	Leu	Thr	
				145					150					155		
agc	gcc	tcc	ccc	tcc	tgg	cag	cgt	tac	cag	cac	cga	gtg	cgg	cgg	gcc	709
Ser	Ala	Ser	Pro	Ser	Trp	Gln	Arg	Tyr	Gln	His	Arg	Val	Arg	Arg	Ala	
			160					165					170			
atg	tgt	gca	ggc	atc	tgg	gtc	ctc	tcg	gcc	atc	atc	ccg	ctg	cct	gag	757
Met	Cys	Ala	Gly	Ile	Trp	Val	Leu	Ser	Ala	Ile	Ile	Pro	Leu	Pro	Glu	
		175					180					185				
gtg	gtc	cac	atc	cag	ctg	gtg	gag	ggc	cct	gag	ccc	atg	tgc	ctc	ttc	805
Val	Val	His	Ile	Gln	Leu	Val	Glu	Gly	Pro	Glu	Pro	Met	Cys	Leu	Phe	
		190				195					200					
atg	gca	cct	ttt	gaa												

Phe Asn Val	Leu Thr Ala Cys Arg	Leu Arg Gln Pro Gly Gln Pro Lys	
240	245	250	
agc cgg cgc cac tgc ttg ctg ctg tgc gcc tac gtg gcc gtc ttt gtc	997		
Ser Arg Arg His Cys Leu Leu Leu Cys Ala Tyr Val Ala Val Phe Val			
255	260	265	
atg tgc tgg ctg ccc tat cat gtg acc ctg ctg ctg ctc aca ctg cat	1045		
Met Cys Trp Leu Pro Tyr His Val Thr Leu Leu Leu Leu Thr Leu His			
270	275	280	
ggg acc cac atc tcc ctc cac tgc cac ctg gtc cac ctg ctc tac ttc	1093		
Gly Thr His Ile Ser Leu His Cys His Leu Val His Leu Leu Tyr Phe			
285	290	295	300
ttc tat gat gtc att gac tgc ttc tcc atg ctg cac tgt gtc atc aac	1141		
Phe Tyr Asp Val Ile Asp Cys Phe Ser Met Leu His Cys Val Ile Asn			
305	310	315	
ccc atc ctt tac aac ttt ctc agc cca cac ttc cgg ggc cgg ctc ctg	1189		
Pro Ile Leu Tyr Asn Phe Leu Ser Pro His Phe Arg Gly Arg Leu Leu			
320	325	330	
aat gct gta gtc cat tac ctt cct aag gac cag acc aag gcg ggc aca	1237		
Asn Ala Val Val His Tyr Leu Pro Lys Asp Gln Thr Lys Ala Gly Thr			
335	340	345	
tgc gcc tcc tct tcc tcc tgt tcc acc cag cat tcc atc atc atc acc	1285		
Cys Ala Ser Ser Ser Ser Cys Ser Thr Gln His Ser Ile Ile Ile Thr			
350	355	360	
aag ggt gat agc cag cct gct gca gca gcc ccc cac cct gag cca agc	1333		
Lys Gly Asp Ser Gln Pro Ala Ala Ala Ala Pro His Pro Glu Pro Ser			
365	370	375	380
ctg agc ttt cag gca cac cat ttg ctt cca aat act tcc ccc atc tct	1381		
Leu Ser Phe Gln Ala His His Leu Leu Pro Asn Thr Ser Pro Ile Ser			
385	390	395	
ccc act cag cct ctt aca ccc agc tgaggtagag gccagactcc tccaacagtg	1435		
Pro Thr Gln Pro Leu Thr Pro Ser			
400			
aaggaaaagg cacagatcac cttagaggcc acgctcccaa gattagttat caccctggca	1495		
gtatgaatac ttccctaagg cctcccatcc atggagggga agagtgggaa ccagctgtta	1555		
cactcagcat ctactgagca ctgatgggag ccctgcctgg gccatgtgct gtggggccaa	1615		
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acctcattaa actatgccaa actttaaaaa aaaaa	1710		

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&lt;211&gt; 1424

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;222&gt; (212) .. (1102)

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gtgccttgaa gccagcaggg ccttgccctac ggatacctcc acccaccctc ctgcccagca 180  
agtggaggcc cgcagcccca gtgtcgccgc c atg gct tcg ccg cag ctc tgc 232  
Met Ala Ser Pro Gln Leu Cys  
1 5  
cgc gcg ctg gtg tcg gcg caa tgg gtg gcg gag gcg ctg cgg gcc ccg 280  
Arg Ala Leu Val Ser Ala Gln Trp Val Ala Glu Ala Leu Arg Ala Pro  
10 15 20  
cgc gct ggg cag cct ctg cag ctg ctg gac gcc tcc tgg tac ctg ccg 328  
Arg Ala Gly Gln Pro Leu Gln Leu Leu Asp Ala Ser Trp Tyr Leu Pro  
25 30 35  
aag ctg ggg cgc gac gcg cga cgc gag ttc gag gag cgc cac atc ccg 376  
Lys Leu Gly Arg Asp Ala Arg Arg Glu Phe Glu Glu Arg His Ile Pro  
40 45 50 55  
ggc gcc gct ttc ttc gac atc gac cag tgc agc gac cgc acc tcg ccc 424  
Gly Ala Ala Phe Phe Asp Ile Asp Gln Cys Ser Asp Arg Thr Ser Pro  
60 65 70  
tac gac cac atg ctg ccc ggg gcc gag cat ttc gcg gag tac gca ggc 472  
Tyr Asp His Met Leu Pro Gly Ala Glu His Phe Ala Glu Tyr Ala Gly  
75 80 85  
cgc ctg ggc gtg ggc gcg gcc acc cac gtc gtg atc tac gac gcc agc 520  
Arg Leu Gly Val Gly Ala Ala Thr His Val Val Ile Tyr Asp Ala Ser  
90 95 100  
gac cag ggc ctc tac tcc gcc ccg cgc gtc tgg tgg atg ttc cgc gcc 568  
Asp Gln Gly Leu Tyr Ser Ala Pro Arg Val Trp Trp Met Phe Arg Ala  
105 110 115  
ttc ggc cac cac gcc gtg tca ctg ctt gat ggc ggc ctc cgc cac tgg 616  
Phe Gly His His Ala Val Ser Leu Leu Asp Gly Gly Leu Arg His Trp  
120 125 130 135  
ctg cgc cag aac ctc ccg ctc agc tcc ggc aag agc caa cct gct ccc 664  
Leu Arg Gln Asn Leu Pro Leu Ser Ser Gly Lys Ser Gln Pro Ala Pro  
140 145 150  
gcc gag ttc cgc gct cag ctc gac ccc gcc ttc atc aag acc tac gag 712  
Ala Glu Phe Arg Ala Gln Leu Asp Pro Ala Phe Ile Lys Thr Tyr Glu  
155 160 165  
gac atc aag gag aac ctg gaa tcc ccg cgc ttc cag gtg gtg gac tcc 760  
Asp Ile Lys Glu Asn Leu Glu Ser Arg Arg Phe Gln Val Val Asp Ser  
170 175 180  
cga gcc act ggc agg ttc cgc ggc acc gag ccc gag ccc cga gac ggc 808  
Arg Ala Thr Gly Arg Phe Arg Gly Thr Glu Pro Glu Pro Arg Asp Gly  
185 190 195  
att gaa cct ggc cac atc cca ggt acc gtg aac atc ccc ttc aca gac 856  
Ile Glu Pro Gly His Ile Pro Gly Thr Val Asn Ile Pro Phe Thr Asp  
200 205 210 215

ttc ctg agc cag gag ggg ctg gag aag agc cct gag gag atc cgc cat 904  
 Phe Leu Ser Gln Glu Gly Leu Glu Lys Ser Pro Glu Glu Ile Arg His  
 220 225 230  
  
 ctg ttc cag gag aag aaa gtg gac ctg tct aag cca ctg gtg gcc acg 952  
 Leu Phe Gln Glu Lys Lys Val Asp Leu Ser Lys Pro Leu Val Ala Thr  
 235 240 245  
  
 tgt ggc tct ggc gtc aca gcc tgc cac gtg gca cta ggg gcc tac ctc 1000  
 Cys Gly Ser Gly Val Thr Ala Cys His Val Ala Leu Gly Ala Tyr Leu  
 250 255 260  
  
 tgc ggc aag cca gac gtg ccc atc tac gat ggc tcc tgg gtg gag tgg 1048  
 Cys Gly Lys Pro Asp Val Pro Ile Tyr Asp Gly Ser Trp Val Glu Trp  
 265 270 275  
  
 tac atg cgc gcc cgg ccc gag gat gtc atc tca gag ggc cgg ggg aag 1096  
 Tyr Met Arg Ala Arg Pro Glu Asp Val Ile Ser Glu Gly Arg Gly Lys  
 280 285 290 295  
  
 acc cac tgaagctggg caggacacag gcgagctcag gtgatgccgg ccaccagcaa 1152  
 Thr His  
  
 tgcttggcct ggtagctccg cttctgcttt caccaagaga gtgtttcttc actcaactca 1212  
 ggtggcattt ggggtgacat ctcaaaggcc aggaattccg ttgacttggt ggctgccagt 1272  
 aggggcgggg gaaaaggcgg aggcgagccc tggaggaggg aggccacaac tccgagctgc 1332  
 ccacctggtg ctgagctggg gccccgcctc cttctgtgtt tatttttgag gaaataaaat 1392  
 aaccaagtgc taaatcttgt aaaaaaaaaa aa 1424

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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (91)..(1425)

<400> 312  
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 gccagcgcca ccgctccgc agccggcacc atg cgc gag atc gtg cac atc 111  
 Met Arg Glu Ile Val His Ile  
 1 5  
  
 cag gcg ggc cag tgc ggc aac cag atc ggc gcc aag ttt tgg gag gtc 159  
 Gln Ala Gly Gln Cys Gly Asn Gln Ile Gly Ala Lys Phe Trp Glu Val  
 10 15 20  
  
 atc agc gat gag cat ggg atc gac ccc aca ggc agt tac cat gga gac 207  
 Ile Ser Asp Glu His Gly Ile Asp Pro Thr Gly Ser Tyr His Gly Asp  
 25 30 35  
  
 agt gac ttg cag ctg gag aga atc aac gtg tac tac aat gag gct gct 255  
 Ser Asp Leu Gln Leu Glu Arg Ile Asn Val Tyr Tyr Asn Glu Ala Ala  
 40 45 50 55

ggt aac aaa tat gta cct cgg gcc atc ctg gtg gat ctg gag cct ggc	303
Gly Asn Lys Tyr Val Pro Arg Ala Ile Leu Val Asp Leu Glu Pro Gly	
60 65 70	
acc atg gac tct gtc agg tct gga ccc ttc ggc cag atc ttc aga cca	351
Thr Met Asp Ser Val Arg Ser Gly Pro Phe Gly Gln Ile Phe Arg Pro	
75 80 85	
gac aac ttc gtg ttc ggc cag agt gga gcc ggg aat aac tgg gcc aag	399
Asp Asn Phe Val Phe Gly Gln Ser Gly Ala Gly Asn Asn Trp Ala Lys	
90 95 100	
ggc cac tac aca gag gga gcc gag ctg gtc gac tcg gtc ctg gat gtg	447
Gly His Tyr Thr Glu Gly Ala Glu Leu Val Asp Ser Val Leu Asp Val	
105 110 115	
gtg agg aag gag tca gag agc tgt gac tgt ctc cag ggc ttc cag ctg	495
Val Arg Lys Glu Ser Glu Ser Cys Asp Cys Leu Gln Gly Phe Gln Leu	
120 125 130 135	
acc cac tct ctg ggg ggc ggc acg ggg tcc ggg atg ggc acc ctg ctc	543
Thr His Ser Leu Gly Gly Gly Thr Gly Ser Gly Met Gly Thr Leu Leu	
140 145 150	
atc agc aag atc cgg gaa gag tac cca gac cgc atc atg aac acc ttc	591
Ile Ser Lys Ile Arg Glu Glu Tyr Pro Asp Arg Ile Met Asn Thr Phe	
155 160 165	
agc gtc atg ccc tca ccc aag gtg tca gac acg gtg gtg gag ccc tac	639
Ser Val Met Pro Ser Pro Lys Val Ser Asp Thr Val Val Glu Pro Tyr	
170 175 180	
aac gcc acc ctc tct gtc cac cag ctg gtg gaa aac aca gat gaâ acc	687
Asn Ala Thr Leu Ser Val His Gln Leu Val Glu Asn Thr Asp Glu Thr	
185 190 195	
tac tcc att gat aac gag gcc ctg tat gac atc tgc ttc cgc acc ctg	735
Tyr Ser Ile Asp Asn Glu Ala Leu Tyr Asp Ile Cys Phe Arg Thr Leu	
200 205 210 215	
aag ctg acc acc ccc acc tac ggg gac ctc aac cac ctg gtg tcg gcc	783
Lys Leu Thr Thr Pro Thr Tyr Gly Asp Leu Asn His Leu Val Ser Ala	
220 225 230	
acc atg agc ggg gtc acc acc tgc ctg cgc ttc ccg ggc cag ctg aac	831
Thr Met Ser Gly Val Thr Thr Cys Leu Arg Phe Pro Gly Gln Leu Asn	
235 240 245	
gca gac ctg cgc aag ctg gcg gtg aac atg gtg ccc ttc cct cgc ctg	879
Ala Asp Leu Arg Lys Leu Ala Val Asn Met Val Pro Phe Pro Arg Leu	
250 255 260	
cac ttc ttc atg ccc ggc ttc gcg ccc ctg acc agc cgg ggc agc cag	927
His Phe Phe Met Pro Gly Phe Ala Pro Leu Thr Ser Arg Gly Ser Gln	
265 270 275	
cag tac cgg gcg ctc acg gtg ccc gag ctc acc cag cag atg ttc gac	975
Gln Tyr Arg Ala Leu Thr Val Pro Glu Leu Thr Gln Gln Met Phe Asp	
280 285 290 295	
tcc aag aac atg atg gcc gcc tgc gac ccg cgc cac ggc cgc tac ctg	1023
Ser Lys Asn Met Met Ala Ala Cys Asp Pro Arg His Gly Arg Tyr Leu	
300 305 310	



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acg gtg gct gcc atc ttc cgg ggc cgc atg tcc atg aag gag gtg gac      1071
Thr Val Ala Ala Ile Phe Arg Gly Arg Met Ser Met Lys Glu Val Asp
          315                      320                      325

gag cag atg ctc aac gtg cag aac aag aac agc agc tac ttc gtg gag      1119
Glu Gln Met Leu Asn Val Gln Asn Lys Asn Ser Ser Tyr Phe Val Glu
          330                      335                      340

tgg atc ccc aac aac gtg aag acg gcc gtg tgc gac atc ccg ccc cgc      1167
Trp Ile Pro Asn Asn Val Lys Thr Ala Val Cys Asp Ile Pro Pro Arg
          345                      350                      355

ggc ctg aag atg tgc gcc acc ttc atc ggc aac agc acg gcc atc cag      1215
Gly Leu Lys Met Ser Ala Thr Phe Ile Gly Asn Ser Thr Ala Ile Gln
          360                      365                      370                      375

gag ctg ttc aag cgc atc tcc gag cag ttc acg gcc atg ttc cgg cgc      1263
Glu Leu Phe Lys Arg Ile Ser Glu Gln Phe Thr Ala Met Phe Arg Arg
          380                      385                      390

aag gcc ttc ctg cac tgg tac acg ggc gag ggc atg gac gag atg gag      1311
Lys Ala Phe Leu His Trp Tyr Thr Gly Glu Gly Met Asp Glu Met Glu
          395                      400                      405

ttc acc gag gcc gag agc aac atg aac gac ctg gtg tcc gag tac cag      1359
Phe Thr Glu Ala Glu Ser Asn Met Asn Asp Leu Val Ser Glu Tyr Gln
          410                      415                      420

cag tac cag gac gcc acg gcc gac gaa caa ggg gag ttc gag gag gag      1407
Gln Tyr Gln Asp Ala Thr Ala Asp Glu Gln Gly Glu Phe Glu Glu Glu
          425                      430                      435

gag ggc gag gac gag gct taaaaa cttctcagat caatcgtgca tccttagtga      1461
Glu Gly Glu Asp Glu Ala
          440                      445

acttctgttg tcctcaagca tgggtctttct acttgtaaac tatggtgctc agttttgcct      1521

ctgttagaaa ttcacactgt tgatgtaatg atgtggaact cctctaaaaa ttacagtatt      1581

gtctgtgaag gtatctatac taataaaaaa gcatgtgtag aaaaaaaaaa      1631

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<210> 313  
 <211> 1047  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (373) .. (912)

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cgcgtagggcg gtttcgtggg ctttacttgg ccgcgctta gggccctcgc ggggggcttg      120
tgggtcctcc tccccctccc actgacaact gccccaactg ctcttcccgc cccggtcaca      180
gtgaaaatgt agacggggtc gttgtccgta cgactgtgcg ccagggctcg gggaggggctg      240

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ccctccgcgt gagcgcccc ctgggaatat tgaacataat cacctctcat tccagactat      300
gttaggtctt aatggtggga ggacgcccga gtgctcggcc cgtttcaccc cgaggaggaa      360
ggacactggg tc      atg acg cca tca gag ggc gcc aga gca ggg acc gga      408
                    Met Thr Pro Ser Glu Gly Ala Arg Ala Gly Thr Gly
                    1          5          10

cgc gag ttg gag atg ttg gac tcg ctg ttg gcc ttg ggc ggc ctg gtg      456
Arg Glu Leu Glu Met Leu Asp Ser Leu Leu Ala Leu Gly Gly Leu Val
    15          20          25

ctg ctt cgg gat tcc gtg gag tgg gag ggg cgc agt ctc ttg aag gcg      504
Leu Leu Arg Asp Ser Val Glu Trp Glu Gly Arg Ser Leu Leu Lys Ala
    30          35          40

ctt gtc aag aaa tct gca ctg tgt ggg gag caa gtg cat atc ctg ggc      552
Leu Val Lys Lys Ser Ala Leu Cys Gly Glu Gln Val His Ile Leu Gly
    45          50          55          60

tgt gaa gtg agc gag gaa gag ttt cgt gaa ggt ttt gac tct gat atc      600
Cys Glu Val Ser Glu Glu Glu Phe Arg Glu Gly Phe Asp Ser Asp Ile
    65          70          75

aac aat cgg ctg gtt tac cat gac ttc ttc aga gac cct ctc aac tgg      648
Asn Asn Arg Leu Val Tyr His Asp Phe Phe Arg Asp Pro Leu Asn Trp
    80          85          90

tca aaa act gag gag gcc ttt cct ggg ggg ccg ctg gga gcc ttg aga      696
Ser Lys Thr Glu Glu Ala Phe Pro Gly Gly Pro Leu Gly Ala Leu Arg
    95          100          105

gcc atg tgc aag agg aca gat cct gtt cct gtc acc att gct ctc gat      744
Ala Met Cys Lys Arg Thr Asp Pro Val Pro Val Thr Ile Ala Leu Asp
    110          115          120

tca ctc agc tgg ctg cta ctt cgc ctt ccc tgc acc aca ctc tgc cag      792
Ser Leu Ser Trp Leu Leu Leu Arg Leu Pro Cys Thr Thr Leu Cys Gln
    125          130          135          140

gtc ctg cat gct gtg agc cat cag gac tct tgt cct ggt gag acc cct      840
Val Leu His Ala Val Ser His Gln Asp Ser Cys Pro Gly Glu Thr Pro
    145          150          155

cct tca ttg ttt ccc ctc ata cat ctc cct ctg cca agg agt gtg ccc      888
Pro Ser Leu Phe Pro Leu Ile His Leu Pro Leu Pro Arg Ser Val Pro
    160          165          170

ctt ttc ctt tct acc cta gaa taa acatctgggt tctccagtca gacctttttt      942
Leu Phe Leu Ser Thr Leu Glu *
    175          180

catttttttg acttttttgt ctgttttttt tttttttact tctccttaat gccatctacc      1002

acttgctttt tttctccaag ttattttttt actcatttgt ttcac      1047

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<210> 314  
 <211> 2013  
 <212> DNA  
 <213> Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (110) .. (919)

&lt;400&gt; 314

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cgctcgggaat tcccgggtcg acccacgcgt ccgcgcagcg ggtgcgggcg ccgacgggcg      60

agagccagcg agcgagcgag cgagccgagc cgagcctccc gccgtcgcc      atg ggc      115
                               Met Gly
                               1

cag aac gac ctg atg ggc acg gcc gag gac ttc gcc gac cag ttc ctc      163
Gln Asn Asp Leu Met Gly Thr Ala Glu Asp Phe Ala Asp Gln Phe Leu
                    5              10              15

cgt gtc aca aag cag tac ctg ccc cac gtg gcg cgc ctc tgt ctg atc      211
Arg Val Thr Lys Gln Tyr Leu Pro His Val Ala Arg Leu Cys Leu Ile
        20              25              30

agc acc ttc ctg gag gac ggc atc cgt atg tgg ttc cag tgg agc gag      259
Ser Thr Phe Leu Glu Asp Gly Ile Arg Met Trp Phe Gln Trp Ser Glu
        35              40              45              50

cag cgc gac tac atc gac acc acc tgg aac tgc gcc tac ctg ctg gcc      307
Gln Arg Asp Tyr Ile Asp Thr Thr Trp Asn Cys Gly Tyr Leu Leu Ala
                    55              60              65

tcg tcc ttc gtc ttc ctc aac ttg ctg gga cag ctg act ggc tgc gtc      355
Ser Ser Phe Val Phe Leu Asn Leu Leu Gly Gln Leu Thr Gly Cys Val
                    70              75              80

ctg gtg ttg agc agg aac ttc gtg cag tac gcc tgc ttc ggg ctc ttt      403
Leu Val Leu Ser Arg Asn Phe Val Gln Tyr Ala Cys Phe Gly Leu Phe
                    85              90              95

gga atc ata gct ctg cag acg att gcc tac agc att tta tgg gac ttg      451
Gly Ile Ile Ala Leu Gln Thr Ile Ala Tyr Ser Ile Leu Trp Asp Leu
        100              105              110

aag ttt ttg atg agg aac ctg gcc ctg gga gga ggc ctg ttg ctg ctc      499
Lys Phe Leu Met Arg Asn Leu Ala Leu Gly Gly Gly Leu Leu Leu Leu
        115              120              125              130

cta gca gaa tcc cgt tct gaa ggg aag agc atg ttt gcg ggc gtc ccc      547
Leu Ala Glu Ser Arg Ser Glu Gly Lys Ser Met Phe Ala Gly Val Pro
                    135              140              145

acc atg cgt gag agc tcc ccc aaa cag tac atg cag ctc gga ggc agg      595
Thr Met Arg Glu Ser Ser Pro Lys Gln Tyr Met Gln Leu Gly Gly Arg
                    150              155              160

gtc ttg ctg gtt ctg atg ttc atg acc ctc ctt cac ttt gac gcc agc      643
Val Leu Leu Val Leu Met Phe Met Thr Leu Leu His Phe Asp Ala Ser
                    165              170              175

ttc ttt tct att gtc cag aac atc gtg ggc aca gct ctg atg att tta      691
Phe Phe Ser Ile Val Gln Asn Ile Val Gly Thr Ala Leu Met Ile Leu
        180              185              190

gtg gcc att ggt ttt aaa acc aag ctg gct gct ttg act ctt gtt gtg      739
Val Ala Ile Gly Phe Lys Thr Lys Leu Ala Ala Leu Thr Leu Val Val
        195              200              205              210

tgg ctc ttt gcc atc aac gta tat ttc aac gcc ttc tgg acc att cca      787

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Trp	Leu	Phe	Ala	Ile	Asn	Val	Tyr	Phe	Asn	Ala	Phe	Trp	Thr	Ile	Pro	
				215					220					225		
gtc	tac	aag	ccc	atg	cat	gac	ttc	ctg	aaa	tac	gac	ttc	ttc	cag	acc	835
Val	Tyr	Lys	Pro	Met	His	Asp	Phe	Leu	Lys	Tyr	Asp	Phe	Phe	Gln	Thr	
			230					235					240			
atg	tcg	gtg	att	ggg	ggc	ttg	ctc	ctg	gtg	gtg	gcc	ctg	ggc	cct	ggg	883
Met	Ser	Val	Ile	Gly	Gly	Leu	Leu	Leu	Val	Val	Ala	Leu	Gly	Pro	Gly	
		245					250					255				
ggt	gtc	tcc	atg	gat	gag	aag	aag	aag	gag	tgg	taa	cagt	cacagatccc			933
Gly	Val	Ser	Met	Asp	Glu	Lys	Lys	Lys	Glu	Trp	*					
		260				265				270						
tacctg	cctg	gctaag	accc	gtggc	cg	tca	aggact	gg	tt	cgggg	gtgg	at	tcaacaaa	ac		993
tgccag	cttt	tatgtat	cct	cttcc	cttcc	cctcc	cttgg	taaagg	caca	gatgt	ttttga					1053
gaacttt	tatt	tg	cagagaca	cctgaga	atc	gatgg	ctcag	tctg	ctctgg	agcc	cacagtc					1113
tggcgt	tctga	cccttc	agtg	caggcc	agcc	tggcag	ctgg	aagc	ctcccc	cacgc	cgagg					1173
ctttgg	agtg	aacag	cctgg	ccag	ctgctc	agacc	agctt	gcagag	ccgc	agccg	ctgtg					1233
ggcaggg	gggt	gtggc	aggag	ctccc	agcac	tggag	accca	cggact	caac	ccag	ttacct					1293
cacatg	gggg	ctttt	ctgag	caagg	tctcg	aaagc	gcagg	ccgcc	ctggc	tgag	cagcac					1353
cgccct	ttcc	cagct	gcact	cgcc	ctgtgg	acag	ccccga	cacacc	actt	tcct	gagget					1413
gtcg	ctcact	cagatt	gtcc	gtttg	ctatg	ccgaat	gcag	ccaaa	attcc	ttttt	tacaat					1473
ttgtg	atgcc	ttacc	gattt	gatct	taatc	ctgtat	ttaa	agtttt	ctaa	cactg	cctta					1533
tactg	tg	ttt	tttgg	gggag	cttaa	ctgct	tg	ctcc	ctg	tcg	tctgc	accat				1593
agtaa	atgcc	acaag	gtag	tcga	acac	ctctg	gcccc	tagac	ctatc	tgggg	acagg					1653
ctgg	ctcagc	ctgt	ctccag	ggct	gctgcg	gccc	agcccc	gagc	ctgc	ct	ctcttggc					1713
ctct	catcca	ttgg	ctctgc	aggg	cagggg	tgagg	caggt	ttct	gctcat	aagt	gctttt					1773
ggaag	tcacc	tacct	tttta	acac	agccga	actag	tcca	acgc	gtttgc	aaat	attccc					1833
ctgg	tagcct	acttc	cttac	cccc	gaatat	tggt	aagatc	gag	caatggc	ttc	aggacat					1893
gggt	tctctt	ctc	ctgtgat	catt	caagt	ctc	actgcat	gaag	actggc	ttat	ctcagt					1953
gttt	caacct	cacc	agggct	gtct	cttgg	ccac	acctcg	ctcc	ctgtta	gtgc	cg	tatg				2013

<210> 315  
 <211> 737  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (346)..(702)

<400> 315

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agaaatgagc aaaaacttca atatatatga ctcaggcaag aaatcagcat ctgtggcaaa      120
tactagaatg aaatgcaaga aagctcactg caaggagtct ccctccctgc agattccaag      180
gctggaatct ttttcttctg gctccaggca gcacagacag ggcctagcct ggagagggtg      240
gacaagatgt cctctcaggg tcttcaatgg ccaagtccat gcccaactgca gaatctttct      300
gtctaccctg aagtatcctt tctgagttc caggcaaagc tgggg      atg tta gcc      354
                                           Met Leu Ala
                                           1

tat gac tgt cat ctg act tgg aag gta cac cta ggg gcc ggg ggg agg      402
Tyr Asp Cys His Leu Thr Trp Lys Val His Leu Gly Ala Gly Gly Arg
      5              10              15

tca gca ggg gag ttt ggg agc cac ttc tcc ccc cac gtg gca ctg gag      450
Ser Ala Gly Glu Phe Gly Ser His Phe Ser Pro His Val Ala Leu Glu
      20              25              30              35

tgt gaa ctg gct cat tct gga cac cag cat gga gcc agc acg gga aca      498
Cys Glu Leu Ala His Ser Gly His Gln His Gly Ala Ser Thr Gly Thr
              40              45              50

ggg ggg cag cct aga gca caa gct cta tct gtg tcc ttc aga gct cct      546
Gly Gly Gln Pro Arg Ala Gln Ala Leu Ser Val Ser Phe Arg Ala Pro
              55              60              65

ggg aaa cat gat gcg ccc tca tgg gaa tgg cat ttt gca tat cac aca      594
Gly Lys His Asp Ala Pro Ser Trp Glu Trp His Phe Ala Tyr His Thr
              70              75              80

ggc tgt cct ggg agt cag gca gac tgg att gtc acg tgc ggt gtg cat      642
Gly Cys Pro Gly Ser Gln Ala Asp Trp Ile Val Thr Cys Gly Val His
      85              90              95

gca gca gct tgt gca ctg cag tgg acc tgt gga cca ttt cta aag gtg      690
Ala Ala Ala Cys Ala Leu Gln Trp Thr Cys Gly Pro Phe Leu Lys Val
      100              105              110              115

cac aac aaa taa taaatgtgtc cttctttgtt tttaaaaaaa aaaaa      737
His Asn Lys *

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<210> 316  
 <211> 722  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (494)..(673)

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<400> 316
tatttcatca aatccaagat ataccaattg taagatgcac cattattata tgcactactg      60
ataattttat gcatcactga tatttttcaa aaggcatcct gaatgttata agaagctgac      120

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tgatatcaga gatgtagaa taggatctca gaacggatga aatatgttat gaaatatggt 180
tatgggttat gaaataccta gtcataacag tcatcaatag aagtgtagct cctttttgcc 240
cacctcaaag gcaaagcctg tgatcatctt atacccta tggaacctaa gactggatca 300
tgatggaatg atggcaataa aaaacataac tgatatctac tgagcacttt atttgtgttg 360
cagcgcaact ttatatgaat taatactcaa gataactttt attgcttggt ttggttaagta 420
ctattattcc cactttgcag ataagggtac tgagacttaa agagaagtta aacatctcaa 480
ccaagttagg aag  atg ctt gga tta caa acc caa gtc tat cta atg cta 529
                  Met Leu Gly Leu Gln Thr Gln Val Tyr Leu Met Leu
                   1           5           10

gat cta cac ctt cta agc cac tgt gtt aca ctg tcc tta agg agg gtc 577
Asp Leu His Leu Leu Ser His Cys Val Thr Leu Ser Leu Arg Arg Val
   15           20           25

agg ttg tgg gtg tca aga cta caa agg caa gta aca cac gtg aga agc 625
Arg Leu Trp Val Ser Arg Leu Gln Arg Gln Val Thr His Val Arg Ser
   30           35           40

tca ggc cag aat cag aga gaa gga tgg tca aga gtt ttg gag atg agg 673
Ser Gly Gln Asn Gln Arg Glu Gly Trp Ser Arg Val Leu Glu Met Arg
   45           50           55           60

taacttaaag aactggctcg tgccgaattc ttggcctcga gggccaaat 722

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<210> 317  
 <211> 1091  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (132)..(824)

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<400> 317
gcacgagcta aagagagccc ggagccagcg tgggaggccg ctgccgtcgc gcgccttggt 60
ttttctgttc cttttttttt ttttttttta acttctgcc tatacacacg cagccatcag 120
cccacaaaga c atg act acc aac gcg ggc ccc ttg cac cca tac tgg cct 170
              Met Thr Thr Asn Ala Gly Pro Leu His Pro Tyr Trp Pro
               1           5           10

cag cac cta aga ctg gac aac ttt gta cct aat gac cgc ccc acc tgg 218
Gln His Leu Arg Leu Asp Asn Phe Val Pro Asn Asp Arg Pro Thr Trp
   15           20           25

cat ata ctg gct ggc ctc ttc tct gtc aca ggg gtc tta gtc gtg acc 266
His Ile Leu Ala Gly Leu Phe Ser Val Thr Gly Val Leu Val Val Thr
   30           35           40           45

aca tgg ctg ttg tca ggt cgt gct gcg gtt gtc cca ttg ggg act tgg 314
Thr Trp Leu Leu Ser Gly Arg Ala Val Val Pro Leu Gly Thr Trp
   50           55           60

cgg cga ctg tcc ctg tgc tgg ttt gca gtg tgt ggg ttc att cac ctg 362

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Arg Arg Leu Ser Leu Cys Trp Phe Ala Val Cys Gly Phe Ile His Leu
      65              70              75

gtg atc gag ggc tgg ttc gtt ctc tac tac gaa gac ctg ctt gga gac      410
Val Ile Glu Gly Trp Phe Val Leu Tyr Tyr Glu Asp Leu Leu Gly Asp
      80              85              90

caa gcc ttc tta tct caa ctc tgg aaa gag tat gcc aag gga gac agc      458
Gln Ala Phe Leu Ser Gln Leu Trp Lys Glu Tyr Ala Lys Gly Asp Ser
      95              100             105

cga tac atc ctg ggt gac aac ttc aca gtg tgc atg gaa acc atc aca      506
Arg Tyr Ile Leu Gly Asp Asn Phe Thr Val Cys Met Glu Thr Ile Thr
     110              115              120             125

gct tgc ctg tgg gga cca ctc agc ctg tgg gtg gtg atc gcc ttt ctc      554
Ala Cys Leu Trp Gly Pro Leu Ser Leu Trp Val Val Ile Ala Phe Leu
      130              135             140

cgc cag cat ccc ctc cgc ttc att cta cag ctt gtg gtc tct gtg ggc      602
Arg Gln His Pro Leu Arg Phe Ile Leu Gln Leu Val Val Ser Val Gly
      145              150             155

cag atc tat ggg gat gtg ctc tac ttc ctg aca gag cac cgc gac gga      650
Gln Ile Tyr Gly Asp Val Leu Tyr Phe Leu Thr Glu His Arg Asp Gly
      160              165             170

ttc cag cac gga gag ctg ggc cac cct ctc tac ttc tgg ttt tac ttt      698
Phe Gln His Gly Glu Leu Gly His Pro Leu Tyr Phe Trp Phe Tyr Phe
      175              180             185

gtc ttc atg aat gcc ctg tgg ctg gtg ctg cct gga gtc ctt gtg ctt      746
Val Phe Met Asn Ala Leu Trp Leu Val Leu Pro Gly Val Leu Val Leu
     190              195              200             205

gat gct gtg aag cac ctc act cat gcc cag agc acg ctg gat gcc aag      794
Asp Ala Val Lys His Leu Thr His Ala Gln Ser Thr Leu Asp Ala Lys
      210              215             220

gcc aca aaa gcc aag agc aag aag aac tga g gagtggtgga ccaggctcga      845
Ala Thr Lys Ala Lys Ser Lys Lys Asn *
      225              230

acactggcgcg aggaggagct ctctgcctgc cagaagagtc tagtcctgct cccacagttt      905

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ataaaggggc tgtgtgaagg cactgctggg agccattaga acacagatac aagagaagcc      1025

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<220>  
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 <222> (117)..(305)

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 atg tca tat tta gat tca gtt gca tca aag tta ttg caa atg gtg aaa 164  
 Met Ser Tyr Leu Asp Ser Val Ala Ser Lys Leu Leu Gln Met Val Lys  
 1 5 10 15  
 aaa tta tcc cag tcc ttt tgc agt aat ttt aaa tat cta aca aaa tat 212  
 Lys Leu Ser Gln Ser Phe Cys Ser Asn Phe Lys Tyr Leu Thr Lys Tyr  
 20 25 30  
 tca aga aaa cag gtt tct gat gaa atc aaa aag tca aga aga act gtg 260  
 Ser Arg Lys Gln Val Ser Asp Glu Ile Lys Lys Ser Arg Arg Thr Val  
 35 40 45  
 gaa tca aat cct ata ttt ttc aag aag aac aag aaa ata cag tga gga 308  
 Glu Ser Asn Pro Ile Phe Phe Lys Lys Asn Lys Lys Ile Gln \*  
 50 55 60  
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tcaccacagt gtagatacag tccgggcttt ctctgtgctt tgcagacctc agtgagacac      891
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ggccctgcag tcccagttct gctgggttaac ctgccacatg cacttctgtc ctgacacaca     1011
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tactctccca aatgcagcct aatcttagta acctgaagt ttatcattct ttaaaaataa     1371
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gattattagc ttaccaacc ctgtgaacac tgagggttgca gaactgccag gttaatccct     1491
gtggcctaga ctactgagga ttctgatagc acatgtaaga ctaagcactc ttcaagctgt     1551
aataaagcat ccacatgtat ctgtgatgat tttcattgct ttagcattgc agccatgtaa     1611
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tttgttttca gcagtgagca gaccgtacag gagcagcaca ccaggagcca tgagaagtgc     1851
cttggaacc aacagggaaa cagaactatc tttatacaca tcccctcatg gacaagagat     1911
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aaaaa                                         2036

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&lt;210&gt; 320

&lt;211&gt; 1721

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1088)..(1417)

&lt;400&gt; 320

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aaactattgc tggcacttcc ccctggaaat aactaatgag gttacgagtt gggcacctgc     180
acagatgtcc ttctctcata gttcctaata cttaggaata gaggagaaat aaaaaaatgg     240
attctctcaa aacactgcca tttgaatagc gacagaagtg ctccccagc ccccaacttt     300

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ggacagcaaa gttgaggaga atgagcagac acagttgttt gcttgatctg aatctctcta 360  
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 gaagcttctt acagcagtga aacggggcac cacctcccc acactcctca ttccccgctt 480  
 aaaacatgga tactttcaaa ttgactggt tcttaaactg ccatcctaag atatggaaaa 540  
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 ccaatctcct tataacacca cagcgtatcc tgccattgac agtghtaatca caattctccc 900  
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 tttttgt atg ata atc aaa tgt aaa ata ctt tta ttt ttg ctg gac agt 1129  
           Met Ile Ile Lys Cys Lys Ile Leu Leu Phe Leu Leu Asp Ser  
           1                  5                  10  
 tgt tat atc atg att att gtg cta cag ttt att gtg cat aat atg aaa 1177  
 Cys Tyr Ile Met Ile Ile Val Leu Gln Phe Ile Val His Asn Met Lys  
       15                  20                  25                  30  
 aac aac tat gac agc ctt cag tcg ggc cag ggt gaa gct gct tat acc 1225  
 Asn Asn Tyr Asp Ser Leu Gln Ser Gly Gln Gly Glu Ala Ala Tyr Thr  
                   35                  40                  45  
 acc tct gcc gtc aga ggg aca tgt ggt gac agc agt ggt gtg gct gca 1273  
 Thr Ser Ala Val Arg Gly Thr Cys Gly Asp Ser Ser Gly Val Ala Ala  
                   50                  55                  60  
 cag ggc gca cta gag aga gct cag cac ccc tgc tgc ccg cca gca gag 1321  
 Gln Gly Ala Leu Glu Arg Ala Gln His Pro Cys Cys Pro Pro Ala Glu  
           65                  70                  75  
 ccc gtg ctg agg gaa tgc cgc aca gat gct gat gca ctg ggt gaa att 1369  
 Pro Val Leu Arg Glu Cys Arg Thr Asp Ala Asp Ala Leu Gly Glu Ile  
       80                  85                  90  
 tct agt att gaa cgt aaa ggt gta cag tgt ctt gct gtt att tta tga 1417  
 Ser Ser Ile Glu Arg Lys Gly Val Gln Cys Leu Ala Val Ile Leu \*  
       95                  100                  105                  110  
 tggaaactga ttttgaaacc aaaaatagct aactaacttt atttaaggaa aggatattaa 1477  
 tttgtactaa cagaggggtga aagctgttca catttgtcaa caaaatctgc ttgctgcagt 1537  
 agtaacctca agtgggttaaa acttgatttc ccgagaaaac taaaaccttt gtgcctaaaa 1597  
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1721

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Asp Ala Val Leu Asp Gln Tyr Ser Met Trp Gly Asn Lys Phe Gly Val				
	170	175	180	
ttg ctt ttt ctg tat tct gta tta ctg aca aag ggc att gaa aac ata				811
Leu Leu Phe Leu Tyr Ser Val Leu Leu Thr Lys Gly Ile Glu Asn Ile				
	185	190	195	
aaa aac gaa att gaa gat gca agt gaa ccc ttg ata gat cct gta tat				859
Lys Asn Glu Ile Glu Asp Ala Ser Glu Pro Leu Ile Asp Pro Val Tyr				
	200	205	210	
gga cat ggc agc caa agt tta att aat ctc ctg ctg acg gga cat gct				907
Gly His Gly Ser Gln Ser Leu Ile Asn Leu Leu Leu Thr Gly His Ala				
	215	220	225	
gtt tct aat gta tgg gat ggt gat aga gag tgc tca gga atg aaa ctt				955
Val Ser Asn Val Trp Asp Gly Asp Arg Glu Cys Ser Gly Met Lys Leu				
	230	235	240	245
ctt ggt ata cat gaa caa gca gca gta gga ttt tta aca cta atg gaa				1003
Leu Gly Ile His Glu Gln Ala Ala Val Gly Phe Leu Thr Leu Met Glu				
	250	255	260	
gct tta aga tac tgt aag gtt ggt tct tac ttg aaa tct cca aaa ttc				1051
Ala Leu Arg Tyr Cys Lys Val Gly Ser Tyr Leu Lys Ser Pro Lys Phe				
	265	270	275	
cct att tgg att gtt ggc agt gag act cac ctc acc gta ttt ttt gcc				1099
Pro Ile Trp Ile Val Gly Ser Glu Thr His Leu Thr Val Phe Phe Ala				
	280	285	290	
aag gat atg gct tta gtt gcc cct gaa gct cct tca gaa caa gcc aga				1147
Lys Asp Met Ala Leu Val Ala Pro Glu Ala Pro Ser Glu Gln Ala Arg				
	295	300	305	
aga gtt ttt caa acc tac gac cca gaa gat aat gga ttc ata ccc gat				1195
Arg Val Phe Gln Thr Tyr Asp Pro Glu Asp Asn Gly Phe Ile Pro Asp				
	310	315	320	325
tca ctt ctg gaa gat gtg atg aaa gca ttg gac ctt gtt tca gat cct				1243
Ser Leu Leu Glu Asp Val Met Lys Ala Leu Asp Leu Val Ser Asp Pro				
	330	335	340	
gaa tat ata aat ctc atg aag aat aaa tta gat cca gaa gga tta gga				1291
Glu Tyr Ile Asn Leu Met Lys Asn Lys Leu Asp Pro Glu Gly Leu Gly				
	345	350	355	
atc ata tta ttg ggc cca ttt ctt caa gaa ttt ttt cct gat cag ggc				1339
Ile Ile Leu Leu Gly Pro Phe Leu Gln Glu Phe Phe Pro Asp Gln Gly				
	360	365	370	
tcc agt ggt cca gaa tct ttt act gtc tac cac tac aat gga ttg aag				1387
Ser Ser Gly Pro Glu Ser Phe Thr Val Tyr His Tyr Asn Gly Leu Lys				
	375	380	385	
cag tca aat tat aat gaa aag gtc atg tac gta gaa ggg act gca gtt				1435
Gln Ser Asn Tyr Asn Glu Lys Val Met Tyr Val Glu Gly Thr Ala Val				
	390	395	400	405
gtg atg ggt ttt gaa gat ccc atg cta cag aca gat gac act cct att				1483
Val Met Gly Phe Glu Asp Pro Met Leu Gln Thr Asp Asp Thr Pro Ile				

410

415

420

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aaa cgc tgt ctg caa acc aaa tgg cca tac att gag tta ctc tgg acc 1531
Lys Arg Cys Leu Gln Thr Lys Trp Pro Tyr Ile Glu Leu Leu Trp Thr
      425              430              435

aca gat cgc tct cct tca cta aat taa tttgt ctaagtatTTT ataaggaaga 1583
Thr Asp Arg Ser Pro Ser Leu Asn *
      440              445

tcttaataac agatgttgaa agaaggagtc aagactggca attggctgga ttaagctaaa 1643

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aaaaa 1708

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tctggcccg cgaagttaag caaccaagag gcgggcctaa gaccggaagc aggaaggagg 180

gcgcaggaag cagggcgccg cagcctgtcg tacggtcctt ctgtgggtct gtcggtgccg 240

agggcagg atg gag aag ctg cgg ctc ctg ggc ctc cgc tac cag gag tac 290
Met Glu Lys Leu Arg Leu Leu Gly Leu Arg Tyr Gln Glu Tyr
      1              5              10

gtg act cgt cac ccg gcc gcc acg gcc cag ctg gag aca gca gtg cgg 338
Val Thr Arg His Pro Ala Ala Thr Ala Gln Leu Glu Thr Ala Val Arg
      15              20              25              30

ggc ttc agt tac ctg ctg gca ggt cga ttc gcc gat tcg cac gag ctg 386
Gly Phe Ser Tyr Leu Leu Ala Gly Arg Phe Ala Asp Ser His Glu Leu
      35              40              45

tca gag ctg gtg tac tct gcc tct aac ctg ctt gtg ctg ctc aat gac 434
Ser Glu Leu Val Tyr Ser Ala Ser Asn Leu Leu Val Leu Leu Asn Asp
      50              55              60

ggg atc cta cgg aag gag ctt cgg aaa aag ttg cct gtg tcg ctg tcc 482
Gly Ile Leu Arg Lys Glu Leu Arg Lys Lys Leu Pro Val Ser Leu Ser
      65              70              75

cag cag aag ctg ctg aca tgg ctg agc gtg ctg gag tgc gtg gag gtg 530
Gln Gln Lys Leu Leu Thr Trp Leu Ser Val Leu Glu Cys Val Glu Val
      80              85              90

ttc atg gag atg gga gct gcc aag gtg tgg ggt gaa gtg ggc cgc tgg 578
Phe Met Glu Met Gly Ala Ala Lys Val Trp Gly Glu Val Gly Arg Trp
      95              100              105              110

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ctt gtc atc gcc ctc atc cag ctg gcc aag gct gta ctg cgg atg ctc Leu Val Ile Ala Leu Ile Gln Leu Ala Lys Ala Val Leu Arg Met Leu 115 120 125	626
ctg ctg ctc tgg ttc aag gct ggc ctc cag act tca ccc cct atc gtt Leu Leu Leu Trp Phe Lys Ala Gly Leu Gln Thr Ser Pro Pro Ile Val 130 135 140	674
cca ctg gac aga gag acc cag gca cag ccc ccg gat ggt gac cac agc Pro Leu Asp Arg Glu Thr Gln Ala Gln Pro Pro Asp Gly Asp His Ser 145 150 155	722
cct ggc aac cat gag cag tcc tac gtg ggg aag cgg tca aac cgg gtg Pro Gly Asn His Glu Gln Ser Tyr Val Gly Lys Arg Ser Asn Arg Val 160 165 170	770
gtg cga acc ctc cag aac acg ccg tcc ctg cac tcc agg cac tgg gga Val Arg Thr Leu Gln Asn Thr Pro Ser Leu His Ser Arg His Trp Gly 175 180 185 190	818
gct ccc cag cag cgg gag gga cgg cag cag cag cat cac gag gag ctg Ala Pro Gln Gln Arg Glu Gly Arg Gln Gln Gln His His Glu Glu Leu 195 200 205	866
agt gcg acc ccc acc ccc ctg ggg ctg cag gag acc atc gca gag ttt Ser Ala Thr Pro Thr Pro Leu Gly Leu Gln Glu Thr Ile Ala Glu Phe 210 215 220	914
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acc agc ctg agc ctc ctg agt gac aga aag ggc ctg acc cgg agg gag Thr Ser Leu Ser Leu Leu Ser Asp Arg Lys Gly Leu Thr Arg Arg Glu 255 260 265 270	1058
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cgc tct cct ttc tac gac cgc ttc tcc gag gcc agg atc ctc ttc ctg Arg Ser Pro Phe Tyr Asp Arg Phe Ser Glu Ala Arg Ile Leu Phe Leu 290 295 300	1154
ctc cag ttg ctg gcc gac cac gtc cct ggc gtt ggc ctg gtc aca agg Leu Gln Leu Leu Ala Asp His Val Pro Gly Val Gly Leu Val Thr Arg 305 310 315	1202
ccg ctc atg gat tac ttg ccc acc tgg cag aaa atc tac ttc tac agt Pro Leu Met Asp Tyr Leu Pro Thr Trp Gln Lys Ile Tyr Phe Tyr Ser 320 325 330	1250
tgg ggc tga cagacct cccggaagga ggggtgtgggg aggggtgggg cagggagccc Trp Gly *	1306
335	
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824



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 <213> Homo sapiens

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 ttaactgaag aactgcaggt tgcaggtgtg tggcatgcac gaggagtctg gcgtctgctc 180  
 ccgttttgac taatagaacc taaaggagct taagaaatca ggtgaatgtg aatcagcttt 240  
 gcacacgtct tttaaattga ttatctttat gtttaggctc taaacaggat tactttatcg 300  
 gcgtcgctaa tagcagttca tttattaagt tgattatcaa taatccctga caaatgagtc 360  
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 tgaaggcgca atggcaatga taa atg aga cag ctc ttg ctt tca aag gct 470  
 Met Arg Gln Leu Leu Leu Ser Lys Ala  
 1 5  
 ata ggg act ctc ggg aaa gca aac agg cat gtg gta gag aca agc acg 518  
 Ile Gly Thr Leu Gly Lys Ala Asn Arg His Val Val Glu Thr Ser Thr  
 10 15 20 25  
 agc agt gag gaa ata tgc tgc agg gga cgt aac tcc agg gag cct tcc 566  
 Ser Ser Glu Glu Ile Cys Cys Arg Gly Arg Asn Ser Arg Glu Pro Ser  
 30 35 40  
 cag agg agg caa tca gag ctg ggc atg gaa gga tga ccgg cagcaaggag 616  
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Val Thr Cys Asn Tyr Glu Ala Arg Lys Leu Gly Val Lys Lys Leu Met  
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Glu Lys His Tyr Gly Arg Glu Ser Arg Gln Cys Pro Ile Pro Ser His			
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Val Ile Gln Lys Leu Gly Thr Gly Asn Tyr Asp Val Met Thr Pro Met			
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Val Asp Ile Leu Met Lys Leu Phe Arg Asn Met Val Asn Val Lys Met			
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Thr His Met Glu Asp Phe Pro Lys Asp Lys Glu Thr Asn Arg Asp Phe			
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Leu Pro Ser Gly Arg Ile Glu Ser Thr Arg Thr Arg Glu Ser Pro Leu			
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Asp Thr Thr Asn Phe Ser Lys Glu Lys Asp Ile Asn Glu Phe Pro Leu			

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Cys Ser Leu Pro Glu Gly Val Asp Gln Glu Val Phe Lys Gln Leu Pro				
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Val Asp Ile Gln Glu Glu Ile Leu Ser Gly Lys Ser Arg Glu Lys Phe				
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Glu Gln Leu Phe Ser Arg Asn His Thr Thr Asp Ser His Lys Gln Thr				
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 Phe Met Leu Leu Gly Thr Leu Cys Glu Pro Gly Ser Gly Gln Ile Arg  
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 Arg Ile Val Ser Arg Gly Arg Thr Gln Leu Phe Ala Leu Asn Pro Arg  
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 Ser Gly Ser Leu Val Thr Ala Gly Arg Ile Asp Arg Glu Glu Leu Cys  
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 Ala Gln Ser Pro Leu Cys Val Val Asn Phe Asn Ile Leu Val Glu Asn  
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Ala Ser His Phe Val Gly Val Asp Gly Val Arg Ala Phe Leu Gln Thr		
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Tyr	Ser	His	Glu	Val	Ser	Leu	Thr	Ala	Asp	Ser	Arg	Lys	Ser	His	Leu		
		755					760					765					
atc	ttt	ccc	cag	ccc	aac	tac	gca	gac	acg	ctc	ctt	agt	gaa	gag	agc	2469	
Ile	Phe	Pro	Gln	Pro	Asn	Tyr	Ala	Asp	Thr	Leu	Ser	Glu	Glu	Ser			
	770				775					780							
tgt	gag	aaa	agc	gag	cct	ctt	ctg	atg	tct	gat	aag	gta	gat	gca	aac	2517	
Cys	Glu	Lys	Ser	Glu	Pro	Leu	Leu	Met	Ser	Asp	Lys	Val	Asp	Ala	Asn		
	785				790					795					800		
aaa	gaa	gaa	cgg	cga	gtt	cag	caa	gcc	ccg	ccc	aac	acg	gac	tgg	cgt	2565	
Lys	Glu	Glu	Arg	Arg	Val	Gln	Gln	Ala	Pro	Pro	Asn	Thr	Asp	Trp	Arg		
			805						810					815			
ttc	tct	cag	gcc	cag	aga	ccc	ggc	acc	agc	ggc	tcc	caa	aat	ggc	gat	2613	
Phe	Ser	Gln	Ala	Gln	Arg	Pro	Gly	Thr	Ser	Gly	Ser	Gln	Asn	Gly	Asp		
			820					825					830				
gac	acc	ggc	acc	tgg	ccc	aac	aac	cag	ttt	gac	aca	gag	atg	ctg	caa	2661	
Asp	Thr	Gly	Thr	Trp	Pro	Asn	Asn	Gln	Phe	Asp	Thr	Glu	Met	Leu	Gln		
		835					840					845					
gcc	atg	atc	ttg	gcg	tcc	gcc	agt	gaa	gct	gct	gat	ggg	agc	tcc	acc	2709	
Ala	Met	Ile	Leu	Ala	Ser	Ala	Ser	Glu	Ala	Ala	Asp	Gly	Ser	Ser	Thr		
	850					855					860						
ctg	gga	ggg	ggt	gcc	ggc	acc	atg	gga	ttg	agc	gcc	cgc	tac	gga	ccc	2757	
Leu	Gly	Gly	Gly	Ala	Gly	Thr	Met	Gly	Leu	Ser	Ala	Arg	Tyr	Gly	Pro		
	865				870					875					880		
cag	ttc	acc	ctg	cag	cac	gtg	ccc	gac	tac	cgc	cag	aat	gtc	tac	atc	2805	
Gln	Phe	Thr	Leu	Gln	His	Val	Pro	Asp	Tyr	Arg	Gln	Asn	Val	Tyr	Ile		
				885					890					895			
cca	ggc	agc	aat	gcc	aca	ctg	acc	aac	gca	gct	ggc	aag	cgg	gat	ggc	2853	
Pro	Gly	Ser	Asn	Ala	Thr	Leu	Thr	Asn	Ala	Ala	Gly	Lys	Arg	Asp	Gly		
			900					905					910				
aag	gcc	cca	gca	ggt	ggc	aat	ggc	aac	aag	aag	aag	tcg	ggc	aag	aag	2901	
Lys	Ala	Pro	Ala	Gly	Gly	Asn	Gly	Asn	Lys	Lys	Lys	Ser	Gly	Lys	Lys		
		915					920					925					
gag	aag	aag	taa													2913	
Glu	Lys	Lys	*														
		930															

&lt;210&gt; 328

&lt;211&gt; 1347

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (167)..(1291)

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1347)

&lt;223&gt; n = a,t,c or g

<400> 328

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gcctgcccgg cttgtctacc atcagagggga gatctctgcc ccctggggct gagagacccc 120

aacctttccc caagctgaag ctgcagggta ttgaggtacc agccag atg tct tcc 175  
Met Ser Ser  
1

cac aaa gga tct gtg gtg gca cag ggg aat ggg gct cct gcc agt aac 223  
His Lys Gly Ser Val Val Ala Gln Gly Asn Gly Ala Pro Ala Ser Asn  
5 10 15

agg gaa gct gac acg gtg gaa ctg gct gaa ctg gga ccc ctg cta gaa 271  
Arg Glu Ala Asp Thr Val Glu Leu Ala Glu Leu Gly Pro Leu Leu Glu  
20 25 30 35

gag aag ggc aaa cgg gta atc gcc aac cca ccc aaa gct gaa gaa gag 319  
Glu Lys Gly Lys Arg Val Ile Ala Asn Pro Pro Lys Ala Glu Glu Glu  
40 45 50

caa aca tgc cca gtg ccc cag gaa gaa gag gag gag gtg cgg gta ctg 367  
Gln Thr Cys Pro Val Pro Gln Glu Glu Glu Glu Glu Val Arg Val Leu  
55 60 65

aca ctt ccc ctg caa gcc cac cac gcc atg gag aag atg gaa gag ttt 415  
Thr Leu Pro Leu Gln Ala His His Ala Met Glu Lys Met Glu Glu Phe  
70 75 80

gtg tac aag gtc tgg gag gga cgt tgg agg gtc atc cca tat gat gtg 463  
Val Tyr Lys Val Trp Glu Gly Arg Trp Arg Val Ile Pro Tyr Asp Val  
85 90 95

ctc cct gac tgg cta aag gac aac gac tat ctg cta cat ggt cat aga 511  
Leu Pro Asp Trp Leu Lys Asp Asn Asp Tyr Leu Leu His Gly His Arg  
100 105 110 115

cct ccc atg ccc tcc ttt cgg gct tgc ttc aag agc atc ttc cgc att 559  
Pro Pro Met Pro Ser Phe Arg Ala Cys Phe Lys Ser Ile Phe Arg Ile  
120 125 130

cat aca gaa act ggc aac atc tgg acc cat ctg ctt ggt ttc gtg ctg 607  
His Thr Glu Thr Gly Asn Ile Trp Thr His Leu Leu Gly Phe Val Leu  
135 140 145

ttt ctc ttt ttg gga atc ttg acc atg ctc aga cca aat atg tac ttc 655  
Phe Leu Phe Leu Gly Ile Leu Thr Met Leu Arg Pro Asn Met Tyr Phe  
150 155 160

atg gcc cct cta cag gag aag gtg gtt ttt ggg atg ttc ttt ttg ggt 703  
Met Ala Pro Leu Gln Glu Lys Val Val Phe Gly Met Phe Phe Leu Gly  
165 170 175

gca gtg ctc tgc ctc agc ttc tcc tgg ctc ttt cac acc gtc tat tgt 751  
Ala Val Leu Cys Leu Ser Phe Ser Trp Leu Phe His Thr Val Tyr Cys  
180 185 190 195

cat tca gag aaa gtc tct cgg act ttt tcc aaa ctg gac tat tca ggg 799  
His Ser Glu Lys Val Ser Arg Thr Phe Ser Lys Leu Asp Tyr Ser Gly  
200 205 210

att gct ctt cta att atg ggg agc ttt gtc ccc tgg ctc tat tat tcc 847  
Ile Ala Leu Leu Ile Met Gly Ser Phe Val Pro Trp Leu Tyr Tyr Ser

215	220	225	
ttc tac tgc tcc cca cag cca cgg ctc atc tac ctc tcc atc gtc tgt			895
Phe Tyr Cys Ser Pro Gln Pro Arg Leu Ile Tyr Leu Ser Ile Val Cys			
230	235	240	
gtc ctg ggc att tct gcc atc att gtg gcg cag tgg gac cgg ttt gcc			943
Val Leu Gly Ile Ser Ala Ile Ile Val Ala Gln Trp Asp Arg Phe Ala			
245	250	255	
act cct aag cac cgg cag aca aga gca ggc gtg ttc ctg gga ctt ggc			991
Thr Pro Lys His Arg Gln Thr Arg Ala Gly Val Phe Leu Gly Leu Gly			
260	265	270	275
ttg agt ggc gtc gtg ccc acc atg cac ttt act atc gct gag ggc ttt			1039
Leu Ser Gly Val Val Pro Thr Met His Phe Thr Ile Ala Glu Gly Phe			
280	285	290	
gtc aag gcc acc aca gtg ggc cag atg ggc tgg ttc ttc ctc atg gct			1087
Val Lys Ala Thr Thr Val Gly Gln Met Gly Trp Phe Phe Leu Met Ala			
295	300	305	
gtg atg tac atc act gga gct ggc ctt tat gct gct cga att cct gag			1135
Val Met Tyr Ile Thr Gly Ala Gly Leu Tyr Ala Ala Arg Ile Pro Glu			
310	315	320	
cgc ttc ttt cct gga aaa ttt gac ata tgg ttc cag tct cat cag att			1183
Arg Phe Phe Pro Gly Lys Phe Asp Ile Trp Phe Gln Ser His Gln Ile			
325	330	335	
ttc cat gtc ctg gtg gtg gca gca gcc ttt gtc cac ttc tat gga gtc			1231
Phe His Val Leu Val Val Ala Ala Ala Phe Val His Phe Tyr Gly Val			
340	345	350	355
tcc aac ctt cag gaa ttc cgt tac ggc cta gaa ggc ggc tgt act gat			1279
Ser Asn Leu Gln Glu Phe Arg Tyr Gly Leu Glu Gly Gly Cys Thr Asp			
360	365	370	
gac acc ctt ctc tga gccttccac ctgcggggtg gaggaggaac ttcccaagtg			1334
Asp Thr Leu Leu			
375			
cttttaaaaa taa			1347

<210> 329  
 <211> 931  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (66)..(539)

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acagc atg aat caa gaa aag tta gcc aaa ctt cag gct cag gtc cgg	107
Met Asn Gln Glu Lys Leu Ala Lys Leu Gln Ala Gln Val Arg	
1 5 10	
ata ggg ggc aag ggt aca gct cgc aga aag aag aag gtg gta cat aga	155

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Ile Gly Gly Lys Gly Thr Ala Arg Arg Lys Lys Lys Val Val His Arg
15                      20                      25                      30

aca gcc aca gct gat gac aaa aag ctt cag agt tct cta aaa aaa ctg      203
Thr Ala Thr Ala Asp Asp Lys Lys Leu Gln Ser Ser Leu Lys Lys Leu
                      35                      40                      45

gct gtg aat aat ata gct ggt att gaa gag gtg aac atg att aaa gat      251
Ala Val Asn Asn Ile Ala Gly Ile Glu Glu Val Asn Met Ile Lys Asp
                      50                      55                      60

gat ggg aca gtt att cat ttc aac aat ccc aaa gtc caa gct tcc ctt      299
Asp Gly Thr Val Ile His Phe Asn Asn Pro Lys Val Gln Ala Ser Leu
                      65                      70                      75

tct gct aat acc ttt gca att act ggt cat gca gaa gcc aaa cca atc      347
Ser Ala Asn Thr Phe Ala Ile Thr Gly His Ala Glu Ala Lys Pro Ile
                      80                      85                      90

aca gaa atg ctt cct gga ata tta agt cag ctt ggt gct gac agt tta      395
Thr Glu Met Leu Pro Gly Ile Leu Ser Gln Leu Gly Ala Asp Ser Leu
                      95                      100                      105                      110

aca agc ctt agg aag tta gct gaa cag ttc cca cgg caa gtc ttg gac      443
Thr Ser Leu Arg Lys Leu Ala Glu Gln Phe Pro Arg Gln Val Leu Asp
                      115                      120                      125

agt aaa gca cca aaa cca gaa gac att gat gag gaa gat gat gat gtt      491
Ser Lys Ala Pro Lys Pro Glu Asp Ile Asp Glu Glu Asp Asp Asp Val
                      130                      135                      140

cca gat ctt gta gaa aat ttt gat gag gca tca aag aat gaa gct aac      539
Pro Asp Leu Val Glu Asn Phe Asp Glu Ala Ser Lys Asn Glu Ala Asn
                      145                      150                      155

taaaagtttg gtttttggaa gctggcatgg actagattta acaaatcagc tatgtggttc      599

caaagtttta cagacatgga gaacatcacc tgttactagt tcagtaatat aaatattttg      659

tatattaata atgctgtttg ttcagcattt ttcggtcatt tgattttgca ttttgcactt      719

cctcccagga tatttttttg gtcaaaatat gaagtattgg tgcaagtttga ggggtgtttg      779

gtttttgatt cctgggtttt ttgttttttg tttgggggat ttttggtgta tgtatgttta      839

tgtatgtgtg tgggtatgtg tgtatacagt ggagagcaaa ttggaaaaca gttctattta      899

tcctcctccc tccccagtag aaataaaaaa aa      931

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&lt;210&gt; 330

&lt;211&gt; 1394

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (230) .. (1036)

&lt;400&gt; 330

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tcggcgaggg aggaggcggg ggagctgcca acaccagac ccaaaccctg acatgctctg      60

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gggaggagag gaggaagcca ggagctgagc gcagccgagg gggctgcttc gccctccggc	120
tccgagcgcc gggctccggg cgccctgccc tgcgcctggg gcagcagcct ttgctggtct	180
tggggggcgcc ccccgcttcc cgccccgggg gtcgcgggcc ggcaggacc	235
	atg ctg Met Leu 1
ctg aaa gag tac cgg atc tgc atg ccg ctc acc gta gac gag tac aaa	283
Leu Lys Glu Tyr Arg Ile Cys Met Pro Leu Thr Val Asp Glu Tyr Lys	
5 10 15	
att gga cag ctg tac atg atc agc aaa cac agc cat gaa cag agt gac	331
Ile Gly Gln Leu Tyr Met Ile Ser Lys His Ser His Glu Gln Ser Asp	
20 25 30	
cgg gga gaa ggg gtg gag gtc gtc cag aat gag ccc ttt gag gac cct	379
Arg Gly Glu Gly Val Glu Val Val Gln Asn Glu Pro Phe Glu Asp Pro	
35 40 45 50	
cac cat ggc aat ggg cag ttc acc gag aag cgg gtg tat ctc aac agc	427
His His Gly Asn Gly Gln Phe Thr Glu Lys Arg Val Tyr Leu Asn Ser	
55 60 65	
aaa ctg cct agt tgg gct aga gct gtt gtc ccc aaa ata ttt tat gtg	475
Lys Leu Pro Ser Trp Ala Arg Ala Val Val Pro Lys Ile Phe Tyr Val	
70 75 80	
aca gag aag gct tgg aac tat tat ccc tac aca att aca gaa tac aca	523
Thr Glu Lys Ala Trp Asn Tyr Tyr Pro Tyr Thr Ile Thr Glu Tyr Thr	
85 90 95	
tgt tcc ttt ctg ccg aaa ttc tcc att cat ata gaa acc aag tat gag	571
Cys Ser Phe Leu Pro Lys Phe Ser Ile His Ile Glu Thr Lys Tyr Glu	
100 105 110	
gac aac aaa gga agc aat gac acc att ttc gac aat gaa gcc aaa gac	619
Asp Asn Lys Gly Ser Asn Asp Thr Ile Phe Asp Asn Glu Ala Lys Asp	
115 120 125 130	
gtg gag aga gaa gtt tgc ttt att gat att gcc tgc gat gaa att cca	667
Val Glu Arg Glu Val Cys Phe Ile Asp Ile Ala Cys Asp Glu Ile Pro	
135 140 145	
gag cgc tac tac aaa gaa tct gag gat cct aag cac ttc aag tca gag	715
Glu Arg Tyr Tyr Lys Glu Ser Glu Asp Pro Lys His Phe Lys Ser Glu	
150 155 160	
aag aca gga cgg gga cag ttg agg gaa ggc tgg aga gat agt cat cag	763
Lys Thr Gly Arg Gly Gln Leu Arg Glu Gly Trp Arg Asp Ser His Gln	
165 170 175	
cct atc atg tgc tcc tac aag ctg gtg act gtg aag ttt gag gtc tgg	811
Pro Ile Met Cys Ser Tyr Lys Leu Val Thr Val Lys Phe Glu Val Trp	
180 185 190	
ggg ctt cag acc aga gtg gaa caa ttt gta cac aag gtg gtc cga gac	859
Gly Leu Gln Thr Arg Val Glu Gln Phe Val His Lys Val Val Arg Asp	
195 200 205 210	
att ctg ctg att gga cat aga cag gct ttt gca tgg gtt gat gag tgg	907
Ile Leu Leu Ile Gly His Arg Gln Ala Phe Ala Trp Val Asp Glu Trp	
215 220 225	

tat gat atg aca atg gat gat gtt cgg gaa tac gag aaa aac atg cat	955
Tyr Asp Met Thr Met Asp Asp Val Arg Glu Tyr Glu Lys Asn Met His	
230 235 240	
 gaa caa acc aac ata aaa gtt tgc aat cag cat tcc tcc cct gtg gat	1003
Glu Gln Thr Asn Ile Lys Val Cys Asn Gln His Ser Ser Pro Val Asp	
245 250 255	
 gac ata gag agt cat gcc caa aca agt aca tga caatggat gaagtccgag	1054
Asp Ile Glu Ser His Ala Gln Thr Ser Thr *	
260 265	
 aatttgaacg agccactcag gaagccacca acaagaaaat cggcattttc ccacctgcaa	1114
tttctatctc cagcatcccc ctgctgcctt cttccgctcg cagtgcgcct tctagtgtc	1174
catccacccc tctctccaca gacgcacccg aatttctgtc cgttcccaaa gatcggtccc	1234
ggaaaaagtc tgccccagaa actctcacac ttccagaccc tgagaaaaaa gccaccctga	1294
atttaccggg catgcactct tcagataagc catgtcggcc caaatctgag taactttata	1354
taaatatctc atgggggtttt atattttcaa aaaaaaaaaa	1394

<210> 331  
 <211> 772  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (301)..(615)

<400> 331	
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gcgtccgcgg acgcgtgggg tgccggcggg agagctggct tggggcgctg gcacctctc	120
ttacagcttt actcctgcc a gcttgggaaa aggcgggaga aggtgaaatt ctgtgtgtc	180
cctccggcga gagactttgt cagctccgc acagtaacat cctgaataaa gtcaaaactc	240
aaccaacagg tggaagtcca agaatccgag tggaggctca ccgaggcgaa ggggccaacc	300
atg gga aag gag agt gga tgg gac tca ggc agg gct gct gta gca gct	348
Met Gly Lys Glu Ser Gly Trp Asp Ser Gly Arg Ala Ala Val Ala Ala	
1 5 10 15	
 gtg gtc gga gga gtt gtg gct gtg ggg act gtg ctc gtg gcg ctc agt	396
Val Val Gly Gly Val Val Ala Val Gly Thr Val Leu Val Ala Leu Ser	
20 25 30	
 gcc atg ggc ttc acc tca gta gga atc gcc gca tcc tcc ata gca gcc	444
Ala Met Gly Phe Thr Ser Val Gly Ile Ala Ala Ser Ser Ile Ala Ala	
35 40 45	
 aag atg atg tct aca gca gcc att gcc aac ggg ggc gga gtt gct gct	492
Lys Met Met Ser Thr Ala Ala Ile Ala Asn Gly Gly Gly Val Ala Ala	
50 55 60	
 ggc agt ctg gtg gct att ctg cag tca gtg ggg gca gct gga ctc tct	540

Gly Ser Leu Val Ala Ile Leu Gln Ser Val Gly Ala Ala Gly Leu Ser  
 65 70 75 80

gtg aca tct aaa gtt atc ggg ggc ttt gct ggg aca gct ctt ggg gcc 588  
 Val Thr Ser Lys Val Ile Gly Gly Phe Ala Gly Thr Ala Leu Gly Ala  
 85 90 95

tgg ctg ggt tca ccc cct tcc agc tga acacc aactgaggc agggagttgg 640  
 Trp Leu Gly Ser Pro Pro Ser Ser \*

100 105

ctctcttggt ggagatgact ttctctgggcc tctggatgac aatcttccaa aggacaagtc 700

tcctactccc aaaactatctt aaggaagcat gaaaaataaa gatgctgggtt atcttctcct 760

aaaaaaaaaa aa 772

<210> 332  
 <211> 931  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (336)..(716)

<400> 332  
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tccggccgcg ggcgcaaagc tggcgcteta tcccacggag ttggttaact cctctcaccg 120

gcccctggaa agggttccaa gtcctttagt acccgacgct gtctgggaat tccgggcgtt 180

tgggtcctt ggtcgcagag gcaggaggcg tgcgtggcag gaggggtcgg gttatatact 240

cctaggtcct gggacagaat agttacgacc tctgggacag gaactcttct ctcttttgtt 300

aataaacttc caactccctc ctacgacccg accgc atg tct gtc atg gac ctc 353  
 Met Ser Val Met Asp Leu  
 1 5

gcc aat act tgc tcc agc ttt cag tcg gac ctg gat ttc tgt tca gat 401  
 Ala Asn Thr Cys Ser Ser Phe Gln Ser Asp Leu Asp Phe Cys Ser Asp  
 10 15 20

tgc ggc tcg gtc ctg cct ctg ccc ggg gct cag gat acg gtc acc tgt 449  
 Cys Gly Ser Val Leu Pro Leu Pro Gly Ala Gln Asp Thr Val Thr Cys  
 25 30 35

att cgc tgt ggc ttc aac atc aac gtt cgg gac ttt gag ggg aag gtt 497  
 Ile Arg Cys Gly Phe Asn Ile Asn Val Arg Asp Phe Glu Gly Lys Val  
 40 45 50

gtg aag act tcg gtt gtg ttc cac caa ctg ggg aca gcc atg cct atg 545  
 Val Lys Thr Ser Val Val Phe His Gln Leu Gly Thr Ala Met Pro Met  
 55 60 65 70

tcg gtg gag gaa ggg cct gag tgc cag gga cct gtg gtt gac agg cgc 593  
 Ser Val Glu Glu Gly Pro Glu Cys Gln Gly Pro Val Val Asp Arg Arg  
 75 80 85



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tgc cct cga tgt ggt cat gaa gga atg gca tac cac acc aga cag atg      641
Cys Pro Arg Cys Gly His Glu Gly Met Ala Tyr His Thr Arg Gln Met
      90                      95                      100

cgt tca gcc gat gaa ggg caa act gtc ttc tac acc tgt acc aac tgc      689
Arg Ser Ala Asp Glu Gly Gln Thr Val Phe Tyr Thr Cys Thr Asn Cys
      105                      110                      115

aag ttc cag gag aag gaa gac tct tga ccttt ttctctgggca actctacagt      741
Lys Phe Gln Glu Lys Glu Asp Ser *
      120                      125

ccctccctcc ttctcggaagg tgaaggatac tgggttttta gatgccttgt ccacctctgc      801

tggttgcaat gttttgctcc cagaagagaa tcagatcatc atgtggggat taccattggt      861

cctggagtag tcctaccctt agttgaattt ccttattaaa gttatatattt tctataaaaa      921

aaaaaaaaaa                                                                931

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<210> 333
<211> 2043
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (189)..(1571)

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<220>
<221> misc_feature
<222> (1)...(2043)
<223> n = a,t,c or g

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<400> 333
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aagggctcgc cgtccttctc cgtttctcgc tgcttcggga cgcgctctct gcggctctgt      120
gagcgccctt gagcgccggc agcggcccg gggggatctt caggttatct tatgatgagg      180
cttttgct atg gct aat gat ccc ttg gaa ggc ttc cat gaa gta aac ctt      230
Met Ala Asn Asp Pro Leu Glu Gly Phe His Glu Val Asn Leu
      1          5          10

gct tca cct act tct ccg gac ctt ctt ggt gtg tat gaa tca gga act      278
Ala Ser Pro Thr Ser Pro Asp Leu Leu Gly Val Tyr Glu Ser Gly Thr
      15          20          25          30

caa gag cag act acc tca cca agt gtc atc tac cgg cca cac cct tca      326
Gln Glu Gln Thr Thr Ser Pro Ser Val Ile Tyr Arg Pro His Pro Ser
      35          40          45

gct tta tcc tct gta cct atc cag gca aat gca tta gat gtt tct gaa      374
Ala Leu Ser Ser Val Pro Ile Gln Ala Asn Ala Leu Asp Val Ser Glu
      50          55          60

ctt cct aca caa ccc gtg tat tca tcc ccc aga cgt tta aat tgt gcg      422
Leu Pro Thr Gln Pro Val Tyr Ser Ser Pro Arg Arg Leu Asn Cys Ala
      65          70          75

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gaa ata tct agt atc agc ttt cat gtt aca gac cca gcc cct tgc tct Glu Ile Ser Ser Ile Ser Phe His Val Thr Asp Pro Ala Pro Cys Ser 80 85 90	470
acc tct gga gtc aca gct gga tta act aaa tta act aca aga aag gac Thr Ser Gly Val Thr Ala Gly Leu Thr Lys Leu Thr Thr Arg Lys Asp 95 100 105 110	518
aac tat aat gca gag aga gag ttt tta cag ggt gct act ata aca gag Asn Tyr Asn Ala Glu Arg Glu Phe Leu Gln Gly Ala Thr Ile Thr Glu 115 120 125	566
gct tgc gat ggc agt gat gat att ttt ggg ttg agt act gat agt ctg Ala Cys Asp Gly Ser Asp Asp Ile Phe Gly Leu Ser Thr Asp Ser Leu 130 135 140	614
tct cgt tta cga agc cca tct gtt ttg gaa gtt aga gaa aag ggc tat Ser Arg Leu Arg Ser Pro Ser Val Leu Glu Val Arg Glu Lys Gly Tyr 145 150 155	662
gaa cga tta aaa gaa gaa ctc gca aaa gct cag agg gaa ctg aag tta Glu Arg Leu Lys Glu Glu Leu Ala Lys Ala Gln Arg Glu Leu Lys Leu 160 165 170	710
aaa gat gaa gaa tgt gag agg ctt tca aaa gtg cga gat caa ctt gga Lys Asp Glu Glu Cys Glu Arg Leu Ser Lys Val Arg Asp Gln Leu Gly 175 180 185 190	758
cag gaa ttg gaa gaa ctc aca gct agt cta ttt gag gaa gct cat aaa Gln Glu Leu Glu Glu Leu Thr Ala Ser Leu Phe Glu Glu Ala His Lys 195 200 205	806
atg gtg aga gaa gca aat atc aag cag gca aca gca gaa aaa cag cta Met Val Arg Glu Ala Asn Ile Lys Gln Ala Thr Ala Glu Lys Gln Leu 210 215 220	854
aaa gaa gca caa gga aaa att gat gta ctt caa gct gaa gta gct gca Lys Glu Ala Gln Gly Lys Ile Asp Val Leu Gln Ala Glu Val Ala Ala 225 230 235	902
ttg aag aca ctt gta ttg tcc agt tct cca aca tca cct acg cag gag Leu Lys Thr Leu Val Leu Ser Ser Ser Pro Thr Ser Pro Thr Gln Glu 240 245 250	950
cct ttg cca ggt gga aag aca cct ttt aaa aag ggg cat aca aga aat Pro Leu Pro Gly Gly Lys Thr Pro Phe Lys Lys Gly His Thr Arg Asn 255 260 265 270	998
aaa agc aca agc agt gct atg agt ggc agt cat cat gac ctc agt gtg Lys Ser Thr Ser Ser Ala Met Ser Gly Ser His His Asp Leu Ser Val 275 280 285	1046
ata cag cca att gta aaa gac tgc aaa gag gct gac tta tcc ttg tat Ile Gln Pro Ile Val Lys Asp Cys Lys Glu Ala Asp Leu Ser Leu Tyr 290 295 300	1094
aat gaa ttc cga ttg tgg aag gat gag ccc aca atg gac agg acg tgt Asn Glu Phe Arg Leu Trp Lys Asp Glu Pro Thr Met Asp Arg Thr Cys 305 310 315	1142
cct ttc tta gac aaa atc tac cag gaa gat atc ttt cca tgt tta aca Pro Phe Leu Asp Lys Ile Tyr Gln Glu Asp Ile Phe Pro Cys Leu Thr 320 325 330	1190

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ttc tca aaa agt gag ttg gct tca gct gtt ctg gag gct gtg gaa aac      1238
Phe Ser Lys Ser Glu Leu Ala Ser Ala Val Leu Glu Ala Val Glu Asn
335                               340                               345                               350

aat act cta agc att gaa cca gtg gga tta caa cct atc cgg ttt gtg      1286
Asn Thr Leu Ser Ile Glu Pro Val Gly Leu Gln Pro Ile Arg Phe Val
355                               360                               365

aaa gct tct gca gtt gaa tgc gga gga cca aaa aaa tgt gct ctc act      1334
Lys Ala Ser Ala Val Glu Cys Gly Gly Pro Lys Lys Cys Ala Leu Thr
370                               375                               380

ggc cag agt aag tcc tgt aaa cac aga att aaa tta ggg gac tca agc      1382
Gly Gln Ser Lys Ser Cys Lys His Arg Ile Lys Leu Gly Asp Ser Ser
385                               390                               395

aac tat tat tat att tct cct ttt tgc aga tac agg atc act tct gta      1430
Asn Tyr Tyr Tyr Ile Ser Pro Phe Cys Arg Tyr Arg Ile Thr Ser Val
400                               405                               410

tgt aac ttt ttt aca tac att cga tac att cag cag gga ctc gtg aaa      1478
Cys Asn Phe Phe Thr Tyr Ile Arg Tyr Ile Gln Gln Gly Leu Val Lys
415                               420                               425                               430

cag cag gat gtt gat cag atg ttt tgg gag gtt atg cag ttg aga aaa      1526
Gln Gln Asp Val Asp Gln Met Phe Trp Glu Val Met Gln Leu Arg Lys
435                               440                               445

gag atg tca ttg gca aag ctg ggt tat ttc aaa gag gaa ctc tga tgc      1574
Glu Met Ser Leu Ala Lys Leu Gly Tyr Phe Lys Glu Glu Leu *
450                               455                               460

tctgcgtggg accatgcctg aactccccga ataactgaaa aatggctgaa tatttttatg      1634

gttacttgat atttatttcc aaggagttag cctaagactt ttttcccctt ttgcaaattg      1694

ctctaagaag taccatgatt tcttttaaac tgatctatgc tgtgtttgct tattcttttag      1754

ttgaacacac tatgaagaat tccaggtgta ctagtgaatg taatttatag ttgccaaaaa      1814

aaagcgcgcg gctgaattta gtagtagagc gacctggaat ccgacggtac tgcagcgtac      1874

actttctata ggagtcgata gagctgcgaa catgtcaagt gttctggtga atgtacgcgc      1934

natcaccaca tcgagcgaca taatgtagct ggggctagag ggcaccata tgctgccatg      1994

cgctcatcgg actgcggcac gcatagacgc acgcggaagc gtcgatggc      2043

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<210> 334
<211> 797
<212> DNA
<213> Homo sapiens

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<222> (94)..(666)

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<222> (1)...(797)
<223> n = a,t,c or g

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aattcccggg tcgacccacg cgtccggcag agc atg gcg gcg ggc gag ctt gag 114  
Met Ala Ala Gly Glu Leu Glu  
1 5

ggt ggc aaa ccc ctg agc ggg ctg ctg aat gcg ctg gcc cag gac act 162  
Gly Gly Lys Pro Leu Ser Gly Leu Leu Asn Ala Leu Ala Gln Asp Thr  
10 15 20

ttc cac ggg tac ccc ggc atc aca gag gag ctg cta cgg agc cag cta 210  
Phe His Gly Tyr Pro Gly Ile Thr Glu Glu Leu Leu Arg Ser Gln Leu  
25 30 35

tat cca gag gtg cca ccc gag gag ttc cgc ccc ttt ctg gca aag atg 258  
Tyr Pro Glu Val Pro Pro Glu Glu Phe Arg Pro Phe Leu Ala Lys Met  
40 45 50 55

agg ggg att ctt aag tct att gcg tct gca gac atg gat ttc aac cag 306  
Arg Gly Ile Leu Lys Ser Ile Ala Ser Ala Asp Met Asp Phe Asn Gln  
60 65 70

ctg gag gca ttc ttg act gct caa acc aaa aag caa ggt ggg atc aca 354  
Leu Glu Ala Phe Leu Thr Ala Gln Thr Lys Lys Gln Gly Gly Ile Thr  
75 80 85

tct gac caa gct gct gtc att tcc aaa ttc tgg aag agc cac aag aca 402  
Ser Asp Gln Ala Ala Val Ile Ser Lys Phe Trp Lys Ser His Lys Thr  
90 95 100

aaa atc cgt gag agc ctc atg aac cag agc cgc tgg aat agc ggg ctt 450  
Lys Ile Arg Glu Ser Leu Met Asn Gln Ser Arg Trp Asn Ser Gly Leu  
105 110 115

cgg ggc ctg agc tgg aga gtt gat ggc aag tct cag tca agg cac tca 498  
Arg Gly Leu Ser Trp Arg Val Asp Gly Lys Ser Gln Ser Arg His Ser  
120 125 130 135

gct caa ata cac aca cct gtt gcc att ata gag ctg gaa tta ggc aaa 546  
Ala Gln Ile His Thr Pro Val Ala Ile Ile Glu Leu Glu Leu Gly Lys  
140 145 150

tat gga cag gaa tct gaa ttt ctg tgt ttg gaa ttt gat gag gtc aaa 594  
Tyr Gly Gln Glu Ser Glu Phe Leu Cys Leu Glu Phe Asp Glu Val Lys  
155 160 165

gtc aac caa att ctg aag acg ctg tca gag gta gaa gaa agt atc agc 642  
Val Asn Gln Ile Leu Lys Thr Leu Ser Glu Val Glu Glu Ser Ile Ser  
170 175 180

aca ctg atc agc cag cct aac tga agatgatgta tgaaggagtt ggagttgttg 696  
Thr Leu Ile Ser Gln Pro Asn \*  
185 190

aaaccaaggt gtccatgac cctccccact gaccttttct aagaaaattc ttgtgcccgc 756

attggtatta aatcctcgca ttcagtctta aaaaaaaaaa a 797

&lt;210&gt; 335

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 <212> DNA  
 <213> Homo sapiens

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 <222> (76)..(408)

<220>  
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 <223> n = a,t,c or g

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 gcttagttag gagct atg gct aaa cat cat cct gat ttg atc ttt tgc cgc 111  
                   Met Ala Lys His His Pro Asp Leu Ile Phe Cys Arg  
                   1                  5                  10  
 aag cag gct ggt gtt gcc atc gga aga ctg tgt gaa aaa tgt gat ggc 159  
 Lys Gln Ala Gly Val Ala Ile Gly Arg Leu Cys Glu Lys Cys Asp Gly  
                   15                  20                  25  
 aag tgt gtg att tgt gac tcc tat gtg cgt ccc tgc act ctg gtg cgc 207  
 Lys Cys Val Ile Cys Asp Ser Tyr Val Arg Pro Cys Thr Leu Val Arg  
                   30                  35                  40  
 ata tgt gat gag tgt aac tat gga tct tac cag ggg cgc tgt gtg atc 255  
 Ile Cys Asp Glu Cys Asn Tyr Gly Ser Tyr Gln Gly Arg Cys Val Ile  
                   45                  50                  55                  60  
 tgt gga gga cct ggg gtc tct gat gcc tat tat tgt aag gag tgc acc 303  
 Cys Gly Gly Pro Gly Val Ser Asp Ala Tyr Tyr Cys Lys Glu Cys Thr  
                   65                  70                  75  
 atc cag gag aag gac aga gat ggc tgc cca aag att gtc aat ctg ggg 351  
 Ile Gln Glu Lys Asp Arg Asp Gly Cys Pro Lys Ile Val Asn Leu Gly  
                   80                  85                  90  
 agc tct aag aca gac ctc ttc tat gaa cgc aaa aaa tac ggc ttc aag 399  
 Ser Ser Lys Thr Asp Leu Phe Tyr Glu Arg Lys Lys Tyr Gly Phe Lys  
                   95                  100                  105  
 aag agg tga ttggtgg gtggccctt cctcccccca acatcagtct gctgcagctg 455  
 Lys Arg \*  
                   110  
 ccagaaaaca tgcctactac taccagcaga aagggagcag agcccagagc atcaccagga 515  
 gtgcctgcta gtgtactggc agcttgccac cccctcctct cccttcaccc agacacgtgg 575  
 tagggatgga aaaggattct tcacagagca ctctggcaca ccatatcgga gaaaacttga 635  
 tagattagtt aatggttttt cttgaattcg agaagcatag atctgttctc catattggta 695  
 tgttctccct caaccaagat cttctaaaaa gaaataatat tttagtcttc tgcttgagga 755  
 actgactgtg aagcgacgcc cagtgaaaaa catgttcttg cagcagctct ggtggcagct 815  
 gtccttgagg aacctttggg gtgtgggtggg aagctatcag aacaagaaat gtaggcattt 875  
 cccgtttttt tggggggggg gggggggggg gccagggctc tgccctcttg aaaggcattt 935

acttgtttaa cacttggtcca gctacagtgg ggtacagtag ctggctattc acaggcatca 995  
 tcatagccca ctagtctcat attattttcc ttttgagaaa ttggaaactc tttctgttgc 1055  
 tattatatta ataaagttgg tgtttatttt ctggtaaaaa aaaaaaa 1102

<210> 336  
 <211> 681  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (125)..(502)

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 gcgtttaaac ttaagcttgg taccgagctc ggatccacta gtccagtgtg gtggaattcg 120  
 cgac atg aaa ctg ctt acc cac aat ctg ctg agc tcg cat gtg cgg ggg 169  
 Met Lys Leu Leu Thr His Asn Leu Leu Ser Ser His Val Arg Gly  
 1 5 10 15  
 gtg ggg tcc cgt ggc ttc ccc ctg cgc ctc cag gcc acc gag gtc cgt 217  
 Val Gly Ser Arg Gly Phe Pro Leu Arg Leu Gln Ala Thr Glu Val Arg  
 20 25 30  
 atc tgc cct gtg gaa ttc aac ccc aac ttc gtg gcg cgt atg ata cct 265  
 Ile Cys Pro Val Glu Phe Asn Pro Asn Phe Val Ala Arg Met Ile Pro  
 35 40 45  
 aaa gtg gag tgg tcg gcg ttc ctg gag gcg gcc gat aac ttg cgt ctg 313  
 Lys Val Glu Trp Ser Ala Phe Leu Glu Ala Ala Asp Asn Leu Arg Leu  
 50 55 60  
 atc cag gtg ccg aaa ggg ccg gtt gag gga tat gag gag aat gag gag 361  
 Ile Gln Val Pro Lys Gly Pro Val Glu Gly Tyr Glu Glu Asn Glu Glu  
 65 70 75  
 ttt ctg agg acc atg cac cac ctg ctg ctg gag gtg gaa gtg ata gag 409  
 Phe Leu Arg Thr Met His His Leu Leu Leu Glu Val Glu Val Ile Glu  
 80 85 90 95  
 ggc acc ctg cag tgc ccg gaa tct gga cgt atg ttc ccc atc agc cgc 457  
 Gly Thr Leu Gln Cys Pro Glu Ser Gly Arg Met Phe Pro Ile Ser Arg  
 100 105 110  
 ggg atc ccc aac atg ctg ctg agt gaa gag gaa act gag agt tga ttg 505  
 Gly Ile Pro Asn Met Leu Leu Ser Glu Glu Glu Thr Glu Ser \*  
 115 120 125  
 tgccaggcgc ccagtttttc ttgttatgac tgtgtatttt tgttgatcta taccctgttt 565  
 ccgaattctg ccgtgtgtat cccaaccct tgaccaatg acaccaaaca cagtgttttt 625  
 gagctcggta ttatatattt tttctcatt aaaggtttaa aaccaaaaaa aaaaaa 681

<210> 337  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (168) .. (1757)

<220>  
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 <222> (1) ... (2352)  
 <223> n = a,t,c or g

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 gccccgggtc cctctgccac aacttctgtc gctctgccgc ctgcaccgtg acccgacta 120  
 ttcacgggag ccctagagag gacaccggga caccagaag ccgggaa atg gat tca 176  
 Met Asp Ser  
 1  
 gtg gcc ttt gag gat gtg gct gtc agc ttc acc cag gag gag tgg gct 224  
 Val Ala Phe Glu Asp Val Ala Val Ser Phe Thr Gln Glu Glu Trp Ala  
 5 10 15  
 ttg ctg gat cct tcc cag aag aat ctc tac agg gat gtg atg cag gaa 272  
 Leu Leu Asp Pro Ser Gln Lys Asn Leu Tyr Arg Asp Val Met Gln Glu  
 20 25 30 35  
 acc ttc aag aac ctg acc tct gta gga aaa aca tgg aaa gtt cag aac 320  
 Thr Phe Lys Asn Leu Thr Ser Val Gly Lys Thr Trp Lys Val Gln Asn  
 40 45 50  
 att gaa gat gag tac aaa aat ccc agg aga aat cta agt ctt atg aga 368  
 Ile Glu Asp Glu Tyr Lys Asn Pro Arg Arg Asn Leu Ser Leu Met Arg  
 55 60 65  
 gag aaa ctc tgt gaa agt aaa gaa agt cat cac tgt gga gaa agc ttc 416  
 Glu Lys Leu Cys Glu Ser Lys Glu Ser His His Cys Gly Glu Ser Phe  
 70 75 80  
 aac cag att gca gat gac atg ctg aac agg aaa act ctt cct gga ata 464  
 Asn Gln Ile Ala Asp Asp Met Leu Asn Arg Lys Thr Leu Pro Gly Ile  
 85 90 95  
 aca cca tgt gaa agc agt gtg tgt gga gaa gtt ggc acg ggt cat tca 512  
 Thr Pro Cys Glu Ser Ser Val Cys Gly Glu Val Gly Thr Gly His Ser  
 100 105 110 115  
 tct ctt aat acg cat atc aga gct gac act gga cac aag tca tct gag 560  
 Ser Leu Asn Thr His Ile Arg Ala Asp Thr Gly His Lys Ser Ser Glu  
 120 125 130  
 tat cag gaa tat gga gag aat cca tat aga aat aag gaa tgt aag aaa 608  
 Tyr Gln Glu Tyr Gly Glu Asn Pro Tyr Arg Asn Lys Glu Cys Lys Lys  
 135 140 145  
 gcc ttc agt tat ctt gac tcc ttt caa tca cat gat aaa gct tgc act 656  
 Ala Phe Ser Tyr Leu Asp Ser Phe Gln Ser His Asp Lys Ala Cys Thr  
 150 155 160  
 aaa gag aaa ccc tat gat ggt aaa gaa tgt aca gaa acc ttc att tcc 704

Lys	Glu	Lys	Pro	Tyr	Asp	Gly	Lys	Glu	Cys	Thr	Glu	Thr	Phe	Ile	Ser	
165						170					175					
cat	tca	tgc	att	caa	aga	cac	agg	gta	atg	cac	agt	gga	gat	gga	cct	752
His	Ser	Cys	Ile	Gln	Arg	His	Arg	Val	Met	His	Ser	Gly	Asp	Gly	Pro	
180					185					190					195	
tat	aaa	tgt	aag	ttt	tgt	ggg	aaa	gcc	ttc	tat	ttt	ctc	aat	tta	tgt	800
Tyr	Lys	Cys	Lys	Phe	Cys	Gly	Lys	Ala	Phe	Tyr	Phe	Leu	Asn	Leu	Cys	
				200					205					210		
ctt	atc	cat	gaa	cga	att	cac	act	ggt	gtg	aaa	cca	tat	aag	tgt	aaa	848
Leu	Ile	His		Glu	Arg	Ile	His	Thr	Gly	Val	Lys	Pro	Tyr	Lys	Cys	
				215					220					225		
caa	tgt	ggt	aag	gcc	ttt	act	cgt	tcc	act	acc	ctt	cca	gta	cat	gaa	896
Gln	Cys	Gly	Lys	Ala	Phe	Thr	Arg	Ser	Thr	Thr	Leu	Pro	Val	His	Glu	
				230				235					240			
aga	act	cac	aca	gga	gtg	aat	gcc	gat	gaa	tgt	aaa	gaa	tgt	ggg	aat	944
Arg	Thr	His	Thr	Gly	Val	Asn	Ala	Asp	Glu	Cys	Lys	Glu	Cys	Gly	Asn	
				245				250					255			
gca	ttc	agt	ttt	cct	agt	gaa	att	cgt	aga	cat	aaa	agg	tct	cac	act	992
Ala	Phe	Ser	Phe	Pro	Ser	Glu	Ile	Arg	Arg	His	Lys	Arg	Ser	His	Thr	
260						265				270					275	
gga	gaa	aaa	ccc	tat	gag	tgt	aag	caa	tgt	ggg	aaa	gtc	ttc	att	tct	1040
Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Lys	Gln	Cys	Gly	Lys	Val	Phe	Ile	Ser	
				280					285					290		
ttc	agt	tcc	att	cag	tat	cat	aag	atg	act	cac	act	gga	gag	aaa	ccc	1088
Phe	Ser	Ser	Ile	Gln	Tyr	His	Lys	Met	Thr	His	Thr	Gly	Glu	Lys	Pro	
				295					300					305		
tat	gaa	tgt	aag	cag	tgt	ggg	aaa	gcc	ttt	aga	tgt	ggc	tca	cac	ctt	1136
Tyr	Glu	Cys	Lys	Gln	Cys	Gly	Lys	Ala	Phe	Arg	Cys	Gly	Ser	His	Leu	
				310				315					320			
caa	aag	cat	gga	agg	act	cac	act	gga	gag	aaa	ccc	tat	gaa	tgt	agg	1184
Gln	Lys	His	Gly	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Arg	
				325				330					335			
caa	tgt	ggt	aaa	gcc	ttc	aga	tgt	acc	tcg	gac	ctt	caa	agg	cat	gaa	1232
Gln	Cys	Gly	Lys	Ala	Phe	Arg	Cys	Thr	Ser	Asp	Leu	Gln	Arg	His	Glu	
340						345				350					355	
aag	aca	cac	act	gag	gat	aaa	ccc	tat	gga	tgt	aag	cag	tgt	ggg	aaa	1280
Lys	Thr	His	Thr	Glu	Asp	Lys	Pro	Tyr	Gly	Cys	Lys	Gln	Cys	Gly	Lys	
				360						365				370		
ggc	ttt	aga	tgt	gct	tca	caa	ctt	caa	att	cat	gaa	agg	acg	cac	agt	1328
Gly	Phe	Arg	Cys	Ala	Ser	Gln	Leu	Gln	Ile	His	Glu	Arg	Thr	His	Ser	
				375					380					385		
gga	gag	aaa	ccc	cat	gaa	tgt	aag	gaa	tgt	gga	aaa	gta	ttc	aag	tat	1376
Gly	Glu	Lys	Pro	His	Glu	Cys	Lys	Glu	Cys	Gly	Lys	Val	Phe	Lys	Tyr	
				390				395					400			
ttt	tct	tcc	ttg	cgt	ata	cat	gaa	agg	acg	cac	act	gga	gag	aag	ccc	1424
Phe	Ser	Ser	Leu	Arg	Ile	His	Glu	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	
				405				410					415			
cat	gaa	tgt	aag	caa	tgt	gga	aaa	gca	ttc	agg	tat	ttc	tct	tcc	ttg	1472



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<210> 338
<211> 2285
<212> DNA
<213> Homo sapiens
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<400> 338  
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tcgccccccc gtcccagcgc cccagccct cccgcgaggg cgcgccggga cggaaggatc	180
caccagtctg tcggcgcccc cggttctcgt ggctcgccgtc gccgtcgctg tgggtgtagt	240
ctccgcccgtc gcctggggcc atg gcc aat tac atc cac gtc cct ccc ggc tcc	292
Met Ala Asn Tyr Ile His Val Pro Pro Gly Ser	
1 5 10	
ccg gag gtg ccc aag ctg aac gtc acc gtt cag gat cag gaggagcatc	341
Pro Glu Val Pro Lys Leu Asn Val Thr Val Gln Asp Gln	
15 20	
gctgccggga gggggccctg agcctcctgc aacacctgcg gcctcactgg gacccccagg	401
aggtgacctt gcagctcttc acagatggaa tcacaaataa acttattggc tggtacgtgg	461
gaaacaccat ggaggatgta gtcctgggtg gaatttatgg caataagact gagttattag	521
tcgatcgaga tgaggaagta aagagttttc gagtgttgca ggctcatggg tgtgcaccac	581
aactctactg taccttcaat aatggactat gctatgaatt tatacaagga gaagcactgg	641
atccaaagca tgtctgcaac ccagccattt tcaggctaata agctcgtcag cttgctaaaa	701
tccatgctat tcatgcacac aatggctgga tccccaaatc taatctttgg ctaaagatgg	761
gaaagtattt ctctctcatt cccacaggat ttgcagatga agacattaat aaaagggtcc	821
taagtgatat cccaagctct cagattctcc aggaagagat gacttggatg aaggagattc	881
tttccaacct gggctcacct gttgtgcttt gccataatga cctattgtgt aagaatataa	941
tctacaatga gaaacaaggt gatgtacagt tcattgatta tgaatattct ggatacaact	1001
acctggcata tgatattgga aatcatttca atgaatttgc aggtgtgagt gatgtagact	1061
atagtctgta tccagataga gaactacaga gtcagtggct gcgtgcttac cttgaagcct	1121
acaaagaatt taagggtctt gggactgaag ttactgaaaa ggaggtagaa atactcttca	1181
ttcaagtcaa tcagtttgca ttggcttctc atttcttttg gggattgtgg gctttgatcc	1241
aagccaaata ctccactatt gagtttgatt tccttgggta tgcaattgtt cgttttaacc	1301
agtactttaa aatgaagcct gaggttactg cattaaaagt gcctgagtaa agaagagatt	1361
taattattct ccagtagctg agcaatgctt gtgaatcttt tcttaagaaa tccccaaaag	1421
ccaatattag ttaaaattct gttgtttaat ttggttatct tgctttataa attatgcctc	1481
taaacaatca aatctatttt tgaaatagac tgaatgatgt caagaaatat acctactgct	1541
atccgtatgt ggtggattag aaatgtgtta aatctgcaaa aggtataaag atgtcagttt	1601
aatttctttg ataatttaac ctatgttgta tgtgaattat ttattataaa cttagcacga	1661
ttctgtgact gtttttctct gtttcacgtt cgttgagtgt aagcaatgaa aatgtcccaa	1721
ataagttttt taagttttac ttttaataaga ttaatttcag taaacattct agttgttcag	1781
tgtaaccttt ttatcttgat gcattgtaag taaaatgaat catttactct tgaaatgcca	1841
gtcattgact gatgtagata atttaggatt ttcatataaa aatagctgtt taggaagggtg	1901

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aaatacattc actgtctctg ttggtggtac atcttggtga attcaatatt agaaagtatt 1961
tctttttggg gtaatataac ttagaattaa atccctgttt ctctatgtag tctggcagta 2021
taaataataa tattttaccat ataatcttgg aataagtatt agttaatggt accaaaaatct 2081
gtattaaata atgttttcaa atgctaaata tggtcgttac tattttcagt tttaaaaaatt 2141
ttatagtatc aaattgtttc taacccaaaaa tttcctttta cttctagaga tgctttatgt 2201
ttttgattat taaatagtca ctagtattgc taatttttga aacaaatacc caaaatttat 2261
catatgtaga aataagaaaa aaaa 2285

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<210> 339
<211> 1069
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (15)..(26)

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<400> 339
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                                     Met Leu Pro Phe
                               1             5             10

ccc aag agt gca gag tgt gga gcg tgg agc gcc ggg act gtg cac gct  98

tga ccg gaa gcc cag acc agt gcg gtc cta gcc aga gag aaa gga cat 146

ttg cca aca atg aga cac gaa gcg ccc atg cag atg gcc tct gcc caa 194

gat gcc agg tac ggc cag aaa gac tcc tct gat cag aac ttt gac tac 242

atg ttc aaa tta ctc atc atc ggc aat agc agt gtg ggg aaa aca tct 290

ttt cta ttc cgt tat gca gat gac tcc ttt aca tct gca ttc gtc agc 338

aca gtt ggg atc gat ttc aaa gta aaa act gta ttc aaa aat gaa aag 386

aga atc aag ctt cag att tgg gac aca gca ggc cag gaa aga tac agg 434

act atc acc aca gcc tat tat cgt gga gcc atg ggc ttt att tta atg 482

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tat gac att aca aat gaa gaa tcc ttc aat gca gta caa gat tgg tca 530

act caa atc aaa aca tac tot tgg gac aat gcc caa gtt att ctg gtt 578

ggg aac aag tgt gac atg gaa gac gag cgg gtc atc tca act gag cga 626

ggg caa cat tta gga gaa cag ctt ggg ttt gag ttt ttt gaa aca agt 674

gcc aag gac aac att aat gtc aag cag aca ttt gag cgc ctt gtg gat 722

atc atc tgc gac aaa atg tca gag agt ttg gag act gat cct gcc atc 770

act gct gca aag cag aac acg aga ctc aag gaa act cct cct cca cgg 818

cag ccc aac tgt gcc tgc tag tgt ccc cgt gca cac agg cag ctc cag 866

ggg gct ctg gtt gcc aac aaa cag cat ttg taa atg gtc tat tag cct 914

tca ttt ata ctg cct aac aat tat ttg aag gaa taa att gat gtc aat 962

ggc tgc tac gca ttc aat tct tgg gag ctt tcc tgt tta ata tgt ggc 1010

aaa tat gtg atc tta aat tta taa gga cta tcc at tgatg ttggagccgg 41

ttagcgaacc ccaagagtgc agagtgtgga gcgtggagcg ccgggactgt gcacgcttga 101

ccggaagccc agaccagtgc ggtcctagcc agagagaaag gacatttgcc aacaatgaga 161

cacgaagcgc ccattgcagat ggcctctgcc caagatgccca ggtacggcca gaaagactcc 221

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gaacagcttg ggtttgagtt ttttgaaaca agtgccaagg acaacattaa tgtcaagcag      701
acatttgagc gccttggtga tatcatctgc gacaaaatgt cagagagttt ggagactgat      761
cctgccatca ctgctgcaaa gcagaacacg agactcaagg aaactcctcc tccaccgcag      821
cccaactgtg cctgctagtg tccccgtgca cacaggcagc tccagggggc tctggttgcc      881
aacaacacgc atttgtaaat ggtctattag ccttcattta tactgcctaa caattatttg      941
aaggaataaa ttgatgtcaa tggctcgtag gcattcaatt cttgggagct ttcctgttta     1001
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 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (3)..(4139)

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cta att cat ctc tcc agc aaa gga cac atc tct cca gca aag gac acc      95
Leu Ile His Leu Ser Ser Lys Gly His Ile Ser Pro Ala Lys Asp Thr
      20             25             30

tct ctc cag caa agg aca cct gca gag atg tcc cca gtc ctt cac ttc      143
Ser Leu Gln Gln Arg Thr Pro Ala Glu Met Ser Pro Val Leu His Phe
      35             40             45

tat gtt cgt ccc tct ggc cat gag ggg gca gcc tct gga cac act cgg      191
Tyr Val Arg Pro Ser Gly His Glu Gly Ala Ala Ser Gly His Thr Arg
      50             55             60

agg aaa ctg caa ggg aaa ctg cca gag ctg cag ggc gtc gag act gaa      239
Arg Lys Leu Gln Gly Lys Leu Pro Glu Leu Gln Gly Val Glu Thr Glu
      65             70             75

ctg tgc tac aac gtg aac tgg aca gct gag gcc ctc ccc agt gct gag      287
Leu Cys Tyr Asn Val Asn Trp Thr Ala Glu Ala Leu Pro Ser Ala Glu
      80             85             90             95

gag aca aag aag ctg atg tgg ctg ttt ggt tgc ccc tta ctg ctg gat      335
Glu Thr Lys Lys Leu Met Trp Leu Phe Gly Cys Pro Leu Leu Leu Asp
      100             105             110

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gat gtt gct cgg gag tcc tgg ctc ctt cct ggc tcc aat gac ctg ctg	383
Asp Val Ala Arg Glu Ser Trp Leu Leu Pro Gly Ser Asn Asp Leu Leu	
115 120 125	
ctg gag gtc ggg ccc agg ctg aac ttc tcc acc cca aca tcc acc aac	431
Leu Glu Val Gly Pro Arg Leu Asn Phe Ser Thr Pro Thr Ser Thr Asn	
130 135 140	
atc gtg tca gtg tgc cgc gcc act ggg ctg ggg cct gtg gat cgt gtg	479
Ile Val Ser Val Cys Arg Ala Thr Gly Leu Gly Pro Val Asp Arg Val	
145 150 155	
gag acc acc cgg cgc tac cgg ctc tcg ttt gcc cac ccc ccg tca gct	527
Glu Thr Thr Arg Arg Tyr Arg Leu Ser Phe Ala His Pro Pro Ser Ala	
160 165 170 175	
gag gtg gaa gcc att gct ctg gct acc ctg cac gac cgg atg aca gag	575
Glu Val Glu Ala Ile Ala Leu Ala Thr Leu His Asp Arg Met Thr Glu	
180 185 190	
cag cac ttc ccc cat ccc atc cag agt ttc tcc cct gag agc atg ccg	623
Gln His Phe Pro His Pro Ile Gln Ser Phe Ser Pro Glu Ser Met Pro	
195 200 205	
gaa ccc ctc aat ggc cct atc aat ata ctg ggt gag ggc cgg ctt gcg	671
Glu Pro Leu Asn Gly Pro Ile Asn Ile Leu Gly Glu Gly Arg Leu Ala	
210 215 220	
ctg gag aag gcc aac cag gag ctt ggt ctg gct tta gac tct tgg gac	719
Leu Glu Lys Ala Asn Gln Glu Leu Gly Leu Ala Leu Asp Ser Trp Asp	
225 230 235	
cta gac ttc tac acc aag cgc ttc cag gag cta cag cgg aac ccg agc	767
Leu Asp Phe Tyr Thr Lys Arg Phe Gln Glu Leu Gln Arg Asn Pro Ser	
240 245 250 255	
act gtg gag gcc ttt gac ttg gcg cag tcc aat agc gag cac agc cga	815
Thr Val Glu Ala Phe Asp Leu Ala Gln Ser Asn Ser Glu His Ser Arg	
260 265 270	
cac tgg ttc ttc aag ggc cag ctc cac gtg gat ggg cag aag ctg gtg	863
His Trp Phe Phe Lys Gly Gln Leu His Val Asp Gly Gln Lys Leu Val	
275 280 285	
cac tca ctg ttt gag tcc atc atg agc acc cag gaa tcc tcg aac ccc	911
His Ser Leu Phe Glu Ser Ile Met Ser Thr Gln Glu Ser Ser Asn Pro	
290 295 300	
aac aac gtc ctc aaa ttc tgt gat aac agc agt gca atc cag gga aag	959
Asn Asn Val Leu Lys Phe Cys Asp Asn Ser Ser Ala Ile Gln Gly Lys	
305 310 315	
gaa gtc cga ttc cta cgg cct gag gac ccc aca cgg cca agc cgc ttc	1007
Glu Val Arg Phe Leu Arg Pro Glu Asp Pro Thr Arg Pro Ser Arg Phe	
320 325 330 335	
cag caa cag caa ggg ctg aga cat gtt gtc ttc aca gca gag act cac	1055
Gln Gln Gln Gln Gly Leu Arg His Val Val Phe Thr Ala Glu Thr His	
340 345 350	
aac ttt ccc aca gga gta tgc ccc ttt agt ggt gca acc act ggc aca	1103
Asn Phe Pro Thr Gly Val Cys Pro Phe Ser Gly Ala Thr Thr Gly Thr	
355 360 365	

ggg ggc cgg att cga gat gtc cag tgc aca ggc cgc ggg gcc cac gtg Gly Gly Arg Ile Arg Asp Val Gln Cys Thr Gly Arg Gly Ala His Val 370 375 380	1151
gtg gct ggc act gcc ggc tat tgc ttt gga aat ctg cat att cca ggt Val Ala Gly Thr Ala Gly Tyr Cys Phe Gly Asn Leu His Ile Pro Gly 385 390 395	1199
tac aat ctg ccc tgg gag gat cta agc ttc cag tat cct ggg aat ttt Tyr Asn Leu Pro Trp Glu Asp Leu Ser Phe Gln Tyr Pro Gly Asn Phe 400 405 410 415	1247
gcc cgg ccc ctg gag gtt gcc att gaa gcc agt aat gga gct tct gac Ala Arg Pro Leu Glu Val Ala Ile Glu Ala Ser Asn Gly Ala Ser Asp 420 425 430	1295
tat ggc aac aag ttt ggg gaa cca gtg ctg gct ggc ttc gcc cgc tcc Tyr Gly Asn Lys Phe Gly Glu Pro Val Leu Ala Gly Phe Ala Arg Ser 435 440 445	1343
ttg ggc ctc cag ctc cca gac ggc cag cgg cgt gag tgg atc aag ccc Leu Gly Leu Gln Leu Pro Asp Gly Gln Arg Arg Glu Trp Ile Lys Pro 450 455 460	1391
atc atg ttt agt ggg ggc att ggg tcc atg gaa gct gac cac ata agc Ile Met Phe Ser Gly Gly Ile Gly Ser Met Glu Ala Asp His Ile Ser 465 470 475	1439
aag gag gcc cca gag cca ggc atg gaa gtt gta aag gtt gga ggt ccc Lys Glu Ala Pro Glu Pro Gly Met Glu Val Val Lys Val Gly Gly Pro 480 485 490 495	1487
gtc tac agg att gga gtt gga ggt gga gct gct tca tct gtg cag gtg Val Tyr Arg Ile Gly Val Gly Gly Ala Ala Ser Ser Val Gln Val 500 505 510	1535
cag gga gat aac acc agt gac ctg gac ttt ggg gct gtg cag cga gga Gln Gly Asp Asn Thr Ser Asp Leu Asp Phe Gly Ala Val Gln Arg Gly 515 520 525	1583
gac ccg gag atg gaa cag aag atg aac cgt gtg atc agg gct tgt gtg Asp Pro Glu Met Glu Gln Lys Met Asn Arg Val Ile Arg Ala Cys Val 530 535 540	1631
gag gcc ccc aag gga aac ccc atc tgc agc ctt cat gat cag ggc gct Glu Ala Pro Lys Gly Asn Pro Ile Cys Ser Leu His Asp Gln Gly Ala 545 550 555	1679
ggt ggc aat ggc aat gtc cta aaa gag ctg agt gac cca gct gga gcc Gly Gly Asn Gly Asn Val Leu Lys Glu Leu Ser Asp Pro Ala Gly Ala 560 565 570 575	1727
atc att tac acc agc cgc ttc cag ctt ggg gac cca acc ctg aat gcc Ile Ile Tyr Thr Ser Arg Phe Gln Leu Gly Asp Pro Thr Leu Asn Ala 580 585 590	1775
ctg gaa atc tgg ggg gct gag tac cag gaa tca aat gct ctt ctg ctg Leu Glu Ile Trp Gly Ala Glu Tyr Gln Glu Ser Asn Ala Leu Leu Leu 595 600 605	1823
agg tcc ccc aac cgg gac ttc ctg act cat gtc agt gcc cgt gaa cgt Arg Ser Pro Asn Arg Asp Phe Leu Thr His Val Ser Ala Arg Glu Arg 610 615 620	1871

tgc ccg gct tgc ttc gtg ggc acc atc act gga gac cgg aga ata gtg	1919
Cys Pro Ala Cys Phe Val Gly Thr Ile Thr Gly Asp Arg Arg Ile Val	
625 630 635	
ctg gtg gac gat cgg gag tgt cct gtc aga aga aat ggc cag ggg gat	1967
Leu Val Asp Asp Arg Glu Cys Pro Val Arg Arg Asn Gly Gln Gly Asp	
640 645 650 655	
gcc ccc ccg aca ccc ccg cca acc cct gtg gac ctg gag ctc gaa tgg	2015
Ala Pro Pro Thr Pro Pro Pro Thr Pro Val Asp Leu Glu Leu Glu Trp	
660 665 670	
gtg ctg ggc aag atg cct cgg aag gag ttc ttc ctg cag agg aag ccc	2063
Val Leu Gly Lys Met Pro Arg Lys Glu Phe Phe Leu Gln Arg Lys Pro	
675 680 685	
ccc atg ctg cag cct ctg gcc ttg ccc cca ggg ctg agc gtg cac cag	2111
Pro Met Leu Gln Pro Leu Ala Leu Pro Pro Gly Leu Ser Val His Gln	
690 695 700	
gct ctg gag agg gtt ctg agg ctg ccc gcc gtg gcc agc aag cgc tac	2159
Ala Leu Glu Arg Val Leu Arg Leu Pro Ala Val Ala Ser Lys Arg Tyr	
705 710 715	
ctc acc aat aag gtg gac cgc tcc gtg gga ggc ctg gtg gcc cag cag	2207
Leu Thr Asn Lys Val Asp Arg Ser Val Gly Gly Leu Val Ala Gln Gln	
720 725 730 735	
cag tgc gtg ggg ccc ctg caa act cct ctg gca gat gta gcg gtt gtg	2255
Gln Cys Val Gly Pro Leu Gln Thr Pro Leu Ala Asp Val Ala Val Val	
740 745 750	
gca ctg agc cat gag gag ctc ata ggg gct gcc aca gcc ttg gga gaa	2303
Ala Leu Ser His Glu Glu Leu Ile Gly Ala Ala Thr Ala Leu Gly Glu	
755 760 765	
cag cca gtc aag agc ctg ctg gac cca aaa gtc gcc gcc cgg ctg gcc	2351
Gln Pro Val Lys Ser Leu Leu Asp Pro Lys Val Ala Ala Arg Leu Ala	
770 775 780	
gtg gcc gaa gcc ctc acc aac ctg gtg ttt gct ctg gtc act gac ctc	2399
Val Ala Glu Ala Leu Thr Asn Leu Val Phe Ala Leu Val Thr Asp Leu	
785 790 795	
cgg gat gtg aag tgt agc ggg aac tgg atg tgg gca gcc aag ctc cca	2447
Arg Asp Val Lys Cys Ser Gly Asn Trp Met Trp Ala Ala Lys Leu Pro	
800 805 810 815	
ggg gag ggc gca gct ttg gcg gat gcc tgt gag gct atg gtg gca gtg	2495
Gly Glu Gly Ala Ala Leu Ala Asp Ala Cys Glu Ala Met Val Ala Val	
820 825 830	
atg gca gcc ctg ggt gtg gca gtg gat ggt ggc aag gac tcc ctc agc	2543
Met Ala Ala Leu Gly Val Ala Val Asp Gly Gly Lys Asp Ser Leu Ser	
835 840 845	
atg gct gct cgg gtt ggc act gag acc gtg cgg gct cct ggg tca ctg	2591
Met Ala Ala Arg Val Gly Thr Glu Thr Val Arg Ala Pro Gly Ser Leu	
850 855 860	
gtc atc tca gcc tat gcc gtc tgc cca gac atc aca gcc act gtg acc	2639
Val Ile Ser Ala Tyr Ala Val Cys Pro Asp Ile Thr Ala Thr Val Thr	
865 870 875	



cca gac ctc aag cat cct gaa ggg aga ggc cat ctg ctc tat gtg gct	2687
Pro Asp Leu Lys His Pro Glu Gly Arg Gly His Leu Leu Tyr Val Ala	
880 885 890 895	
ctg agc cct ggg cag cac cgg ctc ggg ggc aca gct ctg gcc cag tgc	2735
Leu Ser Pro Gly Gln His Arg Leu Gly Gly Thr Ala Leu Ala Gln Cys	
900 905 910	
ttc tcc cag ctt ggg gaa cac cct cca gac ctg gac ctt cct gag aac	2783
Phe Ser Gln Leu Gly Glu His Pro Pro Asp Leu Asp Leu Pro Glu Asn	
915 920 925	
ttg gtg cgg gcc ttc agc atc act cag ggg ctg ctg aaa gac cgc ctc	2831
Leu Val Arg Ala Phe Ser Ile Thr Gln Gly Leu Leu Lys Asp Arg Leu	
930 935 940	
ctc tgc tca ggc cac gat gtc agt gac gga ggc ctc gtc aca tgc ctg	2879
Leu Cys Ser Gly His Asp Val Ser Asp Gly Gly Leu Val Thr Cys Leu	
945 950 955	
ctg gag atg gcc ttt gct gga aat tgc ggg cta cag gtg gat gtg cct	2927
Leu Glu Met Ala Phe Ala Gly Asn Cys Gly Leu Gln Val Asp Val Pro	
960 965 970 975	
gtc ccc agg gtt gat gtc ctg tct gtg ctg ttc gct gag gag cca ggc	2975
Val Pro Arg Val Asp Val Leu Ser Val Leu Phe Ala Glu Glu Pro Gly	
980 985 990	
ctc gtg ctg gag gtg cag gag cca gac ctg gcc cag gtg ctg aag cgt	3023
Leu Val Leu Glu Val Gln Glu Pro Asp Leu Ala Gln Val Leu Lys Arg	
995 1000 1005	
tac cgg gat gct ggc ctc cat tgc ctg gag ctg ggc cac aca ggc gag	3071
Tyr Arg Asp Ala Gly Leu His Cys Leu Glu Leu Gly His Thr Gly Glu	
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gcc ggg ccc cac gcc atg gtc cgg gtg tca gtg aac ggg gct gtg gtt	3119
Ala Gly Pro His Ala Met Val Arg Val Ser Val Asn Gly Ala Val Val	
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Leu Glu Glu Pro Val Gly Glu Leu Arg Ala Leu Trp Glu Glu Thr Ser	
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Phe Gln Leu Asp Arg Leu Gln Ala Glu Pro Arg Cys Val Ala Glu Glu	
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Glu Arg Gly Leu Arg Glu Arg Met Gly Pro Ser Tyr Cys Leu Pro Pro	
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acc ttt ccc aaa gcc tcc gtg ccc cgt gag cct ggt ggt ccc agc ccc	3311
Thr Phe Pro Lys Ala Ser Val Pro Arg Glu Pro Gly Gly Pro Ser Pro	
1090 1095 1100	
cga gtc gcc atc ttg cga gag gag ggc agt aat gga gac cgg gag atg	3359
Arg Val Ala Ile Leu Arg Glu Glu Gly Ser Asn Gly Asp Arg Glu Met	
1105 1110 1115	
gcc gat gcc ttc cac tta gct ggg ttt gag gta tgg gac gtg acc atg	3407
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1120 1125 1130 1135	

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ggg tgg gca gct gct gtg acc ttt cat ccc agg gct ggg gct gag ctg Gly Trp Ala Ala Ala Val Thr Phe His Pro Arg Ala Gly Ala Glu Leu 1170 1175 1180	3551
agg cgc ttc cgg aag cgg cca gac acc ttc agc ctg ggc gtg tgt aat Arg Arg Phe Arg Lys Arg Pro Asp Thr Phe Ser Leu Gly Val Cys Asn 1185 1190 1195	3599
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gag gat gct gca gag atg ggc cct gac tcc cag cca gcc cgg cca ggc Glu Asp Ala Ala Glu Met Gly Pro Asp Ser Gln Pro Ala Arg Pro Gly 1220 1225 1230	3695
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ctg aat ccc aat ggg tcc cca ggg ggc gtg gct ggc atc tgc tcc tgt Leu Asn Pro Asn Gly Ser Pro Gly Gly Val Ala Gly Ile Cys Ser Cys 1315 1320 1325	3983
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<210> 341
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<212> DNA
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<223> n = a,t,c or g

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attccagtgg gccgcttggc ggtgtcgttg cgtaccagg tccgcgtgag gggttcgggg 180

```

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gttctgtggc ggcaca      atg gcg tct cga gca ggc ccg cga gcg gcc gcc      229
Met Ala Ser Arg Ala Gly Pro Arg Ala Ala Gly
      1              5              10

acc gac ggc agc gac ttt cag cac cgg gag cgc gtc gcc atg cac tac      277
Thr Asp Gly Ser Asp Phe Gln His Arg Glu Arg Val Ala Met His Tyr
      15              20              25

cag atg agt gtg acc ctc aag tat gaa atc aag aag ctg atc tac gta      325
Gln Met Ser Val Thr Leu Lys Tyr Glu Ile Lys Lys Leu Ile Tyr Val
      30              35              40

cat ctg gtc ata tgg ctg ctg ctg gtt gct aag atg agc gtg gga cac      373
His Leu Val Ile Trp Leu Leu Val Ala Lys Met Ser Val Gly His
      45              50              55

ctg agg ctc ttg tca cat gat cag gtg gcc atg ccc tat cag tgg gaa      421
Leu Arg Leu Leu Ser His Asp Gln Val Ala Met Pro Tyr Gln Trp Glu
      60              65              70              75

tac ccg tat ttg ctg agc att ttg ccc tct ctc ttg ggc ctt ctc tcc      469
Tyr Pro Tyr Leu Leu Ser Ile Leu Pro Ser Leu Leu Gly Leu Leu Ser
      80              85              90

ttt ccc cgc aac aac att agc tac ctg gtg ctc tcc atg atc agc atg      517
Phe Pro Arg Asn Asn Ile Ser Tyr Leu Val Leu Ser Met Ile Ser Met
      95              100              105

gga ctc ttt tcc atc gct cca ctc att tat ggc agc atg gag atg ttc      565
Gly Leu Phe Ser Ile Ala Pro Leu Ile Tyr Gly Ser Met Glu Met Phe
      110              115              120

cct gct gca cag cag ctc tac cgc cat ggc aag gcc tac cgt ttc ctc      613
Pro Ala Ala Gln Gln Leu Tyr Arg His Gly Lys Ala Tyr Arg Phe Leu
      125              130              135

ttt ggt ttt tct gcc gtt tcc atc atg tac ctg gtg ttg gtg ttg gca      661
Phe Gly Phe Ser Ala Val Ser Ile Met Tyr Leu Val Leu Val Leu Ala
      140              145              150              155

gtg caa gtg cat gcc tgg cag ttg tac tac agc aag aag ctc cta gac      709
Val Gln Val His Ala Trp Gln Leu Tyr Tyr Ser Lys Lys Leu Leu Asp
      160              165              170

tct tgg ttc acc agc aca cag gag aag aag cat aaa tga agcctctttg      758
Ser Trp Phe Thr Ser Thr Gln Glu Lys Lys His Lys *
      175              180

gggtgaagcc tggacatccc atcgaatgaa aggacactag tacagcgggt ccaaaatccc      818

ttctgggtgat tttagcagct gtgatgttg tacctgggtgc agaccaggcc aaagtctcgg      878

aaagctcctt ttgccatctg ctgaggtggc aaaactataa tttattcctg gttggctaga      938

actgggtgac cgacagctat gaaacaaatt tcagctgttt gaagttgaac tttgaggttt      998

ttctttaaga atgagcttcg tccttgccctc tactcgggtca ttctcccat ttccatccat      1058

tacccttag ccattgagac taaaggaaat agggaataaa tcaaattact tcatctctag      1118

gtcacgggtc aggaacatt tgggcagctg ctcccttggc aggctgtggt ctcctctgca      1178

aagcatttta attaaaaacc tcaataaaga tggccctgcc cacactgtgc cttgtgtttg      1238

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 <212> DNA  
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 cccagtcctcg cgggcgtgga gcgcggagg acccgccctc gggctc atg gcg gcc 175  
 Met Ala Ala  
 1  
 ccg gtc cgc ctg ggc cgg aag cgc ccg ctg cct gcc tgt ccc aac ccg 223  
 Pro Val Arg Leu Gly Arg Lys Arg Pro Leu Pro Ala Cys Pro Asn Pro  
 5 10 15  
 ctc ttc gtt cgc tgg ctg acc gag tgg cgg gac gag gcg acc cgc agc 271  
 Leu Phe Val Arg Trp Leu Thr Glu Trp Arg Asp Glu Ala Thr Arg Ser  
 20 25 30 35  
 agg cac cgc acg cgc ttc gta ttt cag aag gcg ctg cgt tcc ctc cga 319  
 Arg His Arg Thr Arg Phe Val Phe Gln Lys Ala Leu Arg Ser Leu Arg  
 40 45 50  
 cgg tac cca ctg ccg ctg cgc agc ggg aag gaa gct aag atc cta cag 367  
 Arg Tyr Pro Leu Pro Leu Arg Ser Gly Lys Glu Ala Lys Ile Leu Gln  
 55 60 65  
 cac ttc gga gac ggg ctc tgc cgg atg ctg gac gag cgg ctg cag cgg 415  
 His Phe Gly Asp Gly Leu Cys Arg Met Leu Asp Glu Arg Leu Gln Arg  
 70 75 80  
 cac cga aca tcg ggc ggt gac cat gcc ccg gac tca cca tct gga gag 463  
 His Arg Thr Ser Gly Gly Asp His Ala Pro Asp Ser Pro Ser Gly Glu  
 85 90 95  
 aac agt cca gcc ccg cag ggg cga ctt gcg gaa gtc cag gac tct tcc 511  
 Asn Ser Pro Ala Pro Gln Gly Arg Leu Ala Glu Val Gln Asp Ser Ser  
 100 105 110 115  
 atg cca gtt cct gcc cag ccc aaa gcg gga ggc tct ggc agc tac tgg 559  
 Met Pro Val Pro Ala Gln Pro Lys Ala Gly Gly Ser Gly Ser Tyr Trp  
 120 125 130  
 cca gct cgg cac tca gga gcc cga gtg ata ctg ctg gtg ctc tac cgg 607  
 Pro Ala Arg His Ser Gly Ala Arg Val Ile Leu Leu Val Leu Tyr Arg  
 135 140 145  
 gag cac ctg aat cct aat ggt cac cac ttc tta acc aag gag gag ctg 655  
 Glu His Leu Asn Pro Asn Gly His His Phe Leu Thr Lys Glu Glu Leu  
 150 155 160  
 ctg cag agg tgt gct cag aag tcc ccc agg gta gcc cct ggg agt gcc 703

Leu	Gln	Arg	Cys	Ala	Gln	Lys	Ser	Pro	Arg	Val	Ala	Pro	Gly	Ser	Ala		
165						170					175						
cca	ccc	tgg	cca	gcc	ctc	cgc	tcc	ctc	ctt	cac	agg	aac	ctg	gtc	ctc	751	
Pro	Pro	Trp	Pro	Ala	Leu	Arg	Ser	Leu	Leu	His	Arg	Asn	Leu	Val	Leu		
180					185					190					195		
agg	aca	cac	cag	cca	gcc	agg	tac	tca	ttg	acc	cca	gag	ggc	ctg	gag	799	
Arg	Thr	His	Gln	Pro	Ala	Arg	Tyr	Ser	Leu	Thr	Pro	Glu	Gly	Leu	Glu		
				200					205					210			
ctg	gcc	cag	aag	ttg	gcc	gag	tca	gaa	ggc	ctg	agc	ttg	ctg	aat	gtg	847	
Leu	Ala	Gln	Lys	Leu	Ala	Glu	Ser	Glu	Gly	Leu	Ser	Leu	Leu	Asn	Val		
			215					220					225				
ggc	atc	ggg	ccc	aag	gag	ccc	cct	ggg	gag	gag	aca	gca	gtg	cca	gga	895	
Gly	Ile	Gly	Pro	Lys	Glu	Pro	Pro	Gly	Glu	Glu	Thr	Ala	Val	Pro	Gly		
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gca	gct	tca	gca	gag	ctt	gcc	agt	gaa	gca	ggg	gtc	cag	cag	cag	cca	943	
Ala	Ala	Ser	Ala	Glu	Leu	Ala	Ser	Glu	Ala	Gly	Val	Gln	Gln	Gln	Pro		
	245					250					255						
ctg	gag	ctg	agg	cct	gga	gag	tac	agg	gtg	ctg	ttg	tgt	gtg	gac	att	991	
Leu	Glu	Leu	Arg	Pro	Gly	Glu	Tyr	Arg	Val	Leu	Leu	Cys	Val	Asp	Ile		
	260				265				270					275			
ggc	gag	acc	cgg	ggg	ggc	ggg	cac	agg	ccg	gag	ctg	ctc	cga	gag	cta	1039	
Gly	Glu	Thr	Arg	Gly	Gly	Gly	His	Arg	Pro	Glu	Leu	Leu	Arg	Glu	Leu		
			280					285						290			
cag	cgg	ctg	cac	gtg	acc	cac	acg	gtg	cgc	aag	ctg	cac	gtt	gga	gat	1087	
Gln	Arg	Leu	His	Val	Thr	His	Thr	Val	Arg	Lys	Leu	His	Val	Gly	Asp		
			295					300					305				
ttt	gtg	tgg	gtg	gct	cag	gag	acc	aat	cct	aga	gac	cca	gca	aac	cct	1135	
Phe	Val	Trp	Val	Ala	Gln	Glu	Thr	Asn	Pro	Arg	Asp	Pro	Ala	Asn	Pro		
	310						315					320					
ggg	gag	ttg	gta	ctg	gat	cac	att	gtg	gag	cgc	aag	cga	ctg	gat	gac	1183	
Gly	Glu	Leu	Val	Leu	Asp	His	Ile	Val	Glu	Arg	Lys	Arg	Leu	Asp	Asp		
	325					330				335							
ctt	tgc	agc	agc	atc	atc	gac	ggc	cgc	ttc	cgg	gag	cag	aag	ttc	cga	1231	
Leu	Cys	Ser	Ser	Ile	Ile	Asp	Gly	Arg	Phe	Arg	Glu	Gln	Lys	Phe	Arg		
	340				345				350					355			
ctg	aag	cgc	tgt	ggt	ctg	gag	cgc	cgg	gta	tac	ctg	gtg	gaa	gag	cat	1279	
Leu	Lys	Arg	Cys	Gly	Leu	Glu	Arg	Arg	Val	Tyr	Leu	Val	Glu	Glu	His		
				360				365					370				
ggt	tcc	gtc	cac	aac	ctc	agc	ctt	cct	gag	agc	aca	ctg	ctg	cag	gct	1327	
Gly	Ser	Val	His	Asn	Leu	Ser	Leu	Pro	Glu	Ser	Thr	Leu	Leu	Gln	Ala		
			375					380					385				
gtc	acc	aac	act	cag	gtc	att	gat	ggc	ttt	ttt	gtg	aag	cgc	aca	gca	1375	
Val	Thr	Asn	Thr	Gln	Val	Ile	Asp	Gly	Phe	Phe	Val	Lys	Arg	Thr	Ala		
	390						395					400					
gac	att	aag	gag	tca	gcc	gcc	tac	ctg	gcc	ctc	ttg	act	cgg	ggc	ctg	1423	
Asp	Ile	Lys	Glu	Ser	Ala	Ala	Tyr	Leu	Ala	Leu	Thr	Arg	Gly	Leu			
	405					410				415							
cag	aga	ctc	tac	cag	ggc	cac	acc	cta	cgc	agc	cgc	ccc	tgg	gga	acc	1471	

**PCT/US01/04098**

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<210> 343
<211> 2013
<212> DNA
<213> Homo sapiens
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<222> (1)...(2013)
<223> n = a,t,c or g
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 tgtgtctctt catctccctg ggaaaggtgc ccccgaggtg aaagag atg gcc tgg 175  
 Met Ala Trp  
 1  
 tgg aaa tcc tgg att gaa cag gag ggt gtc aca gtg aag agc agc tcc 223  
 Trp Lys Ser Trp Ile Glu Gln Glu Gly Val Thr Val Lys Ser Ser Ser  
 5 10 15  
 cac ttc aac cca gac cct gat gca gag acc ctc tac aaa gcc atg aag 271  
 His Phe Asn Pro Asp Pro Asp Ala Glu Thr Leu Tyr Lys Ala Met Lys  
 20 25 30 35  
 ggg atc ggg acc aac gag cag gct atc atc gat gtg ctc acc aag aga 319  
 Gly Ile Gly Thr Asn Glu Gln Ala Ile Ile Asp Val Leu Thr Lys Arg  
 40 45 50  
 agc aac acg cag cgg cag cag atc gcc aag tcc ttc aag gct cag ttc 367  
 Ser Asn Thr Gln Arg Gln Gln Ile Ala Lys Ser Phe Lys Ala Gln Phe  
 55 60 65  
 ggc aag gac ctc act gag acc ttg aag tct gag ctc agt ggc aag ttt 415  
 Gly Lys Asp Leu Thr Glu Thr Leu Lys Ser Glu Leu Ser Gly Lys Phe  
 70 75 80  
 gag agg ctc att gtg gcc ctt atg tac ccg cca tac aga tac gaa gcc 463  
 Glu Arg Leu Ile Val Ala Leu Met Tyr Pro Pro Tyr Arg Tyr Glu Ala  
 85 90 95  
 aag gag ctg cat gac gcc atg aag ggc tta gga acc aag gag ggt gtc 511  
 Lys Glu Leu His Asp Ala Met Lys Gly Leu Gly Thr Lys Glu Gly Val  
 100 105 110 115  
 atc att gag atc ctg gcc tct cgg acc aag aac cag ctg cgg gag ata 559  
 Ile Ile Glu Ile Leu Ala Ser Arg Thr Lys Asn Gln Leu Arg Glu Ile  
 120 125 130  
 atg aag gcg tat gag gaa gac tat ggg tcc agc ctg gag gag gac atc 607  
 Met Lys Ala Tyr Glu Glu Asp Tyr Gly Ser Ser Leu Glu Glu Asp Ile  
 135 140 145  
 caa gca gac aca agt ggc tac ctg gag agg atc ctg gtg tgc ctc ctg 655  
 Gln Ala Asp Thr Ser Gly Tyr Leu Glu Arg Ile Leu Val Cys Leu Leu  
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 cag ggc agc agg gat gat gtg agc agc ttt gtg gac ccg gca ctg gcc 703  
 Gln Gly Ser Arg Asp Asp Val Ser Ser Phe Val Asp Pro Ala Leu Ala  
 165 170 175  
 ctc caa gac gca cag gat ctg tat gcg gca ggc gag aag att cgt ggg 751  
 Leu Gln Asp Ala Gln Asp Leu Tyr Ala Ala Gly Glu Lys Ile Arg Gly  
 180 185 190 195  
 act gat gag atg aaa ttc atc acc atc ctg tgc acg cgc agt gcc act 799  
 Thr Asp Glu Met Lys Phe Ile Thr Ile Leu Cys Thr Arg Ser Ala Thr  
 200 205 210  
 cac ctg ctg aga gtg ttt gaa gag tat gag aaa att gcc aac aag agc 847  
 His Leu Leu Arg Val Phe Glu Glu Tyr Glu Lys Ile Ala Asn Lys Ser  
 215 220 225



att gag gac agc atc aag agt gag acc cat ggc tca ctg gag gag gcc 895  
 Ile Glu Asp Ser Ile Lys Ser Glu Thr His Gly Ser Leu Glu Glu Ala  
 230 235 240  
  
 atg ctc act gtg gtg aaa tgc acc caa aac ctc cac agc tac ttt gca 943  
 Met Leu Thr Val Val Lys Cys Thr Gln Asn Leu His Ser Tyr Phe Ala  
 245 250 255  
  
 gag aga ctc tac tat gcc atg aag gga gca ggg acg cgt gat ggg acc 991  
 Glu Arg Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Arg Asp Gly Thr  
 260 265 270 275  
  
 ctg ata aga aac atc gtt tca agg agc gag att gac tta aat ctt atc 1039  
 Leu Ile Arg Asn Ile Val Ser Arg Ser Glu Ile Asp Leu Asn Leu Ile  
 280 285 290  
  
 aaa tgt cac ttc aag aag atg tac ggc aag acc ctc agc agc atg atc 1087  
 Lys Cys His Phe Lys Lys Met Tyr Gly Lys Thr Leu Ser Ser Met Ile  
 295 300 305  
  
 atg gaa gac acc agc ggc gac tac aag aac gcc ctg ctg agc ctg gtg 1135  
 Met Glu Asp Thr Ser Gly Asp Tyr Lys Asn Ala Leu Leu Ser Leu Val  
 310 315 320  
  
 ggc agc gac ccc tga ggcacagaag aacaagagca aagaccatga agccagagtc 1190  
 Gly Ser Asp Pro \*  
 325  
  
 tccaggactc ctactcaac ctggccatg gacgcagggtt ggggtgtgagg ggggtcccag 1250  
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 <212> DNA  
 <213> Homo sapiens

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&lt;221&gt; CDS

&lt;222&gt; (57) .. (836)

&lt;400&gt; 344

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Met Ala Ala Ser Arg Leu Glu Leu Asn Leu Val Arg Leu Leu Ser Arg	
1 5 10 15	
tgc gag gcg atg gca gcg gag aaa cgg gac ccg gac gag tgg cgc ctg	152
Cys Glu Ala Met Ala Ala Glu Lys Arg Asp Pro Asp Glu Trp Arg Leu	
20 25 30	
gag aag tac gtg gga gcc cta gag gac atg ttg cag gcc ctg aag gtc	200
Glu Lys Tyr Val Gly Ala Leu Glu Asp Met Leu Gln Ala Leu Lys Val	
35 40 45	
cac gcg agc aaa ccg gcc tct gag gtg atc aat gaa tat tcc tgg aag	248
His Ala Ser Lys Pro Ala Ser Glu Val Ile Asn Glu Tyr Ser Trp Lys	
50 55 60	
gtg gat ttt ctg aag ggg atg ctg caa gcc gag aag ctg acc tcc tcc	296
Val Asp Phe Leu Lys Gly Met Leu Gln Ala Glu Lys Leu Thr Ser Ser	
65 70 75 80	
tca gag aaa gca ctg gcc aac cag ttc ctg gcc cct ggc cgt gtg cca	344
Ser Glu Lys Ala Leu Ala Asn Gln Phe Leu Ala Pro Gly Arg Val Pro	
85 90 95	
acc aca gcc aga gag cga gtg ccc gcc aca aag acg gtg cat ctg cag	392
Thr Thr Ala Arg Glu Arg Val Pro Ala Thr Lys Thr Val His Leu Gln	
100 105 110	
tca cgg gcg cgg tac acc agc gag atg cgg agt gag cta cta ggc acg	440
Ser Arg Ala Arg Tyr Thr Ser Glu Met Arg Ser Glu Leu Leu Gly Thr	
115 120 125	
gac tct gca gag cct gag atg gac gta agg aag aga act gga gtg gca	488
Asp Ser Ala Glu Pro Glu Met Asp Val Arg Lys Arg Thr Gly Val Ala	
130 135 140	
ggg tcc cag cca gtg agt gag aag cag tcg gca gct gag cta gac ctc	536
Gly Ser Gln Pro Val Ser Glu Lys Gln Ser Ala Ala Glu Leu Asp Leu	
145 150 155 160	
gtc ctg cag cga cat cag aac ctc cag gaa aag ctg gcg gaa gag atg	584
Val Leu Gln Arg His Gln Asn Leu Gln Glu Lys Leu Ala Glu Glu Met	
165 170 175	
cta gga ctg gcc cgg agc ctc aag acc aat acc ctg gcc gcc cag agt	632
Leu Gly Leu Ala Arg Ser Leu Lys Thr Asn Thr Leu Ala Ala Gln Ser	
180 185 190	
gtc atc aag aag gac aac cag acc ctg tca cac tca ctg aaa atg gcg	680
Val Ile Lys Lys Asp Asn Gln Thr Leu Ser His Ser Leu Lys Met Ala	
195 200 205	
gac cag aac ctg gag aaa ctg aag acg gag tca gag cgt ctg gag cag	728
Asp Gln Asn Leu Glu Lys Leu Lys Thr Glu Ser Glu Arg Leu Glu Gln	
210 215 220	
cac acg cag aag tca gtc aac tgg ctg ctc tgg gcc atg ctc att atc	776

His Thr Gln Lys Ser Val Asn Trp Leu Leu Trp Ala Met Leu Ile Ile  
 225 230 235 240  
 gtc tgc ttc atc ttc att agc atg atc ctc ttc att cga atc atg cct 824  
 Val Cys Phe Ile Phe Ile Ser Met Ile Leu Phe Ile Arg Ile Met Pro  
 245 250 255  
 aaa ctc aaa taa agacccccgc ccacctaataa aaaaaaaaa 864  
 Lys Leu Lys \*  
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<210> 345  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (217)..(618)

<220>  
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 actttttggac ttggattgag ccacgctact ggcacccag gatctccagc ttgcagacag 180  
 cctgtcgtgg gacttcacag cctocataat tataga atg gca atg gtc tct gcg 234  
 Met Ala Met Val Ser Ala  
 1 5  
 atg tcc tgg gtc ctg tat ttg tgg ata agt gct tgt gca atg cta ctc 282  
 Met Ser Trp Val Leu Tyr Leu Trp Ile Ser Ala Cys Ala Met Leu Leu  
 10 15 20  
 tgc cat gga tcc ctt cag cac act ttc cag cag cat cac ctg cac aga 330  
 Cys His Gly Ser Leu Gln His Thr Phe Gln Gln His His Leu His Arg  
 25 30 35  
 cca gaa gga ggg acg tgt gaa gtg ata gca gca cac cga tgt tgt aac 378  
 Pro Glu Gly Gly Thr Cys Glu Val Ile Ala Ala His Arg Cys Cys Asn  
 40 45 50  
 aag aat cgc att gag gag cgg tca caa aca gta aag tgt tcc tgt cta 426  
 Lys Asn Arg Ile Glu Glu Arg Ser Gln Thr Val Lys Cys Ser Cys Leu  
 55 60 65 70  
 cct gga aaa gtg gct gga aca aca aga aac cgg cct tct tgc gtc gat 474  
 Pro Gly Lys Val Ala Gly Thr Thr Arg Asn Arg Pro Ser Cys Val Asp  
 75 80 85  
 gcc tcc ata gtg att ggg aaa tgg tgg tgt gag atg gag cct tgc cta 522  
 Ala Ser Ile Val Ile Gly Lys Trp Trp Cys Glu Met Glu Pro Cys Leu  
 90 95 100

gaa gga gaa gaa tgt aag aca ctc cct gac aat tct gga tgg atg tgc 570  
 Glu Gly Glu Glu Cys Lys Thr Leu Pro Asp Asn Ser Gly Trp Met Cys  
           105                          110                          115  
  
 gca aca ggc aac aaa att aag acc acg aga att cac cca aga acc taa 618  
 Ala Thr Gly Asn Lys Ile Lys Thr Thr Arg Ile His Pro Arg Thr \*  
           120                          125                          130  
  
 cagaagcatt tgtggtagta aagggaac caaccctttg gaaaatacat tttggganc 678  
 tcaaacatc tcacatatat acaagccaaa tgggatttct tacttncact ttgactggct 738  
 accngataat cacagtnctg ttacttgtgt ntaacgaaaa taccctacag tggaggaaga 798  
 cacaggcggtt tttgggcaac accatnggg 827

<210> 346  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (420)..(989)

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 atctttcact ccttggcctg ctaagagtta ctactcagg caatccctgc tccaccagag 180  
 gagactgtcc aattgccaag caaccactg ctggccaatc acagagcttg gaggtgatgt 240  
 catggcaaga gcgagcagtg gtgctgatgt tgagagaagc ccagggtacc actaattgag 300  
 ggagtgagga agagagcagc tcgcttctaa ctggactgca cgttggtgac agcgtcccaa 360  
 gctggtgaca gaccactct gtaactttca gctagattca gccaccagat cccagaac 419  
 atg acc ctt gct gcc tac aaa gag aag atg aag gag ctc ccg ctg gtg 467  
 Met Thr Leu Ala Ala Tyr Lys Glu Lys Met Lys Glu Leu Pro Leu Val  
       1                          5                          10                          15  
  
 tcc ttg ttc tgc tcc tgc ttc ctg gcc gat ccc ctg aat aag tgc tcc 515  
 Ser Leu Phe Cys Ser Cys Phe Leu Ala Asp Pro Leu Asn Lys Ser Ser  
           20                          25                          30  
  
 tac aaa tat gaa gca gac acg gtg gac ctg aat tgg tgc gtc att tcc 563  
 Tyr Lys Tyr Glu Ala Asp Thr Val Asp Leu Asn Trp Cys Val Ile Ser  
           35                          40                          45  
  
 gac atg gaa gtc atc gag ctg aac aaa tgc acc tgc ggc caa tcc ttt 611  
 Asp Met Glu Val Ile Glu Leu Asn Lys Cys Thr Ser Gly Gln Ser Phe  
           50                          55                          60  
  
 gaa gtc atc ctg aag cca ccc tcc ttt gat ggg gtt ccc gag ttc aac 659  
 Glu Val Ile Leu Lys Pro Pro Ser Phe Asp Gly Val Pro Glu Phe Asn  
           65                          70                          75                          80  
  
 gcc tcc ctg cca agg cgg cga gac cca tcc ctg gaa gag atc cag aag 707  
 Ala Ser Leu Pro Arg Arg Arg Asp Pro Ser Leu Glu Glu Ile Gln Lys

85	90	95	
aaa cta gaa gcg gct gag gag cga agg aag tac cag gaa gcg gag ctc			755
Lys Leu Glu Ala Ala Glu Glu Arg Arg Lys Tyr Gln Glu Ala Glu Leu			
100	105	110	
ctg aaa cac cta gca gag aaa cgg gaa cat gag aga gag gtg atc caa			803
Leu Lys His Leu Ala Glu Lys Arg Glu His Glu Arg Glu Val Ile Gln			
115	120	125	
aag gcc att gag gaa aac aac aac ttc atc aag atg gct aag gaa aaa			851
Lys Ala Ile Glu Glu Asn Asn Asn Phe Ile Lys Met Ala Lys Glu Lys			
130	135	140	
ctg gcc cag aag atg gaa tcc aac aag gag aac agg gag gcc cac ctc			899
Leu Ala Gln Lys Met Glu Ser Asn Lys Glu Asn Arg Glu Ala His Leu			
145	150	155	160
gcc gcc atg ttg gaa cgg ctg caa gag aag gac aag cac gcc gag gag			947
Ala Ala Met Leu Glu Arg Leu Gln Glu Lys Asp Lys His Ala Glu Glu			
165	170	175	
gtg cgg aaa aac aag gag ctg aag gaa gag gcc tcc agg taa agcctag			996
Val Arg Lys Asn Lys Glu Leu Lys Glu Glu Ala Ser Arg *			
180	185	190	
aggccaaaga actttccagg tcagccggac agctccagca gctccacgtt ccaggcagcc			1056
tcgcccgcgcg gctgcgctcc cagcactggg gtttgggggg aggggggtgg ccaaggggcg			1116
tttctctctgc ttttggtgtt tgtacatgtt aagaattgac cagtgaagcc atcctatttg			1176
tttccgggga acaatgacgg ggtgggagag gggagaggag agagtttggg aaagggagat			1236
ggagaagaac tcaaggacat tgcaaccctg cccggcgcag atctgatttt cacatctcta			1296
cctggacatt gagcctccag gcaccatgtt gaggagagat gaaaaccagg gcggtagaac			1356
ttcaggggtga aggacagagt cctgggtggg gcagcggctg cagggcgcac cagagaaccc			1416
agccagaggg ggtgtgagta ccagtgggtg tgcttcacc ctgcagcagg tgggatgagg			1476
tctgtgtgtg tgtgtgaacc atcatttttt gatcatcatg accaatgaaa cattgaaaaa			1536
aaaaa			1541

&lt;210&gt; 347

&lt;211&gt; 1220

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (39) .. (998)

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (1220)

&lt;223&gt; n = a,t,c or g

&lt;400&gt; 347

tgatttagtt gattgggggg cagangnaat ttgaaggg	atg atg tat ata act Met Met Tyr Ile Thr 1 5	53
atc tat tcg atg atg aag ata ccc cac caa acc caa aaa aag aga tct Ile Tyr Ser Met Met Lys Ile Pro His Gln Thr Gln Lys Lys Arg Ser 10 15 20		101
ctc gag gat ccg aat tcg cgg ccg cgt cga cgc ggt gtc ctg agc cga Leu Glu Asp Pro Asn Ser Arg Pro Arg Arg Arg Gly Val Leu Ser Arg 25 30 35		149
tta cag cta ggt agt gga gcg ccg ctg ctt acc tgg gtg cag gag aca Leu Gln Leu Gly Ser Gly Ala Pro Leu Leu Thr Trp Val Gln Glu Thr 40 45 50		197
gcc gga gtc gct ggg gga gct ccg cgc cgc cgg acg ccc gtg acc atg Ala Gly Val Ala Gly Gly Ala Pro Arg Arg Arg Thr Pro Val Thr Met 55 60 65		245
tgg agg ctg ctg gct cgc gct agt gcg ccg ctc ctg cgg gtg ccc ttg Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu Arg Val Pro Leu 70 75 80 85		293
tca gat tcc tgg gca ctc ctc ccc gcc agt gct ggc gta aag aca ctg Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly Val Lys Thr Leu 90 95 100		341
ctc cca gta cca agt ttt gaa gat gtt tcc att cct gaa aaa ccc aag Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro Glu Lys Pro Lys 105 110 115		389
ctt aga ttt att gaa agg gca cca ctt gtg cca aaa gta aga aga gaa Leu Arg Phe Ile Glu Arg Ala Pro Leu Val Pro Lys Val Arg Arg Glu 120 125 130		437
cct aaa aat tta agt gac ata cgg gga cct tcc act gaa gct acg gag Pro Lys Asn Leu Ser Asp Ile Arg Gly Pro Ser Thr Glu Ala Thr Glu 135 140 145		485
ttt aca gaa ggc aat ttt gca atc ttg gca ttg ggt ggt ggc tac ctg Phe Thr Glu Gly Asn Phe Ala Ile Leu Ala Leu Gly Gly Gly Tyr Leu 150 155 160 165		533
cat tgg ggc cac ttt gaa atg atg cgc ctg aca atc aac cgc tct atg His Trp Gly His Phe Glu Met Met Arg Leu Thr Ile Asn Arg Ser Met 170 175 180		581
gac ccc aag aac atg ttt gcc ata tgg cga gta cca gcc cct ttc aag Asp Pro Lys Asn Met Phe Ala Ile Trp Arg Val Pro Ala Pro Phe Lys 185 190 195		629
ccc atc act cgc aaa agt gtt ggg cat cgc atg ggg gga ggc aaa ggt Pro Ile Thr Arg Lys Ser Val Gly His Arg Met Gly Gly Gly Lys Gly 200 205 210		677
gct att gac cac tac gtg aca cct gtg aag gct ggc cgc ctt gtt gta Ala Ile Asp His Tyr Val Thr Pro Val Lys Ala Gly Arg Leu Val Val 215 220 225		725
gag atg ggt ggg cgt tgt gaa ttt gaa gaa gtg caa ggt ttc ctt gac Glu Met Gly Gly Arg Cys Glu Phe Glu Glu Val Gln Gly Phe Leu Asp 230 235 240 245		773

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cag gtt gcc cac aag ttg ccc ttc gca gca aag gct gtg agc cgc ggg      821
Gln Val Ala His Lys Leu Pro Phe Ala Ala Lys Ala Val Ser Arg Gly
                250                255                260

act cta gag aag atg cga aaa gat caa gag gaa aga gaa cgt aac aac      869
Thr Leu Glu Lys Met Arg Lys Asp Gln Glu Glu Arg Glu Arg Asn Asn
                265                270                275

cag aac ccc tgg aca ttt gag cga ata gcc act gcc aac atg ctg ggc      917
Gln Asn Pro Trp Thr Phe Glu Arg Ile Ala Thr Ala Asn Met Leu Gly
                280                285                290

ata cgg aaa gta ctg agc cca tat gac ttg acc cac aag ggg aaa tac      965
Ile Arg Lys Val Leu Ser Pro Tyr Asp Leu Thr His Lys Gly Lys Tyr
                295                300                305

tgg ggc aag ttc tac atg ccc aaa cgt gtg tag tgagtgtgta ggagataact    1016
Trp Gly Lys Phe Tyr Met Pro Lys Arg Val *
310                315                320

gtatataggg tactgaaaga aggattctgc atttctattc ccctcagcct acccactgaa    1076

gtctttgggt agctcttaag ccataactaa ggagcagcat ttgagtagat ttctgaaaaa    1136

caatgttatt tgttgattta aaaagaaaac tgtattttta ttaaataaaa tttaaacatc    1196

acttcaggat ataaaaaaaaaaaaa      1220

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<210> 348  
 <211> 2159  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (3) .. (1868)

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<400> 348
tc   cga aac cgc tcc gga att ccc ggg tcg acc cac gcg tcc ggc ggg      47
     Arg Asn Arg Ser Gly Ile Pro Gly Ser Thr His Ala Ser Gly Gly
         1             5             10             15

tcc ggg agc gcg gcg gag acg atg cct gag atc aga gtc acg ccc ttg      95
Ser Gly Ser Ala Ala Glu Thr Met Pro Glu Ile Arg Val Thr Pro Leu
                20                25                30

ggg gcc ggc cag gac gtg ggc cga agc tgc atc ctg gtc tcc att gcg      143
Gly Ala Gly Gln Asp Val Gly Arg Ser Cys Ile Leu Val Ser Ile Ala
                35                40                45

ggc aag aat gtc atg ctg gac tgt gga atg cac atg ggc ttc aat gac      191
Gly Lys Asn Val Met Leu Asp Cys Gly Met His Met Gly Phe Asn Asp
                50                55                60

gac cga cgc ttc cct gac ttc tcc tac atc acc cag aac ggc cgc cta      239
Asp Arg Arg Phe Pro Asp Phe Ser Tyr Ile Thr Gln Asn Gly Arg Leu
                65                70                75

aca gac ttc ctg gac tgt gtg atc att agc cac ttc cac ctg gac cac      287
Thr Asp Phe Leu Asp Cys Val Ile Ile Ser His Phe His Leu Asp His
                80                85                90                95

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tgc ggg gca ctc ccc tac ttc agc gag atg gtg ggc tac gac ggc ccc	335
Cys Gly Ala Leu Pro Tyr Phe Ser Glu Met Val Gly Tyr Asp Gly Pro	
100 105 110	
atc tac atg act cac ccc acc cag gcc atc tgc ccc atc ttg ctg gag	383
Ile Tyr Met Thr His Pro Thr Gln Ala Ile Cys Pro Ile Leu Leu Glu	
115 120 125	
gac tac cgc aag atc gcc gta gac aag aag ggc gag gcc aac ttc ttc	431
Asp Tyr Arg Lys Ile Ala Val Asp Lys Lys Gly Glu Ala Asn Phe Phe	
130 135 140	
acc tcc cag atg atc aaa gac tgc atg aag aag gtg gtg gct gtc cac	479
Thr Ser Gln Met Ile Lys Asp Cys Met Lys Lys Val Val Ala Val His	
145 150 155	
ctc cac cag acg gtc cag gta gat gat gag ctg gag atc aag gcc tac	527
Leu His Gln Thr Val Gln Val Asp Asp Glu Leu Glu Ile Lys Ala Tyr	
160 165 170 175	
tat gca ggc cac gtg ctg ggg gca gcc atg ttc cag att aaa gtg ggc	575
Tyr Ala Gly His Val Leu Gly Ala Ala Met Phe Gln Ile Lys Val Gly	
180 185 190	
tca gag tct gtg gtc tac acg ggt gat tat aac atg acc cca gac cga	623
Ser Glu Ser Val Val Tyr Thr Gly Asp Tyr Asn Met Thr Pro Asp Arg	
195 200 205	
cac tta gga gct gcc tgg att gac aag tgc cgc ccc aac ctg ctc atc	671
His Leu Gly Ala Ala Trp Ile Asp Lys Cys Arg Pro Asn Leu Leu Ile	
210 215 220	
aca gag tcc acg tac gcc acg acc atc cgt gac tcc aag cgc tgc cgg	719
Thr Glu Ser Thr Tyr Ala Thr Thr Ile Arg Asp Ser Lys Arg Cys Arg	
225 230 235	
gag cga gac ttc ctg aag aaa gtc cac gag acc gtg gag cgt ggt ggg	767
Glu Arg Asp Phe Leu Lys Lys Val His Glu Thr Val Glu Arg Gly Gly	
240 245 250 255	
aag gtg ctg ata cct gtg ttc gcg ctg ggc cgc gcc cag gag ctc tgc	815
Lys Val Leu Ile Pro Val Phe Ala Leu Gly Arg Ala Gln Glu Leu Cys	
260 265 270	
atc ctc ctg gag acc ttc tgg gag cgc atg aac ctg aag gtg ccc atc	863
Ile Leu Leu Glu Thr Phe Trp Glu Arg Met Asn Leu Lys Val Pro Ile	
275 280 285	
tac ttc tcc acg ggg ctg acc gag aag gcc aac cac tac tac aag ctg	911
Tyr Phe Ser Thr Gly Leu Thr Glu Lys Ala Asn His Tyr Tyr Lys Leu	
290 295 300	
ttc atc ccc tgg acc aac cag aag atc cgc aag act ttc gtg cag agg	959
Phe Ile Pro Trp Thr Asn Gln Lys Ile Arg Lys Thr Phe Val Gln Arg	
305 310 315	
aac atg ttt gag ttc aag cac atc aag gcc ttc gac cgg gct ttt gct	1007
Asn Met Phe Glu Phe Lys His Ile Lys Ala Phe Asp Arg Ala Phe Ala	
320 325 330 335	
gac aac cca gga ccg atg gtt gtg ttt gcc acg cca gga atg ctg cac	1055
Asp Asn Pro Gly Pro Met Val Val Phe Ala Thr Pro Gly Met Leu His	
340 345 350	



gct ggg cag tcc ctg cag atc ttc cgg aaa tgg gcc gga aac gaa aag	1103
Ala Gly Gln Ser Leu Gln Ile Phe Arg Lys Trp Ala Gly Asn Glu Lys	
355 360 365	
aac atg gtc atc atg ccc ggc tac tgc gtg cag ggc acc gtc ggc cac	1151
Asn Met Val Ile Met Pro Gly Tyr Cys Val Gln Gly Thr Val Gly His	
370 375 380	
aag atc ctc agc ggg cag cgg aag ctc gag atg gag ggg cgg cag gtg	1199
Lys Ile Leu Ser Gly Gln Arg Lys Leu Glu Met Glu Gly Arg Gln Val	
385 390 395	
ctg gag gtc aag atg cag gtg gag tac atg tca ttc agc gca cac gcg	1247
Leu Glu Val Lys Met Gln Val Glu Tyr Met Ser Phe Ser Ala His Ala	
400 405 410 415	
gac gcc aag ggc atc atg cag ctg gtg ggc cag gca gag ccg gag agc	1295
Asp Ala Lys Gly Ile Met Gln Leu Val Gly Gln Ala Glu Pro Glu Ser	
420 425 430	
gtg ctg ctg gtg cat ggc gag gcc aag aag atg gag ttc ctg aag cag	1343
Val Leu Leu Val His Gly Glu Ala Lys Lys Met Glu Phe Leu Lys Gln	
435 440 445	
aag atc gag cag gag ctc cgg gtc aac tgc tac atg ccg gcc aat ggc	1391
Lys Ile Glu Gln Glu Leu Arg Val Asn Cys Tyr Met Pro Ala Asn Gly	
450 455 460	
gag acg gtg acg ctg ccc aca agc ccc agc atc ccc gta ggc atc tcg	1439
Glu Thr Val Thr Leu Pro Thr Ser Pro Ser Ile Pro Val Gly Ile Ser	
465 470 475	
ctg ggg ctg ctg aag cgg gag atg gcg cag ggg ctg ctc cct gag gcc	1487
Leu Gly Leu Leu Lys Arg Glu Met Ala Gln Gly Leu Leu Pro Glu Ala	
480 485 490 495	
aag aag cct cgg ctc ctg cac ggc acc ctg atc atg aag gac agc aac	1535
Lys Lys Pro Arg Leu Leu His Gly Thr Leu Ile Met Lys Asp Ser Asn	
500 505 510	
ttc cgg ctg gtg tcc tca gag caa gcc ctc aaa gag ctg ggt ctg gct	1583
Phe Arg Leu Val Ser Ser Glu Gln Ala Leu Lys Glu Leu Gly Leu Ala	
515 520 525	
gag cac cag ctg cgc ttc acc tgc cgc gtg cac ctg cat gac aca cgc	1631
Glu His Gln Leu Arg Phe Thr Cys Arg Val His Leu His Asp Thr Arg	
530 535 540	
aag gag cag gag acg gca ttg cgc gtc tac agc cac ctc aag agc gtc	1679
Lys Glu Gln Glu Thr Ala Leu Arg Val Tyr Ser His Leu Lys Ser Val	
545 550 555	
ctg aag gac cac tgt gtg cag cac ctc ccg gac ggc tct gtg act gtg	1727
Leu Lys Asp His Cys Val Gln His Leu Pro Asp Gly Ser Val Thr Val	
560 565 570 575	
gag tcc gtc ctc ctc cag gcc gcc gcc cct tct gag gac cca ggc acc	1775
Glu Ser Val Leu Leu Gln Ala Ala Ala Pro Ser Glu Asp Pro Gly Thr	
580 585 590	
aag gtg ctg ctg gtc tcc tgg acc tac cag gac gag gag ctg ggg agc	1823
Lys Val Leu Leu Val Ser Trp Thr Tyr Gln Asp Glu Glu Leu Gly Ser	
595 600 605	

ttc ctc aca tct ctg ctg aag aag ggc ctc ccc cag gcc ccc agc tga 1871  
 Phe Leu Thr Ser Leu Leu Lys Lys Gly Leu Pro Gln Ala Pro Ser  
 610 615 620

ggccggcaac tcacccagcc gccacctctg ccctctccca gctggacaga ccctgggctt 1931  
 gcacttcagg actgtgggtg ccctgggtga acagaccctg caggtcccat ccctggggac 1991  
 agaggccttg tgtcacctgc ctgcccaggc agctgtttgc agctgaagaa acaaactggt 2051  
 ctccaggctg tcttgccctt attcctgggt agggcagggt gtcctagaca gcagtttcca 2111  
 gtaaaagctg aacaaaagac tacttggtac tctcaaaaaa aaaaaaaa 2159

<210> 349  
 <211> 434  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(333)

<400> 349  
 gca cga gca gct ttc cgc cgc ttg ggc gcc ttg tcc gga gct gcg gcc 48  
 Ala Arg Ala Ala Phe Arg Arg Leu Gly Ala Leu Ser Gly Ala Ala Ala  
 1 5 10 15  
 tta ggc ttc gct tcc tac ggg gcg cac ggc gcc caa ttc cca gat gcc 96  
 Leu Gly Phe Ala Ser Tyr Gly Ala His Gly Ala Gln Phe Pro Asp Ala  
 20 25 30  
 tac ggg aag gag ctg ttt gac aag gcc aac aaa cac cac ttc tta cac 144  
 Tyr Gly Lys Glu Leu Phe Asp Lys Ala Asn Lys His His Phe Leu His  
 35 40 45  
 agc ctg gcc ctg tta ggg gtg ccc cat tgc aga aag cca ctc tgg gct 192  
 Ser Leu Ala Leu Leu Gly Val Pro His Cys Arg Lys Pro Leu Trp Ala  
 50 55 60  
 ggg tta ttg cta gct tcc gga acg acc tta ttc tgc acc agc ttt tac 240  
 Gly Leu Leu Leu Ala Ser Gly Thr Thr Leu Phe Cys Thr Ser Phe Tyr  
 65 70 75 80  
 tac cag gct ctg agt gga gac ccc agc atc cag act ttg gcc cct gcg 288  
 Tyr Gln Ala Leu Ser Gly Asp Pro Ser Ile Gln Thr Leu Ala Pro Ala  
 85 90 95  
 gga ggg acc ctg cta ctc ttg ggc tgg ctt gcc ttg gct ctt tga gct 336  
 Gly Gly Thr Leu Leu Leu Leu Gly Trp Leu Ala Leu Ala Leu \*  
 100 105 110  
 cccttttgct taatta'ctgg gttttctggg cagttttttt tttaaagagt tggagtaaga 396  
 agaggattaa aaaggaaagg caaataaaaa aaaaaaaa 434

<210> 350

<211> 1194  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (3)..(1193)

<400> 350

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cc  gcg cgc agt cca gcg gcc ccg cgt gtg tgc cct cgc cct gcc gga      47
    Ala Arg Ser Pro Ala Ala Pro Arg Val Cys Pro Arg Pro Ala Gly
      1              5              10              15

gcg ggg aaa atg gag gct gtg att gag aag gaa tgc agc gcg ctc gga      95
Ala Gly Lys Met Glu Ala Val Ile Glu Lys Glu Cys Ser Ala Leu Gly
              20              25              30

ggc ctc ttc cag acc atc atc agc gac atg aag ggg agc tat cca gtt     143
Gly Leu Phe Gln Thr Ile Ile Ser Asp Met Lys Gly Ser Tyr Pro Val
              35              40              45

tgg gaa gat ttc ata aac aaa gca gga aag ctg cag tcc cag ctt cgg     191
Trp Glu Asp Phe Ile Asn Lys Ala Gly Lys Leu Gln Ser Gln Leu Arg
              50              55              60

aca aca gta gta gca gca gct gcc ttc ttg gac gcc ttt cag aaa gtg     239
Thr Thr Val Val Ala Ala Ala Phe Leu Asp Ala Phe Gln Lys Val
              65              70              75

gct gac atg gcc acc aac aca cgt ggt ggg acc agg gag att gga tct     287
Ala Asp Met Ala Thr Asn Thr Arg Gly Gly Thr Arg Glu Ile Gly Ser
      80              85              90              95

gct ctc acc agg atg tgc atg agg cac aga agc att gaa gcc aag ctg     335
Ala Leu Thr Arg Met Cys Met Arg His Arg Ser Ile Glu Ala Lys Leu
              100              105              110

agg cag ttt tcg agc gct tta att gat tgt ctg ata aac cca ctt caa     383
Arg Gln Phe Ser Ser Ala Leu Ile Asp Cys Leu Ile Asn Pro Leu Gln
              115              120              125

gaa cag atg gaa gaa tgg aag aaa gtg gcc aac cag ctg gat aaa gac     431
Glu Gln Met Glu Glu Trp Lys Lys Val Ala Asn Gln Leu Asp Lys Asp
              130              135              140

cac gca aaa gaa tat aag aaa gcc cgc caa gag ata aaa aag aag tcc     479
His Ala Lys Glu Tyr Lys Lys Ala Arg Gln Glu Ile Lys Lys Lys Ser
              145              150              155

tcg gat acg ctg aaa ctg cag aag aaa gca aaa aaa ggg aga ggt gat     527
Ser Asp Thr Leu Lys Leu Gln Lys Lys Ala Lys Lys Gly Arg Gly Asp
              160              165              170              175

atc cag cct cag ttg gac agt gct ctc caa gat gtc aat gat aag tat     575
Ile Gln Pro Gln Leu Asp Ser Ala Leu Gln Asp Val Asn Asp Lys Tyr
              180              185              190

ctc tta ttg gaa gaa aca gaa aag cag gct gtc cgg aag gct ttg att     623
Leu Leu Leu Glu Glu Thr Glu Lys Gln Ala Val Arg Lys Ala Leu Ile
              195              200              205

gaa gaa cgt ggc cga ttc tgt acc ttc atc tct atg ctg cgg cca gtg     671
Glu Glu Arg Gly Arg Phe Cys Thr Phe Ile Ser Met Leu Arg Pro Val
              210              215              220

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att gaa gaa gaa atc tca atg cta ggg gaa ata acc cac ctt cag acc      719
ile Glu Glu Glu Ile Ser Met Leu Gly Glu Ile Thr His Leu Gln Thr
    225                      230                      235

atc tcg gaa gat cta aaa agc ctg acc atg gac cct cac aaa ctg ccc      767
ile Ser Glu Asp Leu Lys Ser Leu Thr Met Asp Pro His Lys Leu Pro
    240                      245                      250                      255

tcc tca agt gaa cag gtg att ctg gac ttg aaa ggt tct gat tac agc      815
Ser Ser Ser Glu Gln Val Ile Leu Asp Leu Lys Gly Ser Asp Tyr Ser
                      260                      265                      270

tgg tcg tat cag acg cca ccc tct tcc ccc agc acc acc atg tcc aga      863
Trp Ser Tyr Gln Thr Pro Pro Ser Ser Pro Ser Thr Thr Met Ser Arg
                      275                      280                      285

aag tcc agt gtc tgc agc agc ctg aac agt gtc aac agc agt gac tcc      911
Lys Ser Ser Val Cys Ser Ser Leu Asn Ser Val Asn Ser Ser Asp Ser
                      290                      295                      300

cgg tcc agc ggc tcc cac tcg cat tcc ccc agc tca cat tac cgc tac      959
Arg Ser Ser Gly Ser His Ser His Ser Pro Ser Ser His Tyr Arg Tyr
    305                      310                      315

cgc agc tcc aac ctg gcc cag cag gct cct gtg agg ctg tcc agc gtg      1007
Arg Ser Ser Asn Leu Ala Gln Gln Ala Pro Val Arg Leu Ser Ser Val
    320                      325                      330                      335

tcc tcc cat gac tca gga ttc ata tcc cag gat gcc ttc cag tcc aag      1055
Ser Ser His Asp Ser Gly Phe Ile Ser Gln Asp Ala Phe Gln Ser Lys
                      340                      345                      350

tca cca tcc ccc atg ccg cca gag gcc ccc aac cag cgc cgc aaa gag      1103
Ser Pro Ser Pro Met Pro Pro Glu Ala Pro Asn Gln Arg Arg Lys Glu
                      355                      360                      365

aag cga gaa ccg gac ccc aac ggg gga gga ccc act acc gcc agc ggc      1151
Lys Arg Glu Pro Asp Pro Asn Gly Gly Gly Pro Thr Thr Ala Ser Gly
                      370                      375                      380

cca cct gca gca gct gag gag gct cag aga cca cgg agc atg a      1194
Pro Pro Ala Ala Ala Glu Glu Ala Gln Arg Pro Arg Ser Met
    385                      390                      395

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<210> 351  
 <211> 1699  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) .. (834)

<400> 351

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atg aac ctg gaa ggg ctg gag atg gtt gct gtg ctc gtg gtc ctc gct      48
Met Asn Leu Glu Gly Leu Glu Met Val Ala Val Leu Val Val Leu Ala
    1                      5                      10                      15

ctg ttt gtc aag gtc ctg gag cag ttt ggc ctc ttt gag cct gtc tcc      96

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Leu	Phe	Val	Lys	Val	Leu	Glu	Gln	Phe	Gly	Leu	Phe	Glu	Pro	Val	Ser		
			20					25					30				
ttg	gaa	ggc	cac	cct	cca	ggg	ccc	act	aaa	aaa	gcg	ctg	aag	cag	cga	144	
Leu	Glu	Gly	His	Pro	Pro	Gly	Pro	Thr	Lys	Lys	Ala	Leu	Lys	Gln	Arg		
			35				40					45					
ttc	ctc	aag	ctg	ctg	ccg	tgc	tgc	ggg	ccc	caa	gcc	ctg	ccc	tca	gtc	192	
Phe	Leu	Lys	Leu	Leu	Pro	Cys	Cys	Gly	Pro	Gln	Ala	Leu	Pro	Ser	Val		
			50				55					60					
agt	gaa	agc	aag	tgc	ctc	tca	tgt	gct	tcc	ggg	ggc	ggg	gct	cga	tgt	240	
Ser	Glu	Ser	Lys	Cys	Leu	Ser	Cys	Ala	Ser	Gly	Gly	Gly	Ala	Arg	Cys		
			65			70				75					80		
gtg	cac	agc	gtg	gac	gat	gaa	ttt	gaa	ttg	tcc	acc	gtg	tgt	cac	cgg	288	
Val	His	Ser	Val	Asp	Asp	Glu	Phe	Glu	Leu	Ser	Thr	Val	Cys	His	Arg		
				85					90					95			
cct	gag	ggt	ctg	gag	cag	ctg	cag	gag	caa	acc	aaa	ttc	acg	cgc	aag	336	
Pro	Glu	Gly	Leu	Glu	Gln	Leu	Gln	Glu	Gln	Thr	Lys	Phe	Thr	Arg	Lys		
			100					105					110				
gag	ttg	cag	gtc	ctg	tac	cgg	ggc	ttc	aag	aac	gaa	tgt	ccc	agc	gga	384	
Glu	Leu	Gln	Val	Leu	Tyr	Arg	Gly	Phe	Lys	Asn	Glu	Cys	Pro	Ser	Gly		
			115				120					125					
att	gtc	aat	gag	gag	aac	ttc	aag	cag	att	tac	tcc	cag	ttc	ttt	cct	432	
Ile	Val	Asn	Glu	Glu	Asn	Phe	Lys	Gln	Ile	Tyr	Ser	Gln	Phe	Phe	Pro		
			130				135					140					
caa	gga	gac	tcc	agc	acc	tat	gcc	act	ttt	ctc	ttc	aat	gcc	ttt	gac	480	
Gln	Gly	Asp	Ser	Ser	Thr	Tyr	Ala	Thr	Phe	Leu	Phe	Asn	Ala	Phe	Asp		
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Thr	Asn	His	Asp	Gly	Ser	Val	Ser	Phe	Glu	Asp	Phe	Val	Ala	Gly	Leu		
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tcc	gtg	att	ctt	cgg	gga	act	gta	gat	gac	agg	ctt	aat	tgg	gcc	ttc	576	
Ser	Val	Ile	Leu	Arg	Gly	Thr	Val	Asp	Asp	Arg	Leu	Asn	Trp	Ala	Phe		
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Asn	Leu	Tyr	Asp	Leu	Asn	Lys	Asp	Gly	Cys	Ile	Thr	Lys	Glu	Glu	Met		
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ctt	gac	atc	atg	aag	tcc	atc	tat	gac	atg	atg	ggc	aag	tac	acg	tac	672	
Leu	Asp	Ile	Met	Lys	Ser	Ile	Tyr	Asp	Met	Met	Gly	Lys	Tyr	Thr	Tyr		
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Pro	Ala	Leu	Arg	Glu	Glu	Ala	Pro	Arg	Glu	His	Val	Glu	Ser	Phe	Phe		
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Gln	Lys	Met	Asp	Arg	Asn	Lys	Asp	Gly	Val	Val	Thr	Ile	Glu	Glu	Phe		
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Ile	Glu	Ser	Cys	Gln	Lys	Asp	Glu	Asn	Ile	Met	Arg	Ser	Met	Gln	Leu		
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275

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Met Ile Trp  
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tac aca gag aag ggg cac cta acc aag act agg gac ttc aag aag tta 165  
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Arg Lys Leu Ser Gly Ser Gly Asp Ser Trp Ala Arg Ala Pro Thr His  
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cac aca att cag aca aga gct ttg tgg ccc tgt gca aga aag gac ctc 261  
His Thr Ile Gln Thr Arg Ala Leu Trp Pro Cys Ala Arg Lys Asp Leu  
40 45 50  
att att ctt ttt acc tta cag aat gtt gct gag gca cag tgc atc gcc 309  
Ile Ile Leu Phe Thr Leu Gln Asn Val Ala Glu Ala Gln Cys Ile Ala

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	70	75	80	
tta gtg gag acc ttt aac ctc aga cca aat gag ttc aaa tat atg tct				405
Leu Val Glu Thr Phe Asn Leu Arg Pro Asn Glu Phe Lys Tyr Met Ser				
	85	90	95	
gtc atc gct gaa ttg gag caa agc gga ctt gga gca gaa ctg aaa tgt				453
Val Ile Ala Glu Leu Glu Gln Ser Gly Leu Gly Ala Glu Leu Lys Cys				
	100	105	110	115
gcc cag aac caa aat aag act tag aactgtacag gttggccctt cacctagttg				507
Ala Gln Asn Gln Asn Lys Thr *				
	120			
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880



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Cys Glu Lys Asn Ala Lys *	
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Arg Glu Phe Ser Ser Leu Leu Ser Arg Gly Cys Leu Ser Thr Ser Arg	
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Ile Asp Met Asp Ala Leu Glu Asp Tyr Val Trp Pro Arg Ala Thr Ser	
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Glu Leu Ile Leu Leu Pro Val Thr Gly Leu Glu Cys Val Gly Asp Arg	
45 50 55 60	
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Leu Leu Ala Gly Glu Gly Pro Asp Val Leu Val Tyr Ser Leu Asp Phe	
65 70 75	
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Gly Gly His Leu Arg Met Ile Lys Arg Val Gln Asn Leu Leu Gly His	
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Tyr Leu Ile His Gly Phe Arg Val Arg Pro Glu Pro Asn Gly Asp Leu	
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Asp Leu Glu Ala Met Val Ala Val Phe Gly Ser Lys Gly Leu Arg Val	
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Val Lys Ile Ser Trp Gly Gln Gly His Phe Trp Glu Leu Trp Arg Ser	
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Gly Leu Trp Asn Met Ser Asp Trp Ile Trp Asp Ala Arg Trp Leu Glu	
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Pro Val Val Gly Cys Ile Leu Gln Glu Val Pro Cys Thr Asp Arg Cys	
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Thr Leu Ser Ser Ala Cys Leu Ile Gly Asp Ala Trp Lys Glu Leu Thr	
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Ile Val Ala Gly Ala Val Ser Asn Gln Leu Leu Val Trp Tyr Pro Ala	
205 210 215 220	
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Gly Arg Val Lys Val Val Pro Ile Asn Thr Pro Thr Ala Ala Val Asp	
445 450 455 460	
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Gln Thr Leu Phe Pro Gly Lys Val His Ser Leu Ser Trp Ala Leu Arg	
465 470 475	
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Gly Tyr Glu Glu Leu Leu Leu Leu Ala Ser Gly Pro Gly Gly Val Val	
480 485 490	
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Arg Arg Gly Ser Val Leu Leu Phe Pro Ser Gly Pro Gly Arg Asp Gly	
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Ala Tyr Tyr Gln Leu Phe Val Arg Asp Gly Gln Leu Gln Pro Val Leu	
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Ala Phe Ala Tyr Leu Lys Asp Gly Asp Val Met Leu Tyr Arg Ala Leu	
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655 660 665	

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 925 930 935 940  
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 Leu Thr Leu Gln Ala His Ser Cys Gly Ile Asn Ser Leu His Thr Leu  
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Leu Leu Pro Leu Ala Leu Leu Arg Val Arg Cys Thr Pro Tyr Trp Ala
              25              30              35

ggg ttc tta cct ttt gaa atc atg tat ggg agg gcg ctg cct atc ttg      498
Gly Phe Leu Pro Phe Glu Ile Met Tyr Gly Arg Ala Leu Pro Ile Leu
              40              45              50

cct aag cta aga gat gcc caa ttg gca aaa ata tca caa act aat tta      546
Pro Lys Leu Arg Asp Ala Gln Leu Ala Lys Ile Ser Gln Thr Asn Leu
              55              60              65              70

tta cag tac cta cag tct ccc caa cag gta caa gat atc atc ctg cca      594
Leu Gln Tyr Leu Gln Ser Pro Gln Gln Val Gln Asp Ile Ile Leu Pro
              75              80              85

ctt gtt cga gga acc cat ccc aat cca att cct gaa cag aca ggg ccc      642
Leu Val Arg Gly Thr His Pro Asn Pro Ile Pro Glu Gln Thr Gly Pro
              90              95              100

tgc cat tca ttc ccg cca ggt gac ctg ttg ttt gtt aaa aag ttc cag      690
Cys His Ser Phe Pro Pro Gly Asp Leu Leu Phe Val Lys Lys Phe Gln
              105              110              115

aga gaa gga ctc cct cct gct tgg aag aga cct cac acc gtc atc acg      738
Arg Glu Gly Leu Pro Pro Ala Trp Lys Arg Pro His Thr Val Ile Thr
              120              125              130

atg cca acg gct ctg aag gtg gat ggc att cct gcg tgg att cat cac      786
Met Pro Thr Ala Leu Lys Val Asp Gly Ile Pro Ala Trp Ile His His
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tcc cgc atc aaa aag gcc aac aga gcc caa cta gaa aca tgg gtc ccc      834
Ser Arg Ile Lys Lys Ala Asn Arg Ala Gln Leu Glu Thr Trp Val Pro
              155              160              165

agg gct ggg tca ggc ccc tta aaa ctg cac cta agt tgg gtg aag cca      882
Arg Ala Gly Ser Gly Pro Leu Lys Leu His Leu Ser Trp Val Lys Pro
              170              175              180

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tta gat taa ttctttt tcttaatttt gtaaaacaat gcatagett cgtcaaactt 938  
 Leu Asp \*  
 185

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ccccaaaaca caagtgggga atgtagtgtc caacctgggtt ttactaacc ctgttttttag 1058

actctccctt tcttttaatc actcagcctt gtttccacct gaattgactc tcccttagct 1118

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aacttggtga agctgactcc cagcacatcc aagaatgcaa ttaactgata agatactgtg 1238

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catttatcct tttaactttt ttgcctactt tattttctgta aaattgtttt aactagacct 1418

cccctctcct ttctaaacca aagtataaaa gaagatctag ccccttcttc aggccgagag 1478

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ttgcctccaa gccagcttt cagctgggag agggggaaga aggggcagtg gcagcagttc 180

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ttctgttctt ttgggacttc gtcattttt ccaatatgtc ctgggacctc cggagctgta 300

acgggggatgc taaggacacg gtcagtggat tatcgtgact gtacta atg aaa gga 355  
 Met Lys Gly  
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ttc aag ctc tcc tgc act gcc agt aac tcc aac cgc agc acg ccg gcc 403  
 Phe Lys Leu Ser Cys Thr Ala Ser Asn Ser Asn Arg Ser Thr Pro Ala  
 5 10 15

tgc tcg ccc atc ctc cgg aag cgg tct cgc tcg cca acc ccg cag aac 451  
 Cys Ser Pro Ile Leu Arg Lys Arg Ser Arg Ser Pro Thr Pro Gln Asn  
 20 25 30 35

cag gac gga gac acc atg gtg gag aag ggc tca gat cac tcc tcg gac 499  
 Gln Asp Gly Asp Thr Met Val Glu Lys Gly Ser Asp His Ser Ser Asp  
 40 45 50

aag tcc ccg tcc aca ccg gag cag ggc gtg cag cgc agc tgc tcc tcc	547
Lys Ser Pro Ser Thr Pro Glu Gln Gly Val Gln Arg Ser Cys Ser Ser	
55 60 65	
cag tcc ggc cgg agc ggc ggc aag aat tcc aag aaa agc cag agt tgg	595
Gln Ser Gly Arg Ser Gly Gly Lys Asn Ser Lys Lys Ser Gln Ser Trp	
70 75 80	
tat aat gtg tta agc ccc acc tac aag cag aga aat gaa gac ttc aga	643
Tyr Asn Val Leu Ser Pro Thr Tyr Lys Gln Arg Asn Glu Asp Phe Arg	
85 90 95	
aag ctc ttt aag cag ctt cca gac acg gag cgc ctc att gtt gat tac	691
Lys Leu Phe Lys Gln Leu Pro Asp Thr Glu Arg Leu Ile Val Asp Tyr	
100 105 110 115	
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Ser Cys Ala Leu Gln Arg Asp Ile Leu Leu Gln Gly Arg Leu Tyr Leu	
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135 140 145	
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Leu Leu Thr Val Arg Leu Lys Asp Ile Cys Ser Met Thr Lys Glu Lys	
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Lys His Phe Phe Thr Ser Phe Gly Ala Arg Asp Arg Thr Tyr Met Met	
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Met Phe Arg Leu Trp Gln Asn Ala Leu Leu Glu Lys Pro Leu Cys Pro	
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Lys Glu Leu Trp His Phe Val His Gln Cys Tyr Gly Asn Glu Leu Gly	
215 220 225	
ctg acc agt gat gac gag gac tac gtg ccc cct gac gac gac ttc aac	1075
Leu Thr Ser Asp Asp Glu Asp Tyr Val Pro Pro Asp Asp Asp Phe Asn	
230 235 240	
aca atg gga tac tgt gaa gag atc cct gtg gaa gag aat gaa gtg aat	1123
Thr Met Gly Tyr Cys Glu Glu Ile Pro Val Glu Glu Asn Glu Val Asn	
245 250 255	
gac agc tca tcc aag agc agc ata gag acc aag cca gat gcc agt cca	1171
Asp Ser Ser Ser Lys Ser Ser Ile Glu Thr Lys Pro Asp Ala Ser Pro	
260 265 270 275	
cag ctg ccc aag aaa tcc atc acc aac agc aca cta aca tcc aca ggg	1219
Gln Leu Pro Lys Lys Ser Ile Thr Asn Ser Thr Leu Thr Ser Thr Gly	
280 285 290	
agc agt gag gcc ccc gtc tcg ttt gat ggg ctg ccc ctg gag gaa gag	1267
Ser Ser Glu Ala Pro Val Ser Phe Asp Gly Leu Pro Leu Glu Glu Glu	
295 300 305	



gcg ctg gag gga gac ggg tcc ctg gaa aag gag ctc gcc att gac aac Ala Leu Glu Gly Asp Gly Ser Leu Glu Lys Glu Leu Ala Ile Asp Asn 310 315 320	1315
atc atg ggg gag aag att gag atg atc gct cct gtg aac tcc cct tca Ile Met Gly Glu Lys Ile Glu Met Ile Ala Pro Val Asn Ser Pro Ser 325 330 335	1363
ctg gac ttc aat gac aat gag gac atc ccc act gag ctc agt gac tct Leu Asp Phe Asn Asp Asn Glu Asp Ile Pro Thr Glu Leu Ser Asp Ser 340 345 350 355	1411
tcc gac aca cac gat gaa gga gag gtc cag gcc ttc tat gag gac ctg Ser Asp Thr His Asp Glu Gly Glu Val Gln Ala Phe Tyr Glu Asp Leu 360 365 370	1459
agt ggc cgg cag tac gtg aat gaa gtc ttc aac ttc agc gtg gac aag Ser Gly Arg Gln Tyr Val Asn Glu Val Phe Asn Phe Ser Val Asp Lys 375 380 385	1507
ctc tat gac ctc ctc ttc acc aac tcg ccc ttc cag cgg gat ttc atg Leu Tyr Asp Leu Leu Phe Thr Asn Ser Pro Phe Gln Arg Asp Phe Met 390 395 400	1555
gag cag cgg cgc ttc tct gat atc atc ttc cat cca tgg aaa aag gag Glu Gln Arg Arg Phe Ser Asp Ile Ile Phe His Pro Trp Lys Lys Glu 405 410 415	1603
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aac cct ctg gct ccc aaa act gcc act gtc agg gag aca cag acc atg Asn Pro Leu Ala Pro Lys Thr Ala Thr Val Arg Glu Thr Gln Thr Met 440 445 450	1699
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atc gag aag aac ttc tgg agt ggg ctg gag gac tac ttc cgc cat tta Ile Glu Lys Asn Phe Trp Ser Gly Leu Glu Asp Tyr Phe Arg His Leu 520 525 530	1939
gag agc gag ctg gcc aaa acg gag agc act tat ttg gct gag atg cac Glu Ser Glu Leu Ala Lys Thr Glu Ser Thr Tyr Leu Ala Glu Met His 535 540 545	1987
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565                               570                               575

atg agc ccg gtc acc acg ccc aca gat gag gat gtg ggc cac agg atc      2131
Met Ser Pro Val Thr Thr Pro Thr Asp Glu Asp Val Gly His Arg Ile
580                               585                               590                               595

aaa cat gtg gca ggt tcc aca cag acg cgg cat atc ccg gag gac acc      2179
Lys His Val Ala Gly Ser Thr Gln Thr Arg His Ile Pro Glu Asp Thr
600                               605                               610

ccc aac ggt ttc cac ctg cag agc gtg tcc aag ctg ctg ctg gtt atc      2227
Pro Asn Gly Phe His Leu Gln Ser Val Ser Lys Leu Leu Leu Val Ile
615                               620                               625

agc tgt gtg atc tgt ttc agt ctg gtg ctg ctg gtc atc ctt aac atg      2275
Ser Cys Val Ile Cys Phe Ser Leu Val Leu Leu Val Ile Leu Asn Met
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Met Leu Phe Tyr Lys Leu Trp Met Leu Glu Tyr Thr Thr Gln Thr Leu
645                               650                               655

act gcc tgg cag ggt cta agg ctc caa gaa agg tta ccc cag tct cag      2371
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aca gaa tgg gcc cag ctc tta gag tcc caa caa aag tac cac gat act      2419
Thr Glu Trp Ala Gln Leu Leu Glu Ser Gln Gln Lys Tyr His Asp Thr
680                               685                               690

gag ctc caa aaa tgg agg gaa atc atc aaa tcc tca gtg atg ctc ctt      2467
Glu Leu Gln Lys Trp Arg Glu Ile Ile Lys Ser Ser Val Met Leu Leu
695                               700                               705

gac cag atg aag gac tcg ctc atc aac ctt cag aac ggc atc agg tcc      2515
Asp Gln Met Lys Asp Ser Leu Ile Asn Leu Gln Asn Gly Ile Arg Ser
710                               715                               720

cgc gac tac acg tcg gaa agt gaa gaa aag agg aat cgc tat cat tga      2563
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725                               730                               735

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 Phe Lys Leu Ser Cys Thr Ala Ser Asn Ser Asn Arg Ser Thr Pro Ala  
 5 10 15  
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 Cys Ser Pro Ile Leu Arg Lys Arg Ser Arg Ser Pro Thr Pro Gln Asn  
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 Gln Asp Gly Asp Thr Met Val Glu Lys Gly Ser Asp His Ser Ser Asp  
 40 45 50  
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 Lys Ser Pro Ser Thr Pro Glu Gln Gly Val Gln Arg Ser Cys Ser Ser  
 55 60 65  
 cag tcc ggc cgg agc ggc ggc aag aat tcc aag aaa agc cag agt tgg 595  
 Gln Ser Gly Arg Ser Gly Gly Lys Asn Ser Lys Lys Ser Gln Ser Trp  
 70 75 80  
 tat aat gtg tta agc ccc acc tac aag cag aga aat gaa gac ttc aga 643  
 Tyr Asn Val Leu Ser Pro Thr Tyr Lys Gln Arg Asn Glu Asp Phe Arg  
 85 90 95  
 aag ctc ttt aag cag ctt cca gac acg gag cgc ctc att gtt gat tac 691  
 Lys Leu Phe Lys Gln Leu Pro Asp Thr Glu Arg Leu Ile Val Asp Tyr  
 100 105 110 115  
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 Ser Cys Ala Leu Gln Arg Asp Ile Leu Leu Gln Gly Arg Leu Tyr Leu  
 120 125 130  
 tct gaa aat tgg atc tgc ttc tac agc aac atc ttc cgc tgg gaa act 787  
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 135 140 145  
 ctg ctg aca gtc cgt ttg aaa gac atc tgt tcc atg act aaa gaa aaa 835  
 Leu Leu Thr Val Arg Leu Lys Asp Ile Cys Ser Met Thr Lys Glu Lys  
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Tyr Thr Leu Thr Arg Val Ala Arg Asn Lys Ser Arg Leu Arg Val Ser	
485 490 495	
aca gag ctg cgc tat cga aaa cag ccc tgg ggg tta gtg aaa acg ttc	1891
Thr Glu Leu Arg Tyr Arg Lys Gln Pro Trp Gly Leu Val Lys Thr Phe	
500 505 510 515	
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Ile Glu Lys Asn Phe Trp Ser Gly Leu Glu Asp Tyr Phe Arg His Leu	
520 525 530	
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Glu Ser Glu Leu Ala Lys Thr Glu Ser Thr Tyr Leu Ala Glu Met His	
535 540 545	
aga caa tct ccc aaa gag aag gcc agc aag act aca acg gtg cgg agg	2035
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Met Ser Pro Val Thr Thr Pro Thr Asp Glu Asp Val Gly His Arg Ile	
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Ser Cys Val Leu Val Leu Leu Val Ile Leu Asn Met Met Leu Phe Tyr	
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Lys Leu Trp Met Leu Glu Tyr Thr Thr Gln Thr Leu Thr Ala Trp Gln	
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Gly Leu Arg Leu Gln Glu Arg Leu Pro Gln Ser Gln Thr Glu Trp Ala	
660 665 670 675	
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Gln Leu Leu Glu Ser Gln Gln Lys Tyr His Asp Thr Glu Leu Gln Lys	
680 685 690	
tgg agg gaa atc atc aaa tcc tca gtg atg ctc ctt gac cag atg aag	2467
Trp Arg Glu Ile Ile Lys Ser Ser Val Met Leu Leu Asp Gln Met Lys	
695 700 705	
gac tcg ctc atc aac ctt cag aac ggc atc agg tcc cgc gac tac acg	2515
Asp Ser Leu Ile Asn Leu Gln Asn Gly Ile Arg Ser Arg Asp Tyr Thr	
710 715 720	

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 Lys Lys Lys Glu Gln Ser Glu Val Ser Val Ser Pro Arg Ala Ser Lys  
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 Ser Asp Asn Glu Gly Arg Lys His Arg Ser Arg Ser Arg Ser Lys Glu  
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 gga aga aga cat gaa tcc aaa gat aaa tcc tct aag aaa cat aag tct 415  
 Gly Arg Arg His Glu Ser Lys Asp Lys Ser Ser Lys Lys His Lys Ser  
 70 75 80 85  
 gag gaa cat aat gac aaa gaa cat tct tct gat aaa gga aga gag cga 463  
 Glu Glu His Asn Asp Lys Glu His Ser Ser Asp Lys Gly Arg Glu Arg  
 90 95 100  
 cta aat tca tct gaa aat ggt gag gac agg cac aaa cgc aaa gaa aga 511  
 Leu Asn Ser Ser Glu Asn Gly Glu Asp Arg His Lys Arg Lys Glu Arg  
 105 110 115  
 aag tca tca aga ggc aga agt cac tca aga tct agg tct cgt gaa aga 559  
 Lys Ser Ser Arg Gly Arg Ser His Ser Arg Ser Arg Ser Arg Glu Arg  
 120 125 130  
 cgc cat cgt agt aga agc agg gag cgg aag aag tct cga tcc agg agt 607  
 Arg His Arg Ser Arg Ser Arg Glu Arg Lys Lys Ser Arg Ser Arg Ser  
 135 140 145

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Arg Glu Arg Lys Lys Ser Arg Ser Arg Ser Arg Glu Arg Lys Lys Ser	
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aga tcc aga agc agg gaa aga aaa cgg cgg atc agg tct cgt tcc cgc	703
Arg Ser Arg Ser Arg Glu Arg Lys Arg Arg Ile Arg Ser Arg Ser Arg	
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Ser Arg Ser Arg His Arg His Arg Thr Arg Ser Arg Ser Arg Thr Arg	
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Ser Arg Ser Arg Asp Arg Lys Lys Arg Ile Glu Lys Pro Arg Arg Phe	
200 205 210	
agc aga agt tta agc cgg act cca agt cca cct ccc ttc aga ggc aga	847
Ser Arg Ser Leu Ser Arg Thr Pro Ser Pro Pro Pro Phe Arg Gly Arg	
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aac aca gca atg gat gca cag gaa gct tta gct aga agg ttg gaa agg	895
Asn Thr Ala Met Asp Ala Gln Glu Ala Leu Ala Arg Arg Leu Glu Arg	
230 235 240 245	
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Ala Lys Lys Leu Gln Glu Gln Arg Glu Lys Glu Met Val Glu Lys Gln	
250 255 260	
aaa caa caa gaa ata gct gca gca gct gca gct act gga ggt tct gtt	991
Lys Gln Gln Glu Ile Ala Ala Ala Ala Ala Thr Gly Gly Ser Val	
265 270 275	
ctc aat gtt gct gcc ctg ttg gca tca gga aca caa gta aca cct cag	1039
Leu Asn Val Ala Ala Leu Leu Ala Ser Gly Thr Gln Val Thr Pro Gln	
280 285 290	
ata gcc atg gca gct cag atg gca gcc ctg caa gct aaa gct ttg gca	1087
Ile Ala Met Ala Ala Gln Met Ala Ala Leu Gln Ala Lys Ala Leu Ala	
295 300 305	
gag aca gga ata gct gtt cct agc tac tat aac cca gcc gct gtt aat	1135
Glu Thr Gly Ile Ala Val Pro Ser Tyr Tyr Asn Pro Ala Ala Val Asn	
310 315 320 325	
cca atg aaa ttt gct gaa caa gag aaa aaa agg aaa atg ctt tgg cag	1183
Pro Met Lys Phe Ala Glu Gln Glu Lys Lys Arg Lys Met Leu Trp Gln	
330 335 340	
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Gly Lys Lys Glu Gly Asp Lys Ser Gln Ser Ala Glu Ile Trp Glu Lys	
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Leu Asn Phe Gly Asn Lys Asp Gln Asn Val Lys Phe Arg Lys Leu Met	
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Gly Ile Lys Ser Glu Asp Glu Ala Gly Cys Ser Ser Val Asp Glu Glu	
375 380 385	
agt tac aag act ctg aag cag cag gaa gaa gta ttt cga aat tta gat	1375
Ser Tyr Lys Thr Leu Lys Gln Gln Glu Glu Val Phe Arg Asn Leu Asp	
390 395 400 405	

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 Ala Gln Tyr Glu Met Ala Arg Ser Gln Thr His Thr Gln Arg Gly Met  
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 Gly Leu Gly Phe Thr Ser Ser Met Arg Gly Met Asp Ala Val \*  
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acatgaaaga aatgttatgt agatgttctt tagaagatct ggccatttgg tacataatcc 1891

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agggggaaaag tc atg ggc agg gcc tgg tgt ggg atg tgg agg aga cgg 168  
 Met Gly Arg Ala Trp Cys Gly Met Trp Arg Arg Arg  
 1 5 10

cgc ccg ggg agg agg agc gct gtg ccc agg tgg cct cac ttg tca tct 216  
 Arg Pro Gly Arg Arg Ser Ala Val Pro Arg Trp Pro His Leu Ser Ser  
 15 20 25

caa agt ggc gtc gaa ccc cct gac agg tgg acg gga acc ccc ggc tgg 264  
 Gln Ser Gly Val Glu Pro Pro Asp Arg Trp Thr Gly Thr Pro Gly Trp  
 30 35 40

ccc tcc aga gac cag gag gcc cct ggc tca atg atg cca cct gca gct 312  
 Pro Ser Arg Asp Gln Glu Ala Pro Gly Ser Met Met Pro Pro Ala Ala  
 45 50 55 60

gcc caa ccc tcc gcc cat ggt gcc ctt gtt cca cct gcc acc gct cat 360  
 Ala Gln Pro Ser Ala His Gly Ala Leu Val Pro Pro Ala Thr Ala His  
 65 70 75

gaa cct gtg gat cac cca gct ctg cac tgg ctt gcc tgc tgc tgc tgt 408  
 Glu Pro Val Asp His Pro Ala Leu His Trp Leu Ala Cys Cys Cys Cys



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ctc agt tta cct ggg cag ttg ccc ctg gct atc cgg ctg gga tgg gac			456
Leu Ser Leu Pro Gly Gln Leu Pro Leu Ala Ile Arg Leu Gly Trp Asp			
95	100	105	
ttg gac tta gaa gca ggc ccc tcc tct gga aag ctg tgt cct cgg gcc			504
Leu Asp Leu Glu Ala Gly Pro Ser Ser Gly Lys Leu Cys Pro Arg Ala			
110	115	120	
agg agg tgg cag cct cta cct tcc tga gacag ggaccctttt ctgtccatca			556
Arg Arg Trp Gln Pro Leu Pro Ser *			
125	130		
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	Met Lys Thr Leu Phe Leu		
	1 5		
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Gly Val Thr Leu Gly Leu Ala Ala Leu Ser Phe Thr Leu Glu Glu			
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Glu Asp Ile Thr Gly Thr Trp Tyr Val Lys Ala Met Val Val Asp Lys			
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gac ttt ccg gag gac agg agg ccc agg aag gtg tcc cca gtg aag gtg			256
Asp Phe Pro Glu Asp Arg Arg Pro Arg Lys Val Ser Pro Val Lys Val			
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aca gcc ctg ggc ggt ggg aac ttg gaa gcc acg ttc acc ttc atg agg			304
Thr Ala Leu Gly Gly Gly Asn Leu Glu Ala Thr Phe Thr Phe Met Arg			
55 60 65 70			
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Glu Asp Arg Cys Ile Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu			
75 80 85			
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Pro Gly Lys Phe Ser Ala Tyr Gly Gly Arg Lys Leu Ile Tyr Leu Gln			
90 95 100			
gag ctg ccc ggg acg gac gac tac gtc ttt tac tgc aaa gac cag cgc			448

Glu	Leu	Pro	Gly	Thr	Asp	Asp	Tyr	Val	Phe	Tyr	Cys	Lys	Asp	Gln	Arg		
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cgt	ggg	ggc	ctg	cgc	tac	atg	gga	aag	ctt	gtg	gca	tct	gct	ccc	tgc	496	
Arg	Gly	Gly	Leu	Arg	Tyr	Met	Gly	Lys	Leu	Val	Ala	Ser	Ala	Pro	Cys		
		120				125					130						
agg	gcc	gtg	ccg	ctg	tcc	cca	cgt	cgg	ctc	acc	tgg	cca	cct	cac	ctg	544	
Arg	Ala	Val	Pro	Leu	Ser	Pro	Arg	Arg	Leu	Thr	Trp	Pro	Pro	His	Leu		
		135			140					145					150		
cag	gta	gga	atc	cta	ata	cca	acc	tgg	agg	ccc	tgg	aag	aat	tta	aga	592	
Gln	Val	Gly	Ile	Leu	Ile	Pro	Thr	Trp	Arg	Pro	Trp	Lys	Asn	Leu	Arg		
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aat	tgg	tgc	agc	aca	agg	gac	tct	cgg	agg	agg	aca	ttt	tca	tgc	ccc	640	
Asn	Trp	Cys	Ser	Thr	Arg	Asp	Ser	Arg	Arg	Arg	Thr	Phe	Ser	Cys	Pro		
			170				175						180				
tgc	aga	cgg	gaa	gct	gcg	ttc	tcg	aac	act	agg	cag	ccc	ccg	ggt	ctg	688	
Cys	Arg	Arg	Glu	Ala	Ala	Phe	Ser	Asn	Thr	Arg	Gln	Pro	Pro	Gly	Leu		
		185				190						195					
cac	ctc	cag	agc	cca	ccc	tac	cac	cag	aca	cag	agc	ccg	gac	cac	ctg	736	
His	Leu	Gln	Ser	Pro	Pro	Tyr	His	Gln	Thr	Gln	Ser	Pro	Asp	His	Leu		
		200				205					210						
gac	cta	ccc	tcc	agc	cat	gac	cct	tcc	ctg	ctc	cca	ccc	acc	tga		781	
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Met	Arg	Gln	Lys	Arg	Lys	Gly	Asp	Leu	Ser	Pro	Ala	Glu	Leu	Met	Met		
1			5					10						15			
ctg	act	ata	gga	gat	ggt	att	aaa	caa	ctg	att	gaa	gcc	cac	gag	cag	153	
Leu	Thr	Ile	Gly	Asp	Val	Ile	Lys	Gln	Leu	Ile	Glu	Ala	His	Glu	Gln		
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Gly	Lys	Asp	Ile	Asp	Leu	Asn	Lys	Val	Lys	Thr	Lys	Thr	Ala	Ala	Lys		
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tat	ggc	ctt	tct	gcc	cag	ccc	cgc	ctg	gtg	gat	atc	att	gct	gcc	gtc	249	
Tyr	Gly	Leu	Ser	Ala	Gln	Pro	Arg	Leu	Val	Asp	Ile	Ile	Ala	Ala	Val		
		50				55				60							
cct	cct	cag	tat	cgc	aag	gtc	ttg	atg	ccc	aag	tta	aag	gcg	aaa	ccc	297	
Pro	Pro	Gln	Tyr	Arg	Lys	Val	Leu	Met	Pro	Lys	Leu	Lys	Ala	Lys	Pro		

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atc aga act gct agt ggg att gct gtc gtg gct gtg atg tgc aaa ccc				345
Ile Arg Thr Ala Ser Gly Ile Ala Val Val Ala Val Met Cys Lys Pro				
	85	90	95	
cac aga tgt cca cac atc agt ttt aca gga aat ata tgt gta tac tgc				393
His Arg Cys Pro His Ile Ser Phe Thr Gly Asn Ile Cys Val Tyr Cys				
	100	105	110	
cct ggt gga cct gat tct gat ttt gag tat tcc acc cag tct tac act				441
Pro Gly Gly Pro Asp Ser Asp Phe Glu Tyr Ser Thr Gln Ser Tyr Thr				
	115	120	125	
ggc tat gag cca acc tcc atg aga gct atc cgt gcc aga tat gac cct				489
Gly Tyr Glu Pro Thr Ser Met Arg Ala Ile Arg Ala Arg Tyr Asp Pro				
	130	135	140	
ttc cta cag aca aga cac cga ata gaa cag tta aaa caa ctt ggt cat				537
Phe Leu Gln Thr Arg His Arg Ile Glu Gln Leu Lys Gln Leu Gly His				
	145	150	155	160
agt gtg gat aaa gtg gag ttt att gtg atg ggt gga acg ttt atg gcc				585
Ser Val Asp Lys Val Glu Phe Ile Val Met Gly Gly Thr Phe Met Ala				
	165	170	175	
ctt cca gaa gaa tac aga gat tat ttt att cga aat tta cat gat gcc				633
Leu Pro Glu Glu Tyr Arg Asp Tyr Phe Ile Arg Asn Leu His Asp Ala				
	180	185	190	
tta tca gga cat act tcc aac aat att tac gag gca gtc aag tat tct				681
Leu Ser Gly His Thr Ser Asn Asn Ile Tyr Glu Ala Val Lys Tyr Ser				
	195	200	205	
gag aga agc ctc aca aag tgt att gga att act att gaa acc aga cca				729
Glu Arg Ser Leu Thr Lys Cys Ile Gly Ile Thr Ile Glu Thr Arg Pro				
	210	215	220	
gat tac tgc atg aag cga cat tta agt gac atg ttg acc tat ggc tgc				777
Asp Tyr Cys Met Lys Arg His Leu Ser Asp Met Leu Thr Tyr Gly Cys				
	225	230	235	240
aca agg ctg gag att ggg gtg cag agt gtt tat gaa gat gtg gct aga				825
Thr Arg Leu Glu Ile Gly Val Gln Ser Val Tyr Glu Asp Val Ala Arg				
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gac acc aac agg ggc cac act gtg aag gca gtg tgt gag tca ttt cac				873
Asp Thr Asn Arg Gly His Thr Val Lys Ala Val Cys Glu Ser Phe His				
	260	265	270	
ctg gcc aaa gat tcc ggt ttt aaa gtg gtg gcc cat atg atg cct gac				921
Leu Ala Lys Asp Ser Gly Phe Lys Val Val Ala His Met Met Pro Asp				
	275	280	285	
ctg cca aac gtg gga cta gaa aga gac att gaa cag ttc aca gag ttt				969
Leu Pro Asn Val Gly Leu Glu Arg Asp Ile Glu Gln Phe Thr Glu Phe				
	290	295	300	
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Phe Glu Asn Pro Ala Phe Arg Pro Asp Gly Leu Lys Leu Tyr Pro Thr				
	305	310	315	320
ctg gtg att cgt ggg acc ggg ctt tat gag ctt tgg aaa tca gga aga				1065
Leu Val Ile Arg Gly Thr Gly Leu Tyr Glu Leu Trp Lys Ser Gly Arg				

325	330	335	
gat aag agt tac tct cct agt gac ctg gtt gaa ttg gtg gct cgg atc Asp Lys Ser Tyr Ser Pro Ser Asp Leu Val Glu Leu Val Ala Arg Ile 340 345 350			1113
cta gcc ctc gtg cct cca tgg act cga gtg tac cga gta cag agg gat Leu Ala Leu Val Pro Pro Trp Thr Arg Val Tyr Arg Val Gln Arg Asp 355 360 365			1161
att cca atg cct tta gtt agc tca gga gta gag cat ggt aac ctg aga Ile Pro Met Pro Leu Val Ser Ser Gly Val Glu His Gly Asn Leu Arg 370 375 380			1209
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cca tac cag gtt gaa ttg gta agg aga gat tat gtt gca aat ggt ggc Pro Tyr Gln Val Glu Leu Val Arg Arg Asp Tyr Val Ala Asn Gly Gly 420 425 430			1353
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ggc ctc cta cga tta cgc aag tgt tca gaa gaa act ttc cgt ttc gaa Gly Leu Leu Arg Leu Arg Lys Cys Ser Glu Glu Thr Phe Arg Phe Glu 450 455 460			1449
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cat ggg tct ggg aaa atc gct gtg ata tca gga gtg gat gtc ctg ggg His Gly Ser Gly Lys Ile Ala Val Ile Ser Gly Val Asp Val Leu Gly 515 520 525			1641
cag agg cag agg gga ggc cac cac aga agc tgt tca ctc tag gcacttt Gln Arg Gln Arg Gly Gly His His Arg Ser Cys Ser Leu * 530 535 540			1690
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 Met Arg Gln Lys Arg Lys Gly Asp Leu Ser Pro Ala Glu Leu Met Met  
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 Leu Thr Ile Gly Asp Val Ile Lys Gln Leu Ile Glu Ala His Glu Gln  
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 ggg aaa gac atc gat cta aat aag gtg aaa acc aag aca gct gcc aaa 201  
 Gly Lys Asp Ile Asp Leu Asn Lys Val Lys Thr Lys Thr Ala Ala Lys  
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 Tyr Gly Leu Ser Ala Gln Pro Arg Leu Val Asp Ile Ile Ala Ala Val  
 50 55 60  
 cct cct cag tat cgc aag gtc ttg atg ccc aag tta aag gcg aaa ccc 297  
 Pro Pro Gln Tyr Arg Lys Val Leu Met Pro Lys Leu Lys Ala Lys Pro  
 65 70 75 80  
 atc aga act gct agt ggg att gct gtc gtg gct gtg atg tgc aaa ccc 345  
 Ile Arg Thr Ala Ser Gly Ile Ala Val Val Ala Val Met Cys Lys Pro  
 85 90 95  
 cac aga tgt cca cac atc agt ttt aca gga aat ata tgt gta tac tgc 393  
 His Arg Cys Pro His Ile Ser Phe Thr Gly Asn Ile Cys Val Tyr Cys  
 100 105 110  
 cct ggt gga cct gat tct gat ttt gag tat tcc acc cag tct tac act 441  
 Pro Gly Gly Pro Asp Ser Asp Phe Glu Tyr Ser Thr Gln Ser Tyr Thr  
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 ggc tat gag cca acc tcc atg aga gct atc cgt gcc aga tat gac cct 489  
 Gly Tyr Glu Pro Thr Ser Met Arg Ala Ile Arg Ala Arg Tyr Asp Pro  
 130 135 140  
 ttc cta cag aca aga cac cga ata gaa cag tta aaa caa ctt ggt cat 537  
 Phe Leu Gln Thr Arg His Arg Ile Glu Gln Leu Lys Gln Leu Gly His  
 145 150 155 160  
 agt gtg gat aaa gtg gag ttt att gtg atg ggt gga acg ttt atg gcc 585  
 Ser Val Asp Lys Val Glu Phe Ile Val Met Gly Gly Thr Phe Met Ala  
 165 170 175

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195 200 205	
gag aga agc ctc aca aag tgt att gga att act att gaa acc aga cca	729
Glu Arg Ser Leu Thr Lys Cys Ile Gly Ile Thr Ile Glu Thr Arg Pro	
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Asp Tyr Cys Met Lys Arg His Leu Ser Asp Met Leu Thr Tyr Gly Cys	
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Thr Arg Leu Glu Ile Gly Val Gln Ser Val Tyr Glu Asp Val Ala Arg	
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Asp Thr Asn Arg Gly His Thr Val Lys Ala Val Cys Glu Ser Phe His	
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Asp Lys Ser Tyr Ser Pro Ser Asp Leu Val Glu Leu Val Ala Arg Ile	
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cta gcc ctc gtg cct cca tgg act cga gtg tac cga gta cag agg gat	1161
Leu Ala Leu Val Pro Pro Trp Thr Arg Val Tyr Arg Val Gln Arg Asp	
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Ile Pro Met Pro Leu Val Ser Ser Gly Val Glu His Gly Asn Leu Arg	
370 375 380	
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Glu Leu Ala Leu Ala Arg Met Lys Asp Leu Gly Ile Gln Cys Arg Asp	
385 390 395 400	
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Val Arg Thr Arg Glu Val Gly Ile Gln Glu Ile His His Lys Val Arg	
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cca tac cag gtt gaa ttg gta agg aga gat tat gtt gca aat ggt ggc	1353
Pro Tyr Gln Val Glu Leu Val Arg Arg Asp Tyr Val Ala Asn Gly Gly	
420 425 430	

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Trp Glu Thr Phe Leu Ser Tyr Glu Asp Pro Asp Gln Asp Ile Leu Ile	
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Leu Gly Gly Gly Val Ser Ile Val Arg Glu Leu His Val Tyr Gly Ser	
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Val Val Pro Val Ser Ser Arg Asp Pro Thr Lys Phe Gln His Gln Glu	
485 490 495	
ttt ggc atg ctg ctg atg gag gaa gca gaa aga ata gct aga gaa gaa	1593
Phe Gly Met Leu Leu Met Glu Glu Ala Glu Arg Ile Ala Arg Glu Glu	
500 505 510	
cat ggg tct ggg aaa atc gct gtg ata tca ggg gtc ggc acc agg aat	1641
His Gly Ser Gly Lys Ile Ala Val Ile Ser Gly Val Gly Thr Arg Asn	
515 520 525	
tat tat aga aag atc ggc tac aga tta caa ggc ccg tac atg gtg aag	1689
Tyr Tyr Arg Lys Ile Gly Tyr Arg Leu Gln Gly Pro Tyr Met Val Lys	
530 535 540	
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Met Leu Lys *	
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gcttcaccct catcccgag ctgcagagac tggaaactgc cttcaaggcc acggctggtc	1864
atctgctgac cacacccag atccgccctc tctgctgac accccaaaaa atcacttgcg	1924
tttttgaggc ttaaatactc tatccagttt ctacattttg catgaggcct gcagggtggcc	1984
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Met Ala Glu Leu Gln Gln Leu Arg Val Gln Glu Ala Val	
1 5 10	
gag tcc atg gtg aag agt ctg gaa aga gag aac atc cgg aag atg cag	157

904



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ggctttcatt ccatagttgc taatgtcgag cgcccgga ttagtagta gtaggcggcc 2054
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<220>  
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atg aac cgt gaa gac cgg aat gtg ctg cgt atg aaa gaa cgg gaa agg 107
Met Asn Arg Glu Asp Arg Asn Val Leu Arg Met Lys Glu Arg Glu Arg
1 5 10 15

cgg aat cag gaa att cag cag ggc gaa gac gcc ttc cca cct agc tct 155
Arg Asn Gln Glu Ile Gln Gln Gly Glu Asp Ala Phe Pro Pro Ser Ser
20 25 30

cct ctg ttt gca gag cca tac aaa gtt act agc aaa gaa gat aag tta 203
Pro Leu Phe Ala Glu Pro Tyr Lys Val Thr Ser Lys Glu Asp Lys Leu
35 40 45

tca agt cgt att cag agt atg ctt gga aac tac gat gaa atg aag gat 251
Ser Ser Arg Ile Gln Ser Met Leu Gly Asn Tyr Asp Glu Met Lys Asp
50 55 60

ttc ata gga gac aga tct ata cca aag ctt gtt gca att ccc aag cct 299
Phe Ile Gly Asp Arg Ser Ile Pro Lys Leu Val Ala Ile Pro Lys Pro
65 70 75 80

aca gta cca cca tca gca gat gaa aaa tct aac cca aat ttc ttt gaa 347
Thr Val Pro Pro Ser Ala Asp Glu Lys Ser Asn Pro Asn Phe Phe Glu
85 90 95

cag aga cat gga ggc tct cat cag agt agc aaa tgg act cca gta gga 395
Gln Arg His Gly Gly Ser His Gln Ser Ser Lys Trp Thr Pro Val Gly
100 105 110

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ccc gca ccc agc act tct cag tct cag aaa cgg tcc tca ggc tta cag Pro Ala Pro Ser Thr Ser Gln Ser Gln Lys Arg Ser Ser Gly Leu Gln 115 120 125	443
agt gga cat agt agc cag cgg acc agc gca ggt agc agt agt ggc act Ser Gly His Ser Ser Gln Arg Thr Ser Ala Gly Ser Ser Ser Gly Thr 130 135 140	491
aac agt agt ggt cag agg cac gac cgt gag tca tat aac aat agt ggg Asn Ser Ser Gly Gln Arg His Asp Arg Glu Ser Tyr Asn Asn Ser Gly 145 150 155 160	539
agc agt agc cgg aaa aaa ggc cag cat gga tca gaa cac tcc aaa tca Ser Ser Ser Arg Lys Lys Gly Gln His Gly Ser Glu His Ser Lys Ser 165 170 175	587
cgt tct tcc agc cct gga aaa ccc cag gct gtt tct tca tta aac tct Arg Ser Ser Ser Pro Gly Lys Pro Gln Ala Val Ser Ser Leu Asn Ser 180 185 190	635
agt cat tcc agg tct cat ggg aat gat cac cat agc aag gaa cat caa Ser His Ser Arg Ser His Gly Asn Asp His His Ser Lys Glu His Gln 195 200 205	683
cgc tcc aaa tca cct cgg gac cct gat gca aac tgg gat tct cct tcc Arg Ser Lys Ser Pro Arg Asp Pro Asp Ala Asn Trp Asp Ser Pro Ser 210 215 220	731
cgt gta cct ttt tca agt ggg cag cac tca act caa tct ttc cca ccc Arg Val Pro Phe Ser Ser Gly Gln His Ser Thr Gln Ser Phe Pro Pro 225 230 235 240	779
tca ttg atg tca aag tcc aat tca atg tta cag aaa ccc act gcc tat Ser Leu Met Ser Lys Ser Asn Ser Met Leu Gln Lys Pro Thr Ala Tyr 245 250 255	827
gtg cgg ccc atg gac gga cag gag tcc atg gaa cca aag ctg tcc tct Val Arg Pro Met Asp Gly Gln Glu Ser Met Glu Pro Lys Leu Ser Ser 260 265 270	875
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ccc agc agc aaa gca cat ctc acc aag ctg aaa ata cct tcc caa cca Pro Ser Ser Lys Ala His Leu Thr Lys Leu Lys Ile Pro Ser Gln Pro 290 295 300	971
ctg gat gca tca gct tct ggt gat gtg agc tgt gtg gat gaa atc cta Leu Asp Ala Ser Ala Ser Gly Asp Val Ser Cys Val Asp Glu Ile Leu 305 310 315 320	1019
aaa gag atg acg cat tca tgg cct ccc cct cta acg gct att cat aca Lys Glu Met Thr His Ser Trp Pro Pro Pro Leu Thr Ala Ile His Thr 325 330 335	1067
cca tgc aaa aca gaa cct tcc aaa ttt cct ttt cca act aag gag tct Pro Cys Lys Thr Glu Pro Ser Lys Phe Pro Phe Pro Thr Lys Glu Ser 340 345 350	1115
cag cag tcc aat ttt ggc act gga gaa caa aaa aga tat aat cct tct Gln Gln Ser Asn Phe Gly Thr Gly Glu Gln Lys Arg Tyr Asn Pro Ser 355 360 365	1163

aaa act tca aat ggg cac cag tct aaa tct atg tta aaa gat gac tta	1211
Lys Thr Ser Asn Gly His Gln Ser Lys Ser Met Leu Lys Asp Asp Leu	
370 375 380	
aaa cta agc agc agt gaa gac agt gat ggg gaa cag gat tgt gat aag	1259
Lys Leu Ser Ser Ser Glu Asp Ser Asp Gly Glu Gln Asp Cys Asp Lys	
385 390 395 400	
aca atg ccg agg agt aca cca gga agt aac tct gaa cct tca cac cat	1307
Thr Met Pro Arg Ser Thr Pro Gly Ser Asn Ser Glu Pro Ser His His	
405 410 415	
aat agt gaa gga gca gat aac tcc agg gat gat tct agt agc cac agt	1355
Asn Ser Glu Gly Ala Asp Asn Ser Arg Asp Asp Ser Ser Ser His Ser	
420 425 430	
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Gly Ser Glu Ser Ser Ser Gly Ser Asp Ser Glu Ser Glu Ser Ser Ser	
435 440 445	
agt gac agt gag gca aat gag cca tcc cag agt gca tct ccc gag cct	1451
Ser Asp Ser Glu Ala Asn Glu Pro Ser Gln Ser Ala Ser Pro Glu Pro	
450 455 460	
gaa ccc ccg cca aca aac aaa tgg caa ctt gat aat tgg ctg aat aaa	1499
Glu Pro Pro Pro Thr Lys Trp Gln Leu Asp Asn Trp Leu Asn Lys	
465 470 475 480	
gtg aac cca cat aaa gtg tca ccc gcc tct tca gtg gac agt aac atc	1547
Val Asn Pro His Lys Val Ser Pro Ala Ser Ser Val Asp Ser Asn Ile	
485 490 495	
cca tca tct caa ggc tac aaa aag gaa ggc cga gag cag ggc act ggg	1595
Pro Ser Ser Gln Gly Tyr Lys Lys Glu Gly Arg Glu Gln Gly Thr Gly	
500 505 510	
aat agc tac act gat aca agt gga cct aaa gaa acg agt tcc gct act	1643
Asn Ser Tyr Thr Asp Thr Ser Gly Pro Lys Glu Thr Ser Ser Ala Thr	
515 520 525	
ccg gga cga gac tcc aaa acc atc caa aag gga tca gaa agt ggg cgt	1691
Pro Gly Arg Asp Ser Lys Thr Ile Gln Lys Gly Ser Glu Ser Gly Arg	
530 535 540	
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Gly Arg Gln Lys Ser Pro Ala Gln Ser Asp Ser Thr Thr Gln Arg Arg	
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Thr Val Gly Lys Lys Gln Pro Lys Lys Ala Glu Lys Ala Ala Ala Glu	
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Glu Pro Arg Gly Gly Leu Lys Ile Glu Ser Glu Thr Pro Val Asp Leu	
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Ala Ser Ser Met Pro Ser Ser Arg His Lys Ala Ala Thr Lys Gly Ser	
595 600 605	
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Arg Lys Pro Asn Ile Lys Lys Glu Ser Lys Ser Ser Pro Arg Pro Thr	
610 615 620	

gca gag aaa aag aaa tat aag tca aca agt aaa tct tcc cag aaa tca	1979
Ala Glu Lys Lys Lys Tyr Lys Ser Thr Ser Lys Ser Ser Gln Lys Ser	
625 630 635 640	
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Arg Glu Ile Ile Glu Thr Asp Thr Ser Ser Ser Asp Ser Asp Glu Ser	
645 650 655	
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Glu Ser Leu Pro Pro Ser Ser Gln Thr Pro Lys Tyr Pro Glu Ser Asn	
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Leu Ser Glu Pro Asp Asp Arg Tyr Pro Leu Ile Val Lys Ile Asp Leu	
705 710 715 720	
aat ctt ttg act aga ata cca gga aag cct tac aaa gaa aca gag ccg	2267
Asn Leu Leu Thr Arg Ile Pro Gly Lys Pro Tyr Lys Glu Thr Glu Pro	
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ccc aag ggg gaa aag aaa aat gtg cca gaa aag cac acg aga gag gct	2315
Pro Lys Gly Glu Lys Lys Asn Val Pro Glu Lys His Thr Arg Glu Ala	
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Gln Lys Gln Ala Ser Glu Lys Val Ser Asn Lys Gly Lys Arg Glu Ala	
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caaagctgtg gggatgcctt cccctgtttc tccaaagctg tcaccaggca attcaggaaa 3263
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<212> DNA
<213> Homo sapiens

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<222> (191)..(2692)

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taaccaccag ccgaactoga atagtggcag ataccgggac acggtgctgc tgccgcagac 180
gagcttcccc atg aag ctg ctg ggc cgc cag cag ccg gac acg gag ctg 229
          Met Lys Leu Leu Gly Arg Gln Gln Pro Asp Thr Glu Leu
              1              5              10

gag atc cag cag aaa tgt gga ttt tca gaa ctt tat tca tgg caa aga 277
Glu Ile Gln Gln Lys Cys Gly Phe Ser Glu Leu Tyr Ser Trp Gln Arg
    15              20              25

gaa aga aaa gta aag aca gaa ttt tgc ctt cat gat gga cct cct tat 325
Glu Arg Lys Val Lys Thr Glu Phe Cys Leu His Asp Gly Pro Pro Tyr
    30              35              40              45

gca aac ggt gac cct cat gtt gga cat gct tta aat aag att ttg aaa 373
Ala Asn Gly Asp Pro His Val Gly His Ala Leu Asn Lys Ile Leu Lys
    50              55              60

gac ata gcc aat cga ttc cat atg atg aat ggc tcc aaa ata cat ttt 421
Asp Ile Ala Asn Arg Phe His Met Met Asn Gly Ser Lys Ile His Phe
    65              70              75

gtg ccc ggc tgg gat tgt cat ggg ttg ccc att gaa ata aaa gta tta 469
Val Pro Gly Trp Asp Cys His Gly Leu Pro Ile Glu Ile Lys Val Leu

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80	85	90	
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Ser Glu Leu Gly Arg Glu Ala Gln Asn Leu Ser Ala Met Glu Ile Arg			
95	100	105	
aag aaa gct aga tca ttt gct aaa gca gcc att gag aaa cag aaa tca			565
Lys Lys Ala Arg Ser Phe Ala Lys Ala Ala Ile Glu Lys Gln Lys Ser			
110	115	120	125
gca ttt att cgt tgg gga ata atg gca gat tgg aat aat tgc tac tat			613
Ala Phe Ile Arg Trp Gly Ile Met Ala Asp Trp Asn Asn Cys Tyr Tyr			
130	135	140	
aca ttt gat ggg aag tat gaa gcc aaa cag ttg aga act ttt tac caa			661
Thr Phe Asp Gly Lys Tyr Glu Ala Lys Gln Leu Arg Thr Phe Tyr Gln			
145	150	155	
atg tat gat aag ggc ttg gtt tat cga tct tac aaa cct gtg ttt tgg			709
Met Tyr Asp Lys Gly Leu Val Tyr Arg Ser Tyr Lys Pro Val Phe Trp			
160	165	170	
tct ccg tca tct agg act gca ttg gct gaa gca gaa ctt gaa tat aat			757
Ser Pro Ser Ser Arg Thr Ala Leu Ala Glu Ala Glu Leu Glu Tyr Asn			
175	180	185	
cct gag cat gtc agt cgt tca ata tat gta aaa ttt cct ctc tta aag			805
Pro Glu His Val Ser Arg Ser Ile Tyr Val Lys Phe Pro Leu Leu Lys			
190	195	200	205
cct tct cca aaa ttg gca tct ctt ata gat ggt tca tct cct gtt agt			853
Pro Ser Pro Lys Leu Ala Ser Leu Ile Asp Gly Ser Ser Pro Val Ser			
210	215	220	
att ttg gtc tgg acc aca caa cct tgg acg att cca gcc aat gaa gct			901
Ile Leu Val Trp Thr Thr Gln Pro Trp Thr Ile Pro Ala Asn Glu Ala			
225	230	235	
gtt tgc tat atg cct gaa tca aag tat gct gtt gtg aaa tgt tct aag			949
Val Cys Tyr Met Pro Glu Ser Lys Tyr Ala Val Val Lys Cys Ser Lys			
240	245	250	
tct gga gac ctc tac gta ctg gcg gca gat aaa gta gca tct gtt gct			997
Ser Gly Asp Leu Tyr Val Leu Ala Ala Asp Lys Val Ala Ser Val Ala			
255	260	265	
tct act ttg gaa aca aca ttt gag act att tca aca ctt tca ggt gta			1045
Ser Thr Leu Glu Thr Thr Phe Glu Thr Ile Ser Thr Leu Ser Gly Val			
270	275	280	285
gat ttg gaa aat ggt act tgc agt cat cca tta att cct gat aaa gcc			1093
Asp Leu Glu Asn Gly Thr Cys Ser His Pro Leu Ile Pro Asp Lys Ala			
290	295	300	
tct cct ctt tta cct gca aat cat gtg acc atg gca aaa gga acg gga			1141
Ser Pro Leu Leu Pro Ala Asn His Val Thr Met Ala Lys Gly Thr Gly			
305	310	315	
ttg gtt cac aca gcc cca gct cat ggt atg gaa gac tac ggt gta gcg			1189
Leu Val His Thr Ala Pro Ala His Gly Met Glu Asp Tyr Gly Val Ala			
320	325	330	
tct cag cac aac ctg ccc atg gat tgt cta gtg gac gaa gat gga gtt			1237
Ser Gln His Asn Leu Pro Met Asp Cys Leu Val Asp Glu Asp Gly Val			

335	340	345	
ttc aca gat gtt gca ggt cct gaa ctt caa aac aag gct gtc ctt gaa			1285
Phe Thr Asp Val Ala Gly Pro Glu Leu Gln Asn Lys Ala Val Leu Glu			
350	355	360	365
gag gga act gat gtg gtt ata aag atg ctt cag act gca aag aat ttg			1333
Glu Gly Thr Asp Val Val Ile Lys Met Leu Gln Thr Ala Lys Asn Leu			
370	375		380
ttg aaa gag gag aaa ttg gtg cat agc tat ccg tat gac tgg agg acc			1381
Leu Lys Glu Glu Lys Leu Val His Ser Tyr Pro Tyr Asp Trp Arg Thr			
385	390		395
aag aaa cct gtg gtt att cgt gcc agc aag cag tgg ttt ata aac atc			1429
Lys Lys Pro Val Val Ile Arg Ala Ser Lys Gln Trp Phe Ile Asn Ile			
400	405		410
acg gat att aag act gca gcc aag gaa ttg tta aaa aag gtg aaa ttt			1477
Thr Asp Ile Lys Thr Ala Ala Lys Glu Leu Leu Lys Lys Val Lys Phe			
415	420		425
att cct gga tca gca ctg aat ggc atg gtt gaa atg atg gac agg cgg			1525
Ile Pro Gly Ser Ala Leu Asn Gly Met Val Glu Met Met Asp Arg Arg			
430	435	440	445
cca tat tgg tgt ata tca agg caa aga gtt tgg ggt gtt cca att cct			1573
Pro Tyr Trp Cys Ile Ser Arg Gln Arg Val Trp Gly Val Pro Ile Pro			
450	455		460
gtg ttt cat cat aag acc aag gat gaa tac ttg atc aac agc caa acc			1621
Val Phe His His Lys Thr Lys Asp Glu Tyr Leu Ile Asn Ser Gln Thr			
465	470		475
act gag cat att gtt aaa cta gtg gaa caa cac ggc agt gat atc tgg			1669
Thr Glu His Ile Val Lys Leu Val Glu Gln His Gly Ser Asp Ile Trp			
480	485		490
tgg act ctt ccc cct gaa caa ctt ctt cca aaa gaa gtc tta tct gag			1717
Trp Thr Leu Pro Pro Glu Gln Leu Leu Pro Lys Glu Val Leu Ser Glu			
495	500		505
gtt ggt ggc cct gat gcc ttg gaa tat gtg cca ggt cag gat att ttg			1765
Val Gly Gly Pro Asp Ala Leu Glu Tyr Val Pro Gly Gln Asp Ile Leu			
510	515	520	525
gac atc tgg ttt gat agc gga act tca tgg tct tat gtt ctt cca ggt			1813
Asp Ile Trp Phe Asp Ser Gly Thr Ser Trp Ser Tyr Val Leu Pro Gly			
530	535		540
cct gac caa aga gca gat ttg tac ttg gaa gga aaa gac cag ctc ggg			1861
Pro Asp Gln Arg Ala Asp Leu Tyr Leu Glu Gly Lys Asp Gln Leu Gly			
545	550		555
ggt tgg ttt cag tca tcc tta tta aca agt gtg gca gca agg aag aga			1909
Gly Trp Phe Gln Ser Ser Leu Leu Thr Ser Val Ala Ala Arg Lys Arg			
560	565		570
gca cct tat aag aca gtg att gtt cat gga ttt acc ctt gga gaa aag			1957
Ala Pro Tyr Lys Thr Val Ile Val His Gly Phe Thr Leu Gly Glu Lys			
575	580		585
gga gaa aag atg tcc aag tct ctt ggg aat gtc att cat cct gat gtt			2005
Gly Glu Lys Met Ser Lys Ser Leu Gly Asn Val Ile His Pro Asp Val			

590	595	600	605	
gtc gtt aat gga gga caa gat caa agc aaa gag cct ccg tat ggt gct				2053
Val Val Asn Gly Gln Asp Gln Ser Lys Glu Pro Pro Tyr Gly Ala	610	615	620	
gat gtc ctt cgc tgg tgg gta gct gat tcc aat gtc ttc acc gaa gtt				2101
Asp Val Leu Arg Trp Trp Val Ala Asp Ser Asn Val Phe Thr Glu Val	625	630	635	
gca att ggc cca tcc gtg ctc aat gct gcc aga gat gat att agc aag				2149
Ala Ile Gly Pro Ser Val Leu Asn Ala Ala Arg Asp Asp Ile Ser Lys	640	645	650	
ctt agg aat aca ctt cgc ttt ctt ttg gga aat gtg gct gat ttc aac				2197
Leu Arg Asn Thr Leu Arg Phe Leu Leu Gly Asn Val Ala Asp Phe Asn	655	660	665	
cca gaa aca gat tcc atc cct gta aac gat atg tat gtc ata gac cag				2245
Pro Glu Thr Asp Ser Ile Pro Val Asn Asp Met Tyr Val Ile Asp Gln	670	675	680	685
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Tyr Met Leu His Leu Leu Gln Asp Leu Ala Asn Lys Ile Thr Glu Leu	690	695	700	
tac aaa caa tat gat ttt gga aaa gtt gtt cgg ctg tta cgg acg ttt				2341
Tyr Lys Gln Tyr Asp Phe Gly Lys Val Val Arg Leu Leu Arg Thr Phe	705	710	715	
tat acc aga gag ctc tct aac ttt tat ttc agt ata atc aaa gat agg				2389
Tyr Thr Arg Glu Leu Ser Asn Phe Tyr Phe Ser Ile Ile Lys Asp Arg	720	725	730	
ctc tat tgt gaa aag gaa aat gac ccc aaa cga cgc tct tgt cag act				2437
Leu Tyr Cys Glu Lys Glu Asn Asp Pro Lys Arg Arg Ser Cys Gln Thr	735	740	745	
gca tta gtt gaa att ttg gat gta ata gtt cgt tct ttt gct ccc att				2485
Ala Leu Val Glu Ile Leu Asp Val Ile Val Arg Ser Phe Ala Pro Ile	750	755	760	765
ctt cct cac ctg gct gaa gag gtg ttc cag cac ata cct tat att aaa				2533
Leu Pro His Leu Ala Glu Glu Val Phe Gln His Ile Pro Tyr Ile Lys	770	775	780	
gag ccc aag agt gtt ttc cgt act ggg tgg att agt act agt tct atc				2581
Glu Pro Lys Ser Val Phe Arg Thr Gly Trp Ile Ser Thr Ser Ser Ile	785	790	795	
tgg aaa aag ccc ggg ttg gaa gaa gct gtg aga gtg cgt gtg caa tgc				2629
Trp Lys Lys Pro Gly Leu Glu Glu Ala Val Arg Val Arg Val Gln Cys	800	805	810	
gag act cat ttc ttg gaa gca tcc ctg gca aaa atg cag ctg agt aca				2677
Glu Thr His Phe Leu Glu Ala Ser Leu Ala Lys Met Gln Leu Ser Thr	815	820	825	
agg tta tca ctg tga tagaacctgg actgcttttt gagataatag agatgctgca				2732
Arg Leu Ser Leu *				830
gtctgaagag acttcagca cctctcagtt gaatgaatta atgatggctt ctgagtcaac				2792



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tttactggct caggaaccac gagagatgac tgcagatgta atcgagctta aagggaaatt 2852
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aaagccaaga tttaggtaat. gagtggatga gtaaatggtg gaggatggga gcaaaataga 3152
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Met Arg Pro Arg Arg Pro Leu Val Phe Met Ser Leu Val Cys
1 5 10
gca ctc ttg aac aca tgc cag gca cac agg gtg cat gac gac aag cct 155
Ala Leu Leu Asn Thr Cys Gln Ala His Arg Val His Asp Asp Lys Pro
15 20 25 30
aat att gtc cta atc atg gtt gat gac ctg ggt att gga gat ctg ggc 203
Asn Ile Val Leu Ile Met Val Asp Asp Leu Gly Ile Gly Asp Leu Gly
35 40 45
tgc tac ggc aat gac acc atg agg acg cct cac atc gac cgc ctt gcc 251
Cys Tyr Gly Asn Asp Thr Met Arg Thr Pro His Ile Asp Arg Leu Ala
50 55 60
agg gaa ggc gtg cga ctg act cag cac atc tct gcc gcc tcc ctc tgc 299
Arg Glu Gly Val Arg Leu Thr Gln His Ile Ser Ala Ala Ser Leu Cys
65 70 75
agc cca agc cgg tcc gcg ttc ttg acg gga aga tac ccc atc cga tca 347
Ser Pro Ser Arg Ser Ala Phe Leu Thr Gly Arg Tyr Pro Ile Arg Ser
80 85 90
ggt atg gtt tct agt ggt aat aga cgt gtc atc caa aat ctt gca gtc 395
Gly Met Val Ser Ser Gly Asn Arg Arg Val Ile Gln Asn Leu Ala Val
95 100 105 110
ccc gca ggc ctc cct ctt aat gag aca aca ctt gca gcc ttg cta aag 443
Pro Ala Gly Leu Pro Leu Asn Glu Thr Thr Leu Ala Ala Leu Leu Lys
115 120 125
aag caa gga tac agc acg ggg ctt ata ggc aaa tgg cac caa ggc ttg 491
Lys Gln Gly Tyr Ser Thr Gly Leu Ile Gly Lys Trp His Gln Gly Leu
130 135 140

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aac tgc gac tcc cga agt gac cag tgc cac cat cca tat aat tat ggg	539
Asn Cys Asp Ser Arg Ser Asp Gln Cys His His Pro Tyr Asn Tyr Gly	
145 150 155	
ttt gac tac tac tat ggc atg ccg ttc act ctc gtt gac agc tgc tgg	587
Phe Asp Tyr Tyr Tyr Gly Met Pro Phe Thr Leu Val Asp Ser Cys Trp	
160 165 170	
ccg gac ccc tct cgt aac acg gaa tta gcc ttt gag agt cag ctc tgg	635
Pro Asp Pro Ser Arg Asn Thr Glu Leu Ala Phe Glu Ser Gln Leu Trp	
175 180 185 190	
ctc tgt gtg cag cta gtt gcc att gcc atc ctc acc cta acc ttt ggg	683
Leu Cys Val Gln Leu Val Ala Ile Ala Ile Leu Thr Leu Thr Phe Gly	
195 200 205	
aag ctg agc ggc tgg gtc tct gtt ccc tgg ctc ctg atc ttc tcc atg	731
Lys Leu Ser Gly Trp Val Ser Val Pro Trp Leu Leu Ile Phe Ser Met	
210 215 220	
att ctg ttt att ttc ctc ttg ggc tat gct tgg ttc tcc agc cac acg	779
Ile Leu Phe Ile Phe Leu Leu Gly Tyr Ala Trp Phe Ser Ser His Thr	
225 230 235	
tcc cct tta tac tgg gac tgc ctc ctc atg ccg ggg cac gag atc acg	827
Ser Pro Leu Tyr Trp Asp Cys Leu Leu Met Arg Gly His Glu Ile Thr	
240 245 250	
gag cag ccc atg aag gct gaa cga gct gga tcc att atg gtg aag gaa	875
Glu Gln Pro Met Lys Ala Glu Arg Ala Gly Ser Ile Met Val Lys Glu	
255 260 265 270	
gcg att tcc ttt tta gaa agg cac agt aag gaa act ttc ctt ctc ttt	923
Ala Ile Ser Phe Leu Glu Arg His Ser Lys Glu Thr Phe Leu Leu Phe	
275 280 285	
ttc tcc ttt ctt cac gtg cac aca cct ctc ccc acc acg gac gat ttc	971
Phe Ser Phe Leu His Val His Thr Pro Leu Pro Thr Thr Asp Asp Phe	
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act ggc acc agc aag cat ggc ttg tat ggg gat aat gtg gaa gag atg	1019
Thr Gly Thr Ser Lys His Gly Leu Tyr Gly Asp Asn Val Glu Glu Met	
305 310 315	
gac tcc atg gtg ggc aag att ctt gat gct atc gat gat ttt ggc cta	1067
Asp Ser Met Val Gly Lys Ile Leu Asp Ala Ile Asp Asp Phe Gly Leu	
320 325 330	
agg aac aac acc ctt gtc tac ttt aca tca gat cac gga ggg cat ttg	1115
Arg Asn Asn Thr Leu Val Tyr Phe Thr Ser Asp His Gly Gly His Leu	
335 340 345 350	
gaa gct agg cga ggg cat gcc caa ctt ggt gga tgg aat gga ata tac	1163
Glu Ala Arg Arg Gly His Ala Gln Leu Gly Gly Trp Asn Gly Ile Tyr	
355 360 365	
aaa ggt gga aaa ggc atg ggg ggc tgg gaa ggt gga atc cgc gtc cca	1211
Lys Gly Gly Lys Gly Met Gly Gly Trp Glu Gly Gly Ile Arg Val Pro	
370 375 380	
gga att gtc cga tgg cct gga aag gta cca gct gga cgg ttg att aag	1259
Gly Ile Val Arg Trp Pro Gly Lys Val Pro Ala Gly Arg Leu Ile Lys	
385 390 395	

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gaa cct aca agt tta atg gat att tta cca act gtc gca tca gtg tca      1307
Glu Pro Thr Ser Leu Met Asp Ile Leu Pro Thr Val Ala Ser Val Ser
    400                      405                      410

gga gga agt ctc cct cag gac agg gtc att gac ggc cga gac ctc atg      1355
Gly Gly Ser Leu Pro Gln Asp Arg Val Ile Asp Gly Arg Asp Leu Met
    415                      420                      425                      430

ccc ttg ctg cag ggc aac gtc agg cac tcg gag cat gaa ttt ctt ttc      1403
Pro Leu Leu Gln Gly Asn Val Arg His Ser Glu His Glu Phe Leu Phe
    435                      440                      445

cac tac tgt ggc tcc tac ctg cac gcc gtg cgg tgg atc ccc aag gac      1451
His Tyr Cys Gly Ser Tyr Leu His Ala Val Arg Trp Ile Pro Lys Asp
    450                      455                      460

gac agt ggg tca gtt tgg aag gct cac tat gtg acc ccg gta ttc cag      1499
Asp Ser Gly Ser Val Trp Lys Ala His Tyr Val Thr Pro Val Phe Gln
    465                      470                      475

cca cca gct tct ggt ggc tgc tat gtc acc tca tta tgc aga tgt ttc      1547
Pro Pro Ala Ser Gly Gly Cys Tyr Val Thr Ser Leu Cys Arg Cys Phe
    480                      485                      490

gga gaa cag gtt acc tac cac aac ccc cct ctg ctc ttc gat ctc tcc      1595
Gly Glu Gln Val Thr Tyr His Asn Pro Pro Leu Leu Phe Asp Leu Ser
    495                      500                      505                      510

agg gac ccc tca gag tcc aca ccc ctg aca cct gcc aca gag ccc ctc      1643
Arg Asp Pro Ser Glu Ser Thr Pro Leu Thr Pro Ala Thr Glu Pro Leu
    515                      520                      525

tat gat ttt gtg att aaa aag gtg gcc aac gcc ctg aag gaa cac cag      1691
Tyr Asp Phe Val Ile Lys Lys Val Ala Asn Ala Leu Lys Glu His Gln
    530                      535                      540

gaa acc atc gtg cct gtg acc tac caa ctc tca gaa ctg aat cag ggc      1739
Glu Thr Ile Val Pro Val Thr Tyr Gln Leu Ser Glu Leu Asn Gln Gly
    545                      550                      555

agg acg tgg ctg aag cct tgc tgt ggg gtg ttc cca ttt tgt ctg tgt      1787
Arg Thr Trp Leu Lys Pro Cys Cys Gly Val Phe Pro Phe Cys Leu Cys
    560                      565                      570

gac aag gaa gag gaa gtc tct cag cct cgg ggt cct aac gag aag aga      1835
Asp Lys Glu Glu Glu Val Ser Gln Pro Arg Gly Pro Asn Glu Lys Arg
    575                      580                      585                      590

taattacaat caggctacca gaggaagcct ttggtcctaa cgagaagaga taattacaat      1895

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agtcaataaaa ttcattctacc attccagatt attaaaaaaaa aaaaaa      2000

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gac gac cag ctg ctg cag aag ctc agg gcc agt cgc cgc cgc ttc cag	98
Asp Asp Gln Leu Leu Gln Lys Leu Arg Ala Ser Arg Arg Arg Phe Gln	
15 20 25 30	
agg cgc atg cag cgg ctg ata gag aag tac aac cag ccc ttc gag gac	146
Arg Arg Met Gln Arg Leu Ile Glu Lys Tyr Asn Gln Pro Phe Glu Asp	
35 40 45	
acc ccg gtg gtg caa atg gcc acg ctg acc tac gag acg cca cag gga	194
Thr Pro Val Val Gln Met Ala Thr Leu Thr Tyr Glu Thr Pro Gln Gly	
50 55 60	
ttg aga att tgg ggt gga aga cta ata aag gaa aga aac gaa gga gag	242
Leu Arg Ile Trp Gly Gly Arg Leu Ile Lys Glu Arg Asn Glu Gly Glu	
65 70 75	
atc cag gac tcc tcc atg aag ccc gcg gac agg aca gat ggc tcc gtg	290
Ile Gln Asp Ser Ser Met Lys Pro Ala Asp Arg Thr Asp Gly Ser Val	
80 85 90	
caa gct gca gcc tgg ggt cct gag ctt ccc tcg cac cgc aca gtc ctg	338
Gln Ala Ala Ala Trp Gly Pro Glu Leu Pro Ser His Arg Thr Val Leu	
95 100 105 110	
gga gcc gat tca aaa agc ggt gag gtc gat gcc acg tca gac cag gaa	386
Gly Ala Asp Ser Lys Ser Gly Glu Val Asp Ala Thr Ser Asp Gln Glu	
115 120 125	
gag tca gtt gct tgg gcc tta gca cct gca gtg cct caa agc cct ttg	434
Glu Ser Val Ala Trp Ala Leu Ala Pro Ala Val Pro Gln Ser Pro Leu	
130 135 140	
aaa aat gaa tta aga agg aaa tac ttg acc caa gtg gat ata ctg cta	482
Lys Asn Glu Leu Arg Arg Lys Tyr Leu Thr Gln Val Asp Ile Leu Leu	
145 150 155	
caa ggt gca gag tat ttt gag tgt gca ggt aac aga gct gga agg gat	530
Gln Gly Ala Glu Tyr Phe Glu Cys Ala Gly Asn Arg Ala Gly Arg Asp	
160 165 170	
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Val Arg Val Thr Pro Leu Pro Ser Leu Ala Ser Pro Ala Val Pro Ala	
175 180 185 190	
ccc gga tac tgc agt cgt atc tcc aga aag agt cct ggt gac cca gcg	626
Pro Gly Tyr Cys Ser Arg Ile Ser Arg Lys Ser Pro Gly Asp Pro Ala	
195 200 205	
aaa cca gct tca tct ccc aga gaa tgg gat cct ttg cat cct tcc tcc	674
Lys Pro Ala Ser Ser Pro Arg Glu Trp Asp Pro Leu His Pro Ser Ser	
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Thr Asp Met Ala Leu Val Pro Arg Asn Asp Ser Leu Ser Leu Gln Glu	
225 230 235	

acc agt agc agc agc ttc tta agc agc cag ccc ttt gaa gat gat gac	770
Thr Ser Ser Ser Ser Phe Leu Ser Ser Gln Pro Phe Glu Asp Asp Asp	
240 245 250	
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Ile Cys Asn Val Thr Ile Ser Asp Leu Tyr Ala Gly Met Leu His Ser	
255 260 265 270	
atg agc cgg ctg ttg agc aca aag cca tca agc atc atc tcc acc aaa	866
Met Ser Arg Leu Leu Ser Thr Lys Pro Ser Ser Ile Ile Ser Thr Lys	
275 280 285	
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Thr Phe Ile Met Gln Asn Trp Asn Cys Arg Arg Arg His Arg Tyr Lys	
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agc agg atg aac aaa aca tat tgc aaa gga gcc aga cgt tct cag agg	962
Ser Arg Met Asn Lys Thr Tyr Cys Lys Gly Ala Arg Arg Ser Gln Arg	
305 310 315	
agc tcc aag gag aac ttc ata ccc tgc tct gag cct gtg aaa ggg aca	1010
Ser Ser Lys Glu Asn Phe Ile Pro Cys Ser Glu Pro Val Lys Gly Thr	
320 325 330	
ggg gca tta aga gat tgc aag aac gta tta gat gtt tct tgc cgt aag	1058
Gly Ala Leu Arg Asp Cys Lys Asn Val Leu Asp Val Ser Cys Arg Lys	
335 340 345 350	
aca ggt tta aaa ttg gaa aaa gct ttt ctt gaa gtc aac aga ccc caa	1106
Thr Gly Leu Lys Leu Glu Lys Ala Phe Leu Glu Val Asn Arg Pro Gln	
355 360 365	
atc cat aag tta gat cca agt tgg aag gag cgc aaa gtg aca ccc tcg	1154
Ile His Lys Leu Asp Pro Ser Trp Lys Glu Arg Lys Val Thr Pro Ser	
370 375 380	
aag tat tct tcc ttg att tac ttc gac tcc agt gca aca tat aat ctt	1202
Lys Tyr Ser Ser Leu Ile Tyr Phe Asp Ser Ser Ala Thr Tyr Asn Leu	
385 390 395	
gat gag gaa aat aga ttt agg aca tta aaa tgg tta att tct cct gta	1250
Asp Glu Glu Asn Arg Phe Arg Thr Leu Lys Trp Leu Ile Ser Pro Val	
400 405 410	
aaa ata gtt tcc aga cca aca ata cga cag ggc cat gga gag aac cgt	1298
Lys Ile Val Ser Arg Pro Thr Ile Arg Gln Gly His Gly Glu Asn Arg	
415 420 425 430	
cag agg gag att gaa atc cga ttt gat cag ctt cat cgg gaa tat tgc	1346
Gln Arg Glu Ile Glu Ile Arg Phe Asp Gln Leu His Arg Glu Tyr Cys	
435 440 445	
ctg agt ccc agg aac cag cct cgc cgg atg tgc ctc ccg gac tcc tgg	1394
Leu Ser Pro Arg Asn Gln Pro Arg Arg Met Cys Leu Pro Asp Ser Trp	
450 455 460	
gcc atg aac atg tac aga ggg ggt cct gcg agt cct ggt ggc ctt cag	1442
Ala Met Asn Met Tyr Arg Gly Gly Pro Ala Ser Pro Gly Gly Leu Gln	
465 470 475	
ggc tta gaa acc cgc agg ctg agt tta cct tcc agc aaa gca aaa gca	1490
Gly Leu Glu Thr Arg Arg Leu Ser Leu Pro Ser Ser Lys Ala Lys Ala	
480 485 490	

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Lys Ser Leu Ser Glu Ala Phe Glu Asn Leu Gly Lys Arg Ser Leu Glu	
495 500 505 510	
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Ala Gly Arg Cys Leu Pro Lys Ser Asp Ser Ser Ser Ser Leu Pro Lys	
515 520 525	
acc aac ccc aca cac agc gca act cgc ccg cag cag aca tct gac ctt	1634
Thr Asn Pro Thr His Ser Ala Thr Arg Pro Gln Gln Thr Ser Asp Leu	
530 535 540	
cac gtt cag gga aat agt tct gga ata ttt aga aag tca gtg tca ccc	1682
His Val Gln Gly Asn Ser Ser Gly Ile Phe Arg Lys Ser Val Ser Pro	
545 550 555	
agc aaa act ctt tca gtc cca gat aaa gaa gtg cca ggc cac gga agg	1730
Ser Lys Thr Leu Ser Val Pro Asp Lys Glu Val Pro Gly His Gly Arg	
560 565 570	
aat cgt tac gat gaa att aaa gaa gaa ttt gac aag ctt cat caa aag	1778
Asn Arg Tyr Asp Glu Ile Lys Glu Glu Phe Asp Lys Leu His Gln Lys	
575 580 585 590	
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Tyr Cys Leu Lys Ser Pro Gly Gln Met Thr Val Pro Leu Cys Ile Gly	
595 600 605	
gtg tct aca gat aaa gca agt atg gaa gtt cga tat caa aca gaa ggc	1874
Val Ser Thr Asp Lys Ala Ser Met Glu Val Arg Tyr Gln Thr Glu Gly	
610 615 620	
ttc tta gga aaa tta aat cca gac cct cac ttc cag ggt ttc cag aag	1922
Phe Leu Gly Lys Leu Asn Pro Asp Pro His Phe Gln Gly Phe Gln Lys	
625 630 635	
ttg cca tca tca ccc ctg ggg tgc aga aaa agt cta ctg ggc tca act	1970
Leu Pro Ser Ser Pro Leu Gly Cys Arg Lys Ser Leu Leu Gly Ser Thr	
640 645 650	
gca att gag gct cct tca tct aca tgt gtt gct cgt gcc atc acg agg	2018
Ala Ile Glu Ala Pro Ser Ser Thr Cys Val Ala Arg Ala Ile Thr Arg	
655 660 665 670	
gat ggc acg agg gac cat cag ttc cct gca aaa aga ccc agg cta tca	2066
Asp Gly Thr Arg Asp His Gln Phe Pro Ala Lys Arg Pro Arg Leu Ser	
675 680 685	
gaa ccc cag ggc tcc gga cgc cag ggc aat tcc ctg ggt gcc tca gat	2114
Glu Pro Gln Gly Ser Gly Arg Gln Gly Asn Ser Leu Gly Ala Ser Asp	
690 695 700	
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Gly Val Asp Asn Thr Val Arg Pro Gly Asp Gln Gly Ser Ser Ser Gln	
705 710 715	
ccc aac tca gaa gag aga gga gag aac acg tct tac agg atg gaa gag	2210
Pro Asn Ser Glu Glu Arg Gly Glu Asn Thr Ser Tyr Arg Met Glu Glu	
720 725 730	
aaa agt gat ttc atg cta gaa aaa ttg gaa act aaa agt gtg tag cta	2258
Lys Ser Asp Phe Met Leu Glu Lys Leu Glu Thr Lys Ser Val *	
735 740 745	

ggttatttcg gagtggtatt tatcttccca ctgtctctct gtttgatttt ttgttttgtt 2318  
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 Met Asp Pro Ala Leu Ala Ala Gln Met Ser Glu Ala Val Ala Glu Lys  
 1 5 10 15  
 atg ctc cag tac cgg cgg gac aca gca ggc tgg aag att tgc cgg gaa 154  
 Met Leu Gln Tyr Arg Arg Asp Thr Ala Gly Trp Lys Ile Cys Arg Glu  
 20 25 30  
 ggc aat gga gtt tca gtt tcc tgg agg cca tct gtg gag ttt cca ggg 202  
 Gly Asn Gly Val Ser Val Ser Trp Arg Pro Ser Val Glu Phe Pro Gly  
 35 40 45  
 aac ctg tac cga gga gaa ggc att gta tat ggg aca cta gag gag gtg 250  
 Asn Leu Tyr Arg Gly Glu Gly Ile Val Tyr Gly Thr Leu Glu Glu Val  
 50 55 60  
 tgg gac tgt gtg aag cca gct gtt gga ggc cta cga gtg aag tgg gat 298  
 Trp Asp Cys Val Lys Pro Ala Val Gly Gly Leu Arg Val Lys Trp Asp  
 65 70 75 80  
 gag aat gtg acc ggt ttt gaa att atc caa agc atc act gac acc ctg 346  
 Glu Asn Val Thr Gly Phe Glu Ile Ile Gln Ser Ile Thr Asp Thr Leu  
 85 90 95  
 tgt gta agc aga acc tcc act ccc tcc gct gcc atg aag ctc att tct 394  
 Cys Val Ser Arg Thr Ser Thr Pro Ser Ala Ala Met Lys Leu Ile Ser  
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 Pro Arg Asp Phe Val Asp Leu Val Leu Val Lys Arg Tyr Glu Asp Gly  
 115 120 125  
 acc atc agt tcc aac gcc acc cat gtg gag cat ccg tta tgt ccc ccg 490  
 Thr Ile Ser Ser Asn Ala Thr His Val Glu His Pro Leu Cys Pro Pro  
 130 135 140  
 aag cca ggt ttt gtg aga gga ttt aac cat cct tgt ggt tgc ttc tgt 538  
 Lys Pro Gly Phe Val Arg Gly Phe Asn His Pro Cys Gly Cys Phe Cys  
 145 150 155 160  
 gaa cct ctt cca ggg gaa ccc acc aag acc aac ctg gtc aca ttc ttc 586  
 Glu Pro Leu Pro Gly Glu Pro Thr Lys Thr Asn Leu Val Thr Phe Phe

165	170	175	
cat acc gac ctc agc ggt tac ctc cca cag aac gtg gtg gac tcc ttc			634
His Thr Asp Leu Ser Gly Tyr Leu Pro Gln Asn Val Val Asp Ser Phe			
180	185	190	
ttc ccc cgc agc atg acc cgg ttt tat gcc aac ctt cag aaa gca gtg			682
Phe Pro Arg Ser Met Thr Arg Phe Tyr Ala Asn Leu Gln Lys Ala Val			
195	200	205	
aag caa ttc cat gag taa tgctat cggtacttct tggcaaagaa ctcccgtgac			736
Lys Gln Phe His Glu *			
210			
tcacgagga gctccagctg ttgggacacc aaggagcctg ggagcacgca gaggcctgtg			796
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ccgaacatcg tgaagttgca caagtactgg ctggatacct ctgaggcctg cgcgagggtc	180
atcttcatca cagagtacgt gtcatacaggc agcctcaagc aattcctcaa aaagaccaag	240
aagaaccaca aggcc atg aac gcc cgg gcc tgg aag cgc tgg tgc acg cag	291
Met Asn Ala Arg Ala Trp Lys Arg Trp Cys Thr Gln	
1 5 10	
atc ctg tct gcg ctc agc ttc ctg cac gcc tgc acc ccc cca atc atc	339
Ile Leu Ser Ala Leu Ser Phe Leu His Ala Cys Thr Pro Pro Ile Ile	
15 20 25	



cac ggg aac ctg acc agc gac acc atc ttc att cag cac aac ggc ctc His Gly Asn Leu Thr Ser Asp Thr Ile Phe Ile Gln His Asn Gly Leu 30 35 40	387
atc aag atc ggc tcc gtg tgg cac cga atc ttc tcc aat gca ctt cca Ile Lys Ile Gly Ser Val Trp His Arg Ile Phe Ser Asn Ala Leu Pro 45 50 55 60	435
gat gat ctc cga agc ccc atc cgc gct gag cga gag gaa ctt cgg aac Asp Asp Leu Arg Ser Pro Ile Arg Ala Glu Arg Glu Glu Leu Arg Asn 65 70 75	483
ctg cac ttc ttc ccc cca gag tat gga gag gtg gcc gat ggg acc gct Leu His Phe Phe Pro Pro Glu Tyr Gly Glu Val Ala Asp Gly Thr Ala 80 85 90	531
gtg gac atc ttc tcc ttt ggg atg tgt gcg ctg gag atg gct gta ctg Val Asp Ile Phe Ser Phe Gly Met Cys Ala Leu Glu Met Ala Val Leu 95 100 105	579
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cgc gcc agg cac tcg ctg agt gac ccc aac atg cgg gag ttc atc ctt Arg Ala Arg His Ser Leu Ser Asp Pro Asn Met Arg Glu Phe Ile Leu 125 130 135 140	675
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ttc atg gag ctg gac aaa ttc ctg gag gat gtc agg aat gga atc tac Phe Met Glu Leu Asp Lys Phe Leu Glu Asp Val Arg Asn Gly Ile Tyr 225 230 235	963
cca ctg atg aac ttt gca gcc act cga ccc ctg ggg ctg ccc cgt gtg Pro Leu Met Asn Phe Ala Ala Thr Arg Pro Leu Gly Leu Pro Arg Val 240 245 250	1011
ctg gcc cca ccc ccg gag gag gtc caa aag gcc aag acc ccg acg cca Leu Ala Pro Pro Pro Glu Glu Val Gln Lys Ala Lys Thr Pro Thr Pro 255 260 265	1059
gag ccc ttt gac tct gag acc aga aag gtc atc cag atg cag tgc aac Glu Pro Phe Asp Ser Glu Thr Arg Lys Val Ile Gln Met Gln Cys Asn 270 275 280	1107

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ctg gag aga agc gag gac aag gcg cgc tgg cat ctc act ctg ctt ctg      1155
Leu Glu Arg Ser Glu Asp Lys Ala Arg Trp His Leu Thr Leu Leu Leu
285                      290                      295                      300

gtg ctg gaa gac cgg ctg cac cgg cag ctg acc tac gac ctg ctc cca      1203
Val Leu Glu Asp Arg Leu His Arg Gln Leu Thr Tyr Asp Leu Leu Pro
                      305                      310                      315

acg gac agc gcc cag gac ctc gcc tcg gag ctc gtg cac tat ggc ttc      1251
Thr Asp Ser Ala Gln Asp Leu Ala Ser Glu Leu Val His Tyr Gly Phe
                      320                      325                      330

ctc cac gag cac gac cgg atg aag ctg gcc gcc ttc ctg gag agc acc      1299
Leu His Glu His Asp Arg Met Lys Leu Ala Ala Phe Leu Glu Ser Thr
                      335                      340                      345

ttc ctc aag tac cgt ggg acc cag gcc tga c ccggagcccc agccccaggg      1350
Phe Leu Lys Tyr Arg Gly Thr Gln Ala *
                      350                      355

gaccatgccg ggggtgctgcc cgggcaggcc atgttgggga gactccagca ccgtggggct      1410

gccctcctcc atgcgcctgg gagcacaag gccccgtag tgaaggaacc ccccgctctcc      1470

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<210> 370
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gctccgcggc caccgatgcc cggacccctt ctgtcttctg ctagacatgc tcttcctctc      180

ggtgagtgtt tttgctgtcg tcgcgggccc gattcgtggc cttagtcaag cccttgggga      240

ggaggaagga gccgggcccgc ttcgatctgt gtggcctgga tagggcaggg caaaggggaa      300

ctgaccgcgt tcgctcccgg gcctcctcct tttggggcat gttgatccgc ggctgcgtc      360

c      atg ttc cag ttt cat gca ggc tct tgg gaa agc tgg tgc tgc      406
      Met Phe Gln Phe His Ala Gly Ser Trp Glu Ser Trp Cys Cys Cys
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tgc ctg att ccc gcc gac aga cct tgg gac cgg ggc caa cac tgg cag      454
Cys Leu Ile Pro Ala Asp Arg Pro Trp Asp Arg Gly Gln His Trp Gln
          20              25              30

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Ala Val Lys Val Ile Gln Ser Leu Pro Lys Asn Gly Ser Phe Gln Pro	
50 55 60	
aca aat gaa atg atg ctt aaa ttt tat agc ttc tat aag cag gca act	598
Thr Asn Glu Met Met Leu Lys Phe Tyr Ser Phe Tyr Lys Gln Ala Thr	
65 70 75	
gaa gga ccc tgt aaa ctt tca agg cct gga ttt tgg gat cct att gga	646
Glu Gly Pro Cys Lys Leu Ser Arg Pro Gly Phe Trp Asp Pro Ile Gly	
80 85 90 95	
aga tat aaa tgg gat gct tgg agt tca ctg ggt gat atg acc aaa gag	694
Arg Tyr Lys Trp Asp Ala Trp Ser Ser Leu Gly Asp Met Thr Lys Glu	
100 105 110	
gaa gcc atg att gca tat gtt gaa gaa atg aaa aag att att gaa act	742
Glu Ala Met Ile Ala Tyr Val Glu Glu Met Lys Lys Ile Ile Glu Thr	
115 120 125	
atg cca atg act gag aaa gtt gaa gaa ttg ctg cgt gtc ata ggt cca	790
Met Pro Met Thr Glu Lys Val Glu Glu Leu Leu Arg Val Ile Gly Pro	
130 135 140	
ttt tat gaa att gtc gag gac aaa aag agt ggc agg agt tct gat ata	838
Phe Tyr Glu Ile Val Glu Asp Lys Lys Ser Gly Arg Ser Ser Asp Ile	
145 150 155	
ccc tca gtc cga ctg gag aaa atc tct aaa tgt tta gaa gat ctt ggt	886
Pro Ser Val Arg Leu Glu Lys Ile Ser Lys Cys Leu Glu Asp Leu Gly	
160 165 170 175	
aat gtt ctc act tct act ccg aac gcc aaa acc gtt aat ggt aaa gct	934
Asn Val Leu Thr Ser Thr Pro Asn Ala Lys Thr Val Asn Gly Lys Ala	
180 185 190	
gaa agc agt gac agt gga gcc gag tct gag gaa gaa gag gcc caa gaa	982
Glu Ser Ser Asp Ser Gly Ala Glu Ser Glu Glu Glu Glu Ala Gln Glu	
195 200 205	
gaa gtg aaa gga gca gac caa agt gat aat gat aag aaa atg atg aag	1030
Glu Val Lys Gly Ala Asp Gln Ser Asp Asn Asp Lys Lys Met Met Lys	
210 215 220	
aag tca gca gac cat aag aat ttg gaa gtc att gtc act aat ggc tat	1078
Lys Ser Ala Asp His Lys Asn Leu Glu Val Ile Val Thr Asn Gly Tyr	
225 230 235	
gat aaa gat ggc ttt gtt cag gat ata cag aat gac att cat gcc agt	1126
Asp Lys Asp Gly Phe Val Gln Asp Ile Gln Asn Asp Ile His Ala Ser	
240 245 250 255	
tct tcc ctg aat ggc aga agc act gaa gaa gta aag ccc att gat gaa	1174
Ser Ser Leu Asn Gly Arg Ser Thr Glu Glu Val Lys Pro Ile Asp Glu	
260 265 270	
aac ttg ggg caa act gga aaa tct gct gtt tgc att cac caa gat ata	1222
Asn Leu Gly Gln Thr Gly Lys Ser Ala Val Cys Ile His Gln Asp Ile	
275 280 285	

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gat tca gac agt gaa gtt tac tgt gat tct atg gaa caa ttt gga caa Asp Ser Asp Ser Glu Val Tyr Cys Asp Ser Met Glu Gln Phe Gly Gln 305 310 315	1318
gaa gag tct tta gac agc ttt acg tcc aac aat gga cca ttt cag tat Glu Glu Ser Leu Asp Ser Phe Thr Ser Asn Asn Gly Pro Phe Gln Tyr 320 325 330 335	1366
tac ttg ggt ggt cat tcc agt caa ccc atg gaa aat tct gga ttt cgt Tyr Leu Gly Gly His Ser Ser Gln Pro Met Glu Asn Ser Gly Phe Arg 340 345 350	1414
gaa gat att caa gta cct cct gga aat ggc aac att ggg aat atg cag Glu Asp Ile Gln Val Pro Pro Gly Asn Gly Asn Ile Gly Asn Met Gln 355 360 365	1462
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ggc agg aat aac agc gga gca cca cac cgg gag aag cga ggc gga gaa Gly Arg Asn Asn Ser Gly Ala Pro His Arg Glu Lys Arg Gly Gly Glu 385 390 395	1558
act gac gaa ttc tct aat gtt aga aga gga aga gga cat agg atg caa Thr Asp Glu Phe Ser Asn Val Arg Arg Gly Arg Gly His Arg Met Gln 400 405 410 415	1606
cac ttg agc gaa gga acc aag ggc cgg cag gtg gga agt gga ggt gat His Leu Ser Glu Gly Thr Lys Gly Arg Gln Val Gly Ser Gly Gly Asp 420 425 430	1654
ggg gag cgc tgg ggc tcc gac aga ggg tcc cga ggc agc ctc aat gag Gly Glu Arg Trp Gly Ser Asp Arg Gly Ser Arg Gly Ser Leu Asn Glu 435 440 445	1702
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tca tca aca tca aca ttg cag act gct cct cag ccc acc tca cag aga Ser Ser Thr Ser Thr Leu Gln Thr Ala Pro Gln Pro Thr Ser Gln Arg 480 485 490 495	1846
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 atattttgca ctacacaaac gataacattt taaggactaa tattgctgat acttgaataa 2176  
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 <213> Homo sapiens

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 cgccccaggc gccgcgcgcg cggccccgcg gctctgaggt tgctcgcgcg cccccgccga 180  
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 Met Asp Arg Met Lys Lys Ile Lys Arg Gln Leu Ser Met Thr  
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 Leu Arg Gly Gly Arg Gly Ile Asp Lys Thr Asn Gly Ala Pro Glu Gln  
 15 20 25 30  
 ata ggc ctg gat gag agt ggt ggt ggt ggc ggc agt gac cct gga gag 323  
 Ile Gly Leu Asp Glu Ser Gly Gly Gly Gly Gly Ser Asp Pro Gly Glu  
 35 40 45  
 gcc ccc aca cgt gct gct cct ggg gaa ctt cgt tct gca cgg ggc cca 371  
 Ala Pro Thr Arg Ala Ala Pro Gly Glu Leu Arg Ser Ala Arg Gly Pro  
 50 55 60  
 ctc agc tct gca cca gag att gtg cac gag gac ttg aag atg ggg tct 419  
 Leu Ser Ser Ala Pro Glu Ile Val His Glu Asp Leu Lys Met Gly Ser  
 65 70 75  
 gat ggg gag agt gac cag gct tca gcc acg tcc tcg gat gag gtg cag 467  
 Asp Gly Glu Ser Asp Gln Ala Ser Ala Thr Ser Ser Asp Glu Val Gln  
 80 85 90  
 tct cca gtg aga gtg cgt atg cgc aac cat ccc cca cgc aag atc tcc 515  
 Ser Pro Val Arg Val Arg Met Arg Asn His Pro Pro Arg Lys Ile Ser  
 95 100 105 110

act gag gac atc aac aag cgc cta tca cta cca gct gac atc cgg ctg	563
Thr Glu Asp Ile Asn Lys Arg Leu Ser Leu Pro Ala Asp Ile Arg Leu	
115 120 125	
cct gag ggc tac ctg gag aag ctg acc ctc aat agc ccc atc ttt gac	611
Pro Glu Gly Tyr Leu Glu Lys Leu Thr Leu Asn Ser Pro Ile Phe Asp	
130 135 140	
aag ccc ctc agc cgc cgc ctc cgt cgt gtc agc cta tct gag att ggc	659
Lys Pro Leu Ser Arg Arg Leu Arg Arg Val Ser Leu Ser Glu Ile Gly	
145 150 155	
ttt ggg aaa ctg gag acc tac att aag ctg gac aaa ctg ggc gag ggt	707
Phe Gly Lys Leu Glu Thr Tyr Ile Lys Leu Asp Lys Leu Gly Glu Gly	
160 165 170	
acc tat gcc acc gtc tac aaa ggc aaa agc aag ctc aca gac aac ctt	755
Thr Tyr Ala Thr Val Tyr Lys Gly Lys Ser Lys Leu Thr Asp Asn Leu	
175 180 185 190	
gtg gca ctc aag gag atc aga ctg gaa cat gaa gag ggg gca ccc tgc	803
Val Ala Leu Lys Glu Ile Arg Leu Glu His Glu Glu Gly Ala Pro Cys	
195 200 205	
acc gcc atc cgg gaa gtg tcc ctg ctc aag gac ctc aaa cac gcc aac	851
Thr Ala Ile Arg Glu Val Ser Leu Leu Lys Asp Leu Lys His Ala Asn	
210 215 220	
atc gtt acg cta cat gac att atc cac acg gag aag tcc ctc acc ctt	899
Ile Val Thr Leu His Asp Ile Ile His Thr Glu Lys Ser Leu Thr Leu	
225 230 235	
gtc ttt gag tac ctg gac aag gac ctg aag cag tac ctg gat gac tgt	947
Val Phe Glu Tyr Leu Asp Lys Asp Leu Lys Gln Tyr Leu Asp Asp Cys	
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Gly Asn Ile Ile Asn Met His Asn Val Lys Leu Phe Leu Phe Gln Leu	
255 260 265 270	
ctc cgt ggc ctg gcc tac tgc cac cgg cag aag gtg cta cac cga gat	1043
Leu Arg Gly Leu Ala Tyr Cys His Arg Gln Lys Val Leu His Arg Asp	
275 280 285	
ctc aag ccc cag aac ctg ctc atc aac gag agg gga gag ctc aag ctg	1091
Leu Lys Pro Gln Asn Leu Leu Ile Asn Glu Arg Gly Glu Leu Lys Leu	
290 295 300	
gct gac ttt ggc ctg gcc cga gcc aag tca atc cca aca aag aca tac	1139
Ala Asp Phe Gly Leu Ala Arg Ala Lys Ser Ile Pro Thr Lys Thr Tyr	
305 310 315	
tcc aat gag gtg gtg aca ctg tgg tac cgg ccc cct gac atc ctg ctt	1187
Ser Asn Glu Val Val Thr Leu Trp Tyr Arg Pro Pro Asp Ile Leu Leu	
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Ile Phe Tyr Glu Met Ala Thr Gly Arg Pro Leu Phe Pro Gly Ser Thr	
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gag gag acg tgg cca ggc atc ctg tcc aac gag gag ttc aag aca tac	1379
Glu Glu Thr Trp Pro Gly Ile Leu Ser Asn Glu Glu Phe Lys Thr Tyr	
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aac tac ccc aag tac cga gcc gag gcc ctt ttg agc cac gca ccc cga	1427
Asn Tyr Pro Lys Tyr Arg Ala Glu Ala Leu Leu Ser His Ala Pro Arg	
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ctc agt ctg ggg gag cgg atc cac aaa ctt cct gac act act tcc ata	1571
Leu Ser Leu Gly Glu Arg Ile His Lys Leu Pro Asp Thr Thr Ser Ile	
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Phe Ala Leu Lys Glu Ile Gln Leu Gln Lys Glu Ala Ser Leu Arg Ser	
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Glu Phe *	
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ttgatcgccg cgtttaagtt gcgctcgggg cggcc      atg tcg gcc ggc gag gtc      173
                                         Met Ser Ala Gly Glu Val
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gag cgc cta gtg tcg gag ctg agc ggc ggg acc gga ggg gat gag gag      221
Glu Arg Leu Val Ser Glu Leu Ser Gly Gly Thr Gly Gly Asp Glu Glu
              10              15              20

gaa gag tgg ctc tat ggc gat gaa aat gaa gtt gaa agg cca gaa gaa      269
Glu Glu Trp Leu Tyr Gly Asp Glu Asn Glu Val Glu Arg Pro Glu Glu
              25              30              35

gaa aat gcc agt gct aat cct cca tct gga att gaa gat gaa act gct      317
Glu Asn Ala Ser Ala Asn Pro Pro Ser Gly Ile Glu Asp Glu Thr Ala
              40              45              50

gaa aat ggt gta cca aaa ccg aaa gtg act gag acc gaa gat gat agt      365
Glu Asn Gly Val Pro Lys Pro Lys Val Thr Glu Thr Glu Asp Asp Ser
              55              60              65              70

gat agt gac agc gat gat gat gaa gat gat gtt cat gtc act ata gga      413
Asp Ser Asp Ser Asp Asp Asp Glu Asp Asp Val His Val Thr Ile Gly
              75              80              85

gac att aaa acg gga gca cca cag tat ggg agt tat ggt aca gca cct      461
Asp Ile Lys Thr Gly Ala Pro Gln Tyr Gly Ser Tyr Gly Thr Ala Pro
              90              95              100

gta aat ctt aac atc aag aca ggg gga aga gtt tat gga act aca ggg      509
Val Asn Leu Asn Ile Lys Thr Thr Gly Arg Val Tyr Gly Thr Thr Gly
              105              110              115

aca aaa gtc aaa gga gta gac ctt gat gca cct gga agc att aat gga      557
Thr Lys Val Lys Gly Val Asp Leu Asp Ala Pro Gly Ser Ile Asn Gly
              120              125              130

gtt cca ctc tta gag gta gat ttg gat tct ttt gaa gat aaa cca tgg      605
Val Pro Leu Leu Glu Val Asp Leu Asp Ser Phe Glu Asp Lys Pro Trp
              135              140              145              150

cgt aaa cct ggt gct gat ctt tct gat tat ttt aat tat ggg ttt aat      653
Arg Lys Pro Gly Ala Asp Leu Ser Asp Tyr Phe Asn Tyr Gly Phe Asn
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gaa gat acc tgg aaa gct tac tgt gaa aaa caa aag agg ata cga atg      701
Glu Asp Thr Trp Lys Ala Tyr Cys Glu Lys Gln Lys Arg Ile Arg Met
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gga ctt gaa gtt ata cca gta acc tct act aca aat aaa att acg gta      749
Gly Leu Glu Val Ile Pro Val Thr Ser Thr Thr Asn Lys Ile Thr Val
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cca ccg agc aga aac agc act tct tct cag tct cag aca agt act gcc Pro Pro Ser Arg Asn Ser Thr Ser Ser Gln Ser Gln Thr Ser Thr Ala 235 240 245	893
tcc aga aaa gcc aat tca agc gtt ggg aag tgg cag gat cga tat ggg Ser Arg Lys Ala Asn Ser Ser Val Gly Lys Trp Gln Asp Arg Tyr Gly 250 255 260	941
agg gcc gaa tca cct gat cta agg aga tta cct ggg gca att gat gtt Arg Ala Glu Ser Pro Asp Leu Arg Arg Leu Pro Gly Ala Ile Asp Val 265 270 275	989
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aag ttt act ccc aga tcc ttc tgg ggc tcg cgt cct aaa cat act ggg   1179
Lys Phe Thr Pro Arg Ser Phe Trp Gly Ser Arg Pro Lys His Thr Gly
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ggc aga tct gag atg agg gcc cac gtt ccc cag gcc cct tgg gca agg   1227
Gly Arg Ser Glu Met Arg Ala His Val Pro Gln Ala Pro Trp Ala Arg
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Gln Ala Pro Pro Val Leu Pro Leu Trp Thr Val Val Asn Asp His Pro
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cat gag aaa cct gtt tca aga ccc cag aat aca tag agac acacacatgg   1325
His Glu Lys Pro Val Ser Arg Pro Gln Asn Thr  *
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at 2947

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tttccaagag cagcagaaa atg aat aaa tcc ctg ggg cca gtg tca ttc aag 172
          Met Asn Lys Ser Leu Gly Pro Val Ser Phe Lys
              1              5              10
gac gtg gct gtg gac ttc acc cag gag gaa tgg cag cag ctg gat cct 220
Asp Val Ala Val Asp Phe Thr Gln Glu Trp Gln Gln Leu Asp Pro
          15              20              25

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gag cag aag ata act tac agg gat gtg atg ctg gag aac tac agc aat	268
Glu Gln Lys Ile Thr Tyr Arg Asp Val Met Leu Glu Asn Tyr Ser Asn	
30 35 40	
cta gtt tct gtg ggg tat cac att atc aaa ccg gat gtt atc agc aag	316
Leu Val Ser Val Gly Tyr His Ile Ile Lys Pro Asp Val Ile Ser Lys	
45 50 55	
ttg gag caa gga gaa gag cca tgg ata gta gaa gga gaa ttc cta ctt	364
Leu Glu Gln Gly Glu Glu Pro Trp Ile Val Glu Gly Glu Phe Leu Leu	
60 65 70 75	
cag agc tat cca gat gaa gtc tgg caa act gat gac cta ata gag aga	412
Gln Ser Tyr Pro Asp Glu Val Trp Gln Thr Asp Asp Leu Ile Glu Arg	
80 85 90	
atc cag gaa gag gaa aat aaa cct tca agg caa act gtg ttc att gag	460
Ile Gln Glu Glu Glu Asn Lys Pro Ser Arg Gln Thr Val Phe Ile Glu	
95 100 105	
acc ctg att gaa gag aga ggt aat gtt cct ggt aaa act ttt gat gta	508
Thr Leu Ile Glu Glu Arg Gly Asn Val Pro Gly Lys Thr Phe Asp Val	
110 115 120	
gaa acg aac cct gtt cct tca aga aaa ata gcc tat aaa aat agc ctc	556
Glu Thr Asn Pro Val Pro Ser Arg Lys Ile Ala Tyr Lys Asn Ser Leu	
125 130 135	
tgt gac tca tgt gaa aag tgt tta acg tct gtt tca gaa tat att agt	604
Cys Asp Ser Cys Glu Lys Cys Leu Thr Ser Val Ser Glu Tyr Ile Ser	
140 145 150 155	
agt gat gga agc tat gca aga atg aaa gct gat gaa tgt agt gga tgt	652
Ser Asp Gly Ser Tyr Ala Arg Met Lys Ala Asp Glu Cys Ser Gly Cys	
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Gly Lys Ser Leu Leu His Ile Lys Leu Glu Lys Thr His Pro Gly Asp	
175 180 185	
caa gct tat gaa ttt aat caa aat ggg gaa cct tat act cta aat gaa	748
Gln Ala Tyr Glu Phe Asn Gln Asn Gly Glu Pro Tyr Thr Leu Asn Glu	
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gaa agt ctt tat cag aaa att cgt att ttg gag aaa cct ttt gaa tat	796
Glu Ser Leu Tyr Gln Lys Ile Arg Ile Leu Glu Lys Pro Phe Glu Tyr	
205 210 215	
att gaa tgc cag aaa gcc ttc caa aag gac act gtt ttt gtt aat cac	844
Ile Glu Cys Gln Lys Ala Phe Gln Lys Asp Thr Val Phe Val Asn His	
220 225 230 235	
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Met Glu Glu Lys Pro Tyr Lys Trp Asn Gly Ser Glu Ile Ala Phe Leu	
240 245 250	
cag atg tgc gac ctc act gta cat cag aca tct cat atg gaa atg aag	940
Gln Met Ser Asp Leu Thr Val His Gln Thr Ser His Met Glu Met Lys	
255 260 265	
ccc tat gaa tgc agt gaa tgt ggg aaa tcc ttc tgt aaa aag tca aaa	988
Pro Tyr Glu Cys Ser Glu Cys Gly Lys Ser Phe Cys Lys Lys Ser Lys	
270 275 280	

ttt att ata cat cag agg act cac aca gga gag aaa cct tac gaa tgt	1036
Phe Ile Ile His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys	
285 290 295	
aat cag tgt ggg aaa tcc ttc tgc cag aag gga acc ctt act gtg cat	1084
Asn Gln Cys Gly Lys Ser Phe Cys Gln Lys Gly Thr Leu Thr Val His	
300 305 310 315	
cag aga aca cac aca ggg gag aag ccc tat gaa tgt aat gaa tgt ggg	1132
Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Asn Glu Cys Gly	
320 325 330	
aag aac ttt tac cag aag tta cac ctc att cag cat cag aga act cac	1180
Lys Asn Phe Tyr Gln Lys Leu His Leu Ile Gln His Gln Arg Thr His	
335 340 345	
tca gga gag aag ccc tat gaa tgt agt tat tgt gga aaa tcc ttt tgc	1228
Ser Gly Glu Lys Pro Tyr Glu Cys Ser Tyr Cys Gly Lys Ser Phe Cys	
350 355 360	
cag aag aca cac ctc aca caa cat cag aga aca cat tca gga gag aga	1276
Gln Lys Thr His Leu Thr Gln His Gln Arg Thr His Ser Gly Glu Arg	
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Pro Tyr Val Cys His Asp Cys Gly Lys Thr Phe Ser Gln Lys Ser Ala	
380 385 390 395	
ctt aat gac cat cag aaa att cac aca ggt gtg aaa ctc tac aag tgt	1372
Leu Asn Asp His Gln Lys Ile His Thr Gly Val Lys Leu Tyr Lys Cys	
400 405 410	
agt gaa tgt ggg aaa tgc ttc tgc cgc aag tct act ctc acg acc cac	1420
Ser Glu Cys Gly Lys Cys Phe Cys Arg Lys Ser Thr Leu Thr Thr His	
415 420 425	
ctg agg acc cac aca gga gag aaa ccg tat gaa tgt aat gag tgt gga	1468
Leu Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Asn Glu Cys Gly	
430 435 440	
aaa gcc ttc tct cgg atg tca tac ctc act gta cat tat aga act cat	1516
Lys Ala Phe Ser Arg Met Ser Tyr Leu Thr Val His Tyr Arg Thr His	
445 450 455	
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Ser Gly Glu Lys Pro Tyr Glu Cys Thr Glu Cys Gly Lys Lys Phe Tyr	
460 465 470 475	
cac aaa tca gca ttc aac agc cat cag aga att cat agg aga ggc aat	1612
His Lys Ser Ala Phe Asn Ser His Gln Arg Ile His Arg Arg Gly Asn	
480 485 490	
atg aat gta ata gat gtg gga agg ctt ctc tga agtcagac ctcattttat	1663
Met Asn Val Ile Asp Val Gly Arg Leu Leu *	
495 500	
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acatcagaga gttcacacag gttagtgtgg acatcccctt gtgtgttgga ctcataatct	1783
gaagactcac agaattggaaa ccatgattat aacaagacca catggtataa caataactaga	1843
ctatagacaa gtaaaaaattt ataaaatatta agaattgtata tacatgtcac catggattgg	1903

aactgttttg catatcaggg aaatcatagc caaggggaaa tctatcagta taaggaatgt 1963  
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 ccgtcagccc agaagacgta aagcaggcta ccagcaattt tgagaacttg caaaaacagc 180  
 ttgcaaggaa a atg aag ctt cct att ttc ata gca gat gca ttc aca gca 230  
                   Met Lys Leu Pro Ile Phe Ile Ala Asp Ala Phe Thr Ala  
                   1                  5                  10  
 aga gca ttt cgt ggg aat cct gct gct gtt tgc ctc cta gaa aat gaa 278  
 Arg Ala Phe Arg Gly Asn Pro Ala Ala Val Cys Leu Leu Glu Asn Glu  
                   15                  20                  25  
 ttg gat gaa gac atg cat cag aaa att gca agg gag atg aac ctc tct 326  
 Leu Asp Glu Asp Met His Gln Lys Ile Ala Arg Glu Met Asn Leu Ser  
                   30                  35                  40                  45  
 gaa act gct ttt atc cga aaa ctg cac ccg aca gac aac ttt gca caa 374  
 Glu Thr Ala Phe Ile Arg Lys Leu His Pro Thr Asp Asn Phe Ala Gln  
                   50                  55                  60  
 agt tcc tgc ttt gga ctg aga tgg ttt aca cca gcg agt gag gtc cca 422  
 Ser Ser Cys Phe Gly Leu Arg Trp Phe Thr Pro Ala Ser Glu Val Pro  
                   65                  70                  75  
 ctc tgt ggc cat gcc acc ctg gct tct gca gct gtg ctg ttt cac aaa 470  
 Leu Cys Gly His Ala Thr Leu Ala Ser Ala Ala Val Leu Phe His Lys  
                   80                  85                  90  
 ata aaa aac atg aat agc acg ctc acg ttt gtc act ctg agt gga gaa 518  
 Ile Lys Asn Met Asn Ser Thr Leu Thr Phe Val Thr Leu Ser Gly Glu  
                   95                  100                  105  
 cta agg gcc aga cga gca gag gac ggc atc gtc ctg gac ttg cct ctt 566  
 Leu Arg Ala Arg Arg Ala Glu Asp Gly Ile Val Leu Asp Leu Pro Leu  
                   110                  115                  120                  125  
 tat cca gcc cac ccc cag gac ttc cat gaa gta gag gac ttg ata aag 614  
 Tyr Pro Ala His Pro Gln Asp Phe His Glu Val Glu Asp Leu Ile Lys  
                   130                  135                  140  
 act gcc ata ggc aac aca ctg gtc cag gac atc tgt tat tct cca gat 662  
 Thr Ala Ile Gly Asn Thr Leu Val Gln Asp Ile Cys Tyr Ser Pro Asp

145	150	155	
acc caa aag ctc ctc gtc cgc ctc agt gac gtt tac aac agg tcg ttt			710
Thr Gln Lys Leu Leu Val Arg Leu Ser Asp Val Tyr Asn Arg Ser Phe			
160	165	170	
ctg gag aac ctg aaa gtg aac acg gag aat ctg ctg caa gtt gaa aac			758
Leu Glu Asn Leu Lys Val Asn Thr Glu Asn Leu Leu Gln Val Glu Asn			
175	180	185	
aca ggg aag gtg aaa ggg ctt att ctt acc ctt aaa gga gag cct ggt			806
Thr Gly Lys Val Lys Gly Leu Ile Leu Thr Leu Lys Gly Glu Pro Gly			
190	195	200	205
ggg cag acc caa gca ttt gac ttt tac tca aga tat ttt gca ccg tgg			854
Gly Gln Thr Gln Ala Phe Asp Phe Tyr Ser Arg Tyr Phe Ala Pro Trp			
210	215	220	
gtt ggt gtg gct gaa gac cca gtg aca ggg tct gca cac gct gtt ctc			902
Val Gly Val Ala Glu Asp Pro Val Thr Gly Ser Ala His Ala Val Leu			
225	230	235	
agc agc tac tgg tcc cag cat ctg ggg aag aaa gaa atg cat gct ttt			950
Ser Ser Tyr Trp Ser Gln His Leu Gly Lys Lys Glu Met His Ala Phe			
240	245	250	
cag tgt tcc cac cga gga gga gag ctg gga att tcc ctt cgt cca gac			998
Gln Cys Ser His Arg Gly Gly Glu Leu Gly Ile Ser Leu Arg Pro Asp			
255	260	265	
gga agg gtt gac att aga gga ggt gca gct gtt gtt tta gag ggc aca			1046
Gly Arg Val Asp Ile Arg Gly Gly Ala Ala Val Val Leu Glu Gly Thr			
270	275	280	285
ctg aca gcc tag agg tggttatgct gtgacgctgc tgtctctaac caccaagtat			1101
Leu Thr Ala *			
tttctgctta aaaagaaatg taaggggctg cctttagcaa atgtgcgtag tagtctactt			1161
aatcctcatg ttaaaaaatcg aaaaatgggc caggcgcagt ggctcatgcc tgtaatcgta			1221
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Met Asn

1

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Met Phe Lys Glu Ala Val Thr Phe Lys Asp Val Ala Val Thr Phe Thr	
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gag gag gaa ttg ggg ctg ctg ggc cct gcc cag agg aag ctg tac cga	273
Glu Glu Glu Leu Gly Leu Leu Gly Pro Ala Gln Arg Lys Leu Tyr Arg	
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gat gtg atg gtg gag aac ttt agg aac ctg ctg tca gtg ggg cat cca	321
Asp Val Met Val Glu Asn Phe Arg Asn Leu Ser Val Gly His Pro	
35 40 45 50	
ccc ttc aaa caa gat gta tca cct ata gaa aga aat gag cag ctt tgg	369
Pro Phe Lys Gln Asp Val Ser Pro Ile Glu Arg Asn Glu Gln Leu Trp	
55 60 65	
ata atg acg aca gca acc cga aga cag gga aat tta gat acc tta ctt	417
Ile Met Thr Thr Ala Thr Arg Arg Gln Gly Asn Leu Asp Thr Leu Leu	
70 75 80	
gta aaa gct ctt ttg ctc tat gac ctg gct caa act taa acttggattt	466
Val Lys Ala Leu Leu Leu Tyr Asp Leu Ala Gln Thr *	
85 90 95	
gaagttagaa gaaatgttgg aagtcattta tatatgaaga aatgttggaa ggactcatat	526
atgcatacat tccttgagtg actatgaatg actgccgggc agtaacttct gggctgtggt	586
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ccagcagctg ctgttgccac caccactagt tcaagcacc	174
atg cag ttt acc tca	
Met Gln Phe Thr Ser	
1 5	
ata tca aat tct ttg acc tcc act gct gct att ggg ctc tca ttt aca	222
Ile Ser Asn Ser Leu Thr Ser Thr Ala Ala Ile Gly Leu Ser Phe Thr	
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act tca acg act acc acc gcc act ttc acc acc aac act act acc aca	270
Thr Ser Thr Thr Thr Thr Ala Thr Phe Thr Thr Asn Thr Thr Thr Thr	
25 30 35	

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atc acc agt ggc ttt act gtg aac caa aac caa ctg tta tca aga ggg      318
Ile Thr Ser Gly Phe Thr Val Asn Gln Asn Gln Leu Leu Ser Arg Gly
      40      45      50

ttt gaa aac ctt gta cct tat act tca act gtt agt gta gta gca act      366
Phe Glu Asn Leu Val Pro Tyr Thr Ser Thr Val Ser Val Val Ala Thr
      55      60      65

cct gtg atg aca tat ggt cat ctg gag ggt ctt ata aat gag tgg aac      414
Pro Val Met Thr Tyr Gly His Leu Glu Gly Leu Ile Asn Glu Trp Asn
      70      75      80      85

ctt gag ctg gaa gat caa gag aag tac ttt ctt ctc cag gcc act cag      462
Leu Glu Leu Glu Asp Gln Glu Lys Tyr Phe Leu Leu Gln Ala Thr Gln
      90      95      100

gtc aat gct tgg gac cat aca ttg att gag aat ggt gag atg att cgt      510
Val Asn Ala Trp Asp His Thr Leu Ile Glu Asn Gly Glu Met Ile Arg
      105      110      115

att tta cat gga gaa gtg aac aaa gtg aaa ctg gat cag aaa aga ttg      558
Ile Leu His Gly Glu Val Asn Lys Val Lys Leu Asp Gln Lys Arg Leu
      120      125      130

gaa caa gaa ttg gat ttt atc ctg tca cag cag cag gaa cta gaa ttt      606
Glu Gln Glu Leu Asp Phe Ile Leu Ser Gln Gln Gln Glu Leu Glu Phe
      135      140      145

ctg ttg act tat tta gag gag tct acg cgc gac cag agt gga ctt cat      654
Leu Leu Thr Tyr Leu Glu Glu Ser Thr Arg Asp Gln Ser Gly Leu His
      150      155      160      165

tat ctg cag gat gca gat gag gag cat gtg gag atc tcc acc aga tct      702
Tyr Leu Gln Asp Ala Asp Glu Glu His Val Glu Ile Ser Thr Arg Ser
      170      175      180

gca gaa ttc tga atg cccatatgga ctccctgcag tggattgatc ggaattcagg      757
Ala Glu Phe *
      185

catgctgcga aggaaggtag aagtggtaac acgggttttt cgaggattat cattcacgag      817

gggtcttttca catcatgttc atcactgttt tttagtgtat tgaccctttt ttcagcttgt      877

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atgatcaaaa taaatacatc tgggtttaac ctgaatcacc atttagtaac atagtcatca      180

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tatacttcat gtgttaggaa cctgtgacta catgttctga actgttagta agaaaaatgg	360
tattggatac cttactcttt aagattttta attatttttg gtaaaactgg gaaatagccg	420
tctgatttgc attttatttt cttttgtatt ttaaggat	473
atg gaa tat tat ctt	
Met Glu Tyr Tyr Leu	
1 5	
gta aaa tgg aaa gga tgg cca gat tct aca aat act tgg gaa cct ttg	521
Val Lys Trp Lys Gly Trp Pro Asp Ser Thr Asn Thr Trp Glu Pro Leu	
10 15 20	
caa aat ctg aag tgc ccg tta ctg ctt cag caa ttc tct aat gac aag	569
Gln Asn Leu Lys Cys Pro Leu Leu Leu Gln Gln Phe Ser Asn Asp Lys	
25 30 35	
cat aat tat tta tct cag gta aag aaa ggc aaa gca ata act cca aaa	617
His Asn Tyr Leu Ser Gln Val Lys Lys Gly Lys Ala Ile Thr Pro Lys	
40 45 50	
gac aat aac aaa act ttg aaa cct gcc att gct gag tac att gtg aag	665
Asp Asn Asn Lys Thr Leu Lys Pro Ala Ile Ala Glu Tyr Ile Val Lys	
55 60 65	
aag gct aaa caa agg ata gct ctg cag aga tgg caa gat gaa ctc aac	713
Lys Ala Lys Gln Arg Ile Ala Leu Gln Arg Trp Gln Asp Glu Leu Asn	
70 75 80 85	
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Ala Pro Gly Ile Ser Leu Val Asn Glu Ala Thr Phe Gly Cys Ser Cys	
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Ser Asn Gly Arg Gly Trp Gly Val Lys Thr Leu Val Lys Ile Lys Arg	
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Ser Val Thr Ala His Leu Ala Ala Lys Trp Pro Glu Thr Pro Leu Leu	
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Leu Glu Ala Ser Glu Phe Met Ala Glu Glu Ser Asn Glu Lys Phe Trp	
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Gln Phe Leu Glu Thr Val Gln Glu Leu Ala Ile Tyr Lys Gln Thr Glu	
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Ser Asp Tyr Ser Tyr Tyr Asn Leu Ile Leu Lys Lys Ala Gly Gln Phe	
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Lys Glu Asn Leu Pro Val Val Ile Leu Tyr Ala Glu Met Gly Thr Arg	
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Thr Val Glu Asp Glu Thr Glu Thr Asn Glu Val Gln Gly Phe Leu Phe	
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Val Asp Met Asp Val Tyr Asp Ala Phe Ser Ile Leu Asp Met Leu Lys	
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Gly Ile His Ser Lys Tyr Asp Glu Glu Arg Lys Ala Gly Ala Ser Phe	
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Cys Ser Arg Ser Arg Ser Gly Arg Met Glu Gly Ala Lys Gly Lys Glu			
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Cys Thr Ala Gly His Ser Trp Pro Ala Pro Ala Leu Trp Cys Leu Leu			
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 Gln Phe Leu Glu Thr Val Gln Glu Leu Ala Ile Tyr Lys Gln Thr Glu  
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Leu Leu Leu Glu Gly Gln Cys Phe Asp Lys Val Thr Glu Gln Pro Pro	
1090 1095 1100 1105	
cgg ggt ctg cag ttc aca cta ggc aca aaa aat aaa cct gct gtg gtt	3478
Arg Gly Leu Gln Phe Thr Leu Gly Thr Lys Asn Lys Pro Ala Val Val	
1110 1115 1120	
gat aca ata gtg atg gca cat cat ggg tat ttt caa tta aaa gca aac	3526
Asp Thr Ile Val Met Ala His His Gly Tyr Phe Gln Leu Lys Ala Asn	
1125 1130 1135	
cca ggt gct tgg ata ctg agg tta cac caa gga aaa tct gaa gat att	3574
Pro Gly Ala Trp Ile Leu Arg Leu His Gln Gly Lys Ser Glu Asp Ile	
1140 1145 1150	
tat caa ata gtt ggg cat gaa gga act gac tct caa gca gac cta gaa	3622
Tyr Gln Ile Val Gly His Glu Gly Thr Asp Ser Gln Ala Asp Leu Glu	
1155 1160 1165	
gat atc att gtt gta tta aac agc ttc aaa agc aag ata ctc aaa gta	3670
Asp Ile Ile Val Val Leu Asn Ser Phe Lys Ser Lys Ile Leu Lys Val	
1170 1175 1180 1185	
aaa gtg aaa aaa gaa aca gac aaa att aag gaa gat atc ctt acc gat	3718
Lys Val Lys Lys Glu Thr Asp Lys Ile Lys Glu Asp Ile Leu Thr Asp	
1190 1195 1200	

gaa gat gaa aaa aca aaa gga ctg tgg gat tcc att aaa agt ttc aca Glu Asp Glu Lys Thr Lys Gly Leu Trp Asp Ser Ile Lys Ser Phe Thr 1205 1210 1215	3766
gta agc ttg cat aaa gaa aac aaa aag gaa aaa gat gtc cta aac att Val Ser Leu His Lys Glu Asn Lys Lys Glu Lys Asp Val Leu Asn Ile 1220 1225 1230	3814
ttt tca gtt gct tct ggt cat tta tat gaa cgt ttt tta aga att atg Phe Ser Val Ala Ser Gly His Leu Tyr Glu Arg Phe Leu Arg Ile Met 1235 1240 1245	3862
atg ctt tct gtt ttg cgt aac acc aaa aca cca gtg aaa ttc tgg ttg Met Leu Ser Val Leu Arg Asn Thr Lys Thr Pro Val Lys Phe Trp Leu 1250 1255 1260 1265	3910
cta aaa aat tat ctc tca ccg aca ttt aaa gaa gta att cct cac atg Leu Lys Asn Tyr Leu Ser Pro Thr Phe Lys Glu Val Ile Pro His Met 1270 1275 1280	3958
gct aaa gag tat gga ttc cga tat gaa cta gtt caa tat agg tgg ccc Ala Lys Glu Tyr Gly Phe Arg Tyr Glu Leu Val Gln Tyr Arg Trp Pro 1285 1290 1295	4006
cgt tgg ctt cgt caa cag act gaa aga cag agg att att tgg ggt tac Arg Trp Leu Arg Gln Gln Thr Glu Arg Gln Arg Ile Ile Trp Gly Tyr 1300 1305 1310	4054
aaa att ctt ttc ctt gat gtt ctt ttc cca cta gca gtg gac aaa atc Lys Ile Leu Phe Leu Asp Val Leu Phe Pro Leu Ala Val Asp Lys Ile 1315 1320 1325	4102
att ttt gtt gat gct gac cag att gtg aga cat gat cta aaa gaa ctt Ile Phe Val Asp Ala Asp Gln Ile Val Arg His Asp Leu Lys Glu Leu 1330 1335 1340 1345	4150
cga gat ttc gat ctg gat gga gct cct tat ggg tat act cca ttt tgt Arg Asp Phe Asp Leu Asp Gly Ala Pro Tyr Gly Tyr Thr Pro Phe Cys 1350 1355 1360	4198
gat agc cgc agg gaa atg gat gga tat cgt ttc tgg aaa aca gga tac Asp Ser Arg Arg Glu Met Asp Gly Tyr Arg Phe Trp Lys Thr Gly Tyr 1365 1370 1375	4246
tgg gca tca cat ctt tta aga cgg aaa tac cat atc agt gct tta tat Trp Ala Ser His Leu Leu Arg Arg Lys Tyr His Ile Ser Ala Leu Tyr 1380 1385 1390	4294
gta gtg gat ctc aag aag ttc agg aga att gga gca ggt gac agg ctc Val Val Asp Leu Lys Lys Phe Arg Arg Ile Gly Ala Gly Asp Arg Leu 1395 1400 1405	4342
agg agc cag tat caa gct ctc agt caa gat cca aac agt ctt tca aac Arg Ser Gln Tyr Gln Ala Leu Ser Gln Asp Pro Asn Ser Leu Ser Asn 1410 1415 1420 1425	4390
cta gat cag gat ctc ccc aat aat atg att tac caa gtc gcc att aag Leu Asp Gln Asp Leu Pro Asn Asn Met Ile Tyr Gln Val Ala Ile Lys 1430 1435 1440	4438
tct ctt cct caa gac tgg ctg tgg tgt gaa acc tgg tgt gat gat gaa Ser Leu Pro Gln Asp Trp Leu Trp Cys Glu Thr Trp Cys Asp Asp Glu 1445 1450 1455	4486



tcc aaa caa aga gcc aaa aca att gat ctg tgc aat aat ccc aaa aca 4534  
 Ser Lys Gln Arg Ala Lys Thr Ile Asp Leu Cys Asn Asn Pro Lys Thr  
 1460 1465 1470

aaa gaa tcc aaa cta aaa gct gct gcc aga att gtc cca gaa tgg gtg 4582  
 Lys Glu Ser Lys Leu Lys Ala Ala Ala Arg Ile Val Pro Glu Trp Val  
 1475 1480 1485

gag tat gat gct gag ata aga caa cta tta gat cat ctt gaa aac aag 4630  
 Glu Tyr Asp Ala Glu Ile Arg Gln Leu Leu Asp His Leu Glu Asn Lys  
 1490 1495 1500 1505

aag caa gat aca att ttg aca cat gat gaa ctc tag cact ggtgtatatg 4680  
 Lys Gln Asp Thr Ile Leu Thr His Asp Glu Leu \*  
 1510 1515

agaaggaagg cgaaagcatg acaggaaacc tgccgcctgc tggggaagtc tggagcccct 4740

gctgagacga tttggaagtc tcgttaagat cagtgcacata ttctttaatt ttaaaaaatt 4800

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aaccttggtg tgttatctga ccaacttccc acatacgtg aagagaagtg cacatggcca 180

tcaaaggcac gcgccccccc cttcccttca gctgccttgg cagctgccga acccaccctc 240

gcagtggctg cccagaacct ttacacatgt atgtgtgcgc gtgtgcagag catgacaagg 300

caggtggctg gggctccagc ctggctaaag agaacttgcc cttaggggca agagagggag 360

gcactgcatt tccagtttcg ttctggaagt gccacctga catctgtggt gccactgat 420

ctttacagat atcctgctgg atgacattgt ccttaccat tctctcttcc tcccagcgga 480

gaaatttctg caggagctac accagtactt tggtcgggca ggaggc atg gag ggc 535  
 Met Glu Gly  
 1

cct gaa ggg ctg ggc cgg aag caa gcc tgt cta gcc atg ctt ctc cat 583  
 Pro Glu Gly Leu Gly Arg Lys Gln Ala Cys Leu Ala Met Leu Leu His  
 5 10 15

ttc ttg gac acc tac cag ggg ctg ctt caa gag gaa gag ggg gcc ggc 631  
 Phe Leu Asp Thr Tyr Gln Gly Leu Leu Gln Glu Glu Gly Ala Gly

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cac atc atc aag gat cta tac ctg cta att atg aag gac gag tcc ctt				679
His Ile Ile Lys Asp Leu Tyr Leu Leu Ile Met Lys Asp Glu Ser Leu				
	40	45	50	
tac cag ggc ctc cga gag gac act ctg agg ctg cac cag ctg gtg gag				727
Tyr Gln Gly Leu Arg Glu Asp Thr Leu Arg Leu His Gln Leu Val Glu				
	55	60	65	
acg gtg gaa cta aag att cca gag gag aac cag cca ccc agc aag cag				775
Thr Val Glu Leu Lys Ile Pro Glu Glu Asn Gln Pro Pro Ser Lys Gln				
	70	75	80	
gtg aag cca ctc ttc cgc cac ttc cgc cgg ata gac tcc tgt ctg cag				823
Val Lys Pro Leu Phe Arg His Phe Arg Arg Ile Asp Ser Cys Leu Gln				
	85	90	95	
acc cgg gtg gcc ttc cgg ggc tct gat gag atc ttc tgc cgt gta tac				871
Thr Arg Val Ala Phe Arg Gly Ser Asp Glu Ile Phe Cys Arg Val Tyr				
100	105	110	115	
atg cct gac cac tct tat gtg acc ata cgc agc cgc ctt tca gca tct				919
Met Pro Asp His Ser Tyr Val Thr Ile Arg Ser Arg Leu Ser Ala Ser				
	120	125	130	
gtg cag gac att ctg ggc tct gtg acg gag aaa ctt caa tat tca gag				967
Val Gln Asp Ile Leu Gly Ser Val Thr Glu Lys Leu Gln Tyr Ser Glu				
	135	140	145	
gag ccc gcg ggg cgt gag gat tcc ctc atc ctg gta gct gtg tcc tcc				1015
Glu Pro Ala Gly Arg Glu Asp Ser Leu Ile Leu Val Ala Val Ser Ser				
	150	155	160	
tct gga gag aag gtc ctt ctc cag ccc act gag gac tgt gtt ttc acc				1063
Ser Gly Glu Lys Val Leu Leu Gln Pro Thr Glu Asp Cys Val Phe Thr				
	165	170	175	
gca ctg ggc atc aac agc cac ctg ttt gcc tgt act cgg gac agc tat				1111
Ala Leu Gly Ile Asn Ser His Leu Phe Ala Cys Thr Arg Asp Ser Tyr				
180	185	190	195	
gag gct ctg gtg ccc ctc ccc gag gag atc cag gtc tcc cct gga gac				1159
Glu Ala Leu Val Pro Leu Pro Glu Glu Ile Gln Val Ser Pro Gly Asp				
	200	205	210	
aca gag atc cac cga gtg gag cct gag gac gtt gcc aac cac cta act				1207
Thr Glu Ile His Arg Val Glu Pro Glu Asp Val Ala Asn His Leu Thr				
	215	220	225	
gcc ttc cac tgg gag ctg ttc cga tgt gtg cat gag ctg gag ttc gtg				1255
Ala Phe His Trp Glu Leu Phe Arg Cys Val His Glu Leu Glu Phe Val				
	230	235	240	
gac tac gtg ttc cac ggg gag cgc ggc cgc cgg gag acg gcc aac ttg				1303
Asp Tyr Val Phe His Gly Glu Arg Gly Arg Arg Glu Thr Ala Asn Leu				
	245	250	255	
gag ctg ctg ctg cag cgc tgc agc gag gtc acg cac tgg gtg gcc acc				1351
Glu Leu Leu Leu Gln Arg Cys Ser Glu Val Thr His Trp Val Ala Thr				
	260	265	270	275
gaa gtg ctg ctc tgc gag gcc ccg ggc aag cgc gcg cag ctg ctc aag				1399
Glu Val Leu Leu Cys Glu Ala Pro Gly Lys Arg Ala Gln Leu Leu Lys				

280	285	290	
aag ttc atc aag atc gcg gcc ctc tgc aag cag aac cag gac ctg ctg			1447
Lys Phe Ile Lys Ile Ala Ala Leu Cys Lys Gln Asn Gln Asp Leu Leu			
295	300	305	
tct ttc tac gcc gtg gtc atg ggg ctg gac aac gcc gct gtc agc cgc			1495
Ser Phe Tyr Ala Val Val Met Gly Leu Asp Asn Ala Ala Val Ser Arg			
310	315	320	
ctt cga ctc acc tgg gag aag ctg cca ggg aaa ttc aag aac ttg ttt			1543
Leu Arg Leu Thr Trp Glu Lys Leu Pro Gly Lys Phe Lys Asn Leu Phe			
325	330	335	
cgc aaa ttt gag aac ctg acg gac ccc tgc agg aac cac aaa agc tac			1591
Arg Lys Phe Glu Asn Leu Thr Asp Pro Cys Arg Asn His Lys Ser Tyr			
340	345	350	355
cga gaa gtg atc tcc aaa atg aag ccc cct gtg att ccc ttc gtg cct			1639
Arg Glu Val Ile Ser Lys Met Lys Pro Pro Val Ile Pro Phe Val Pro			
360	365	370	
ctg atc ctc aaa gac ctg act ttc ctg cac gaa ggg agt aag acc ctt			1687
Leu Ile Leu Lys Asp Leu Thr Phe Leu His Glu Gly Ser Lys Thr Leu			
375	380	385	
gta gat ggt ttg gtg aac atc gag aag ctg cat tca gtg gcc gaa aaa			1735
Val Asp Gly Leu Val Asn Ile Glu Lys Leu His Ser Val Ala Glu Lys			
390	395	400	
gtg agg aca atc cgc aaa tac cgg agc cgg ccc ctt tgc ctg gac atg			1783
Val Arg Thr Ile Arg Lys Tyr Arg Ser Arg Pro Leu Cys Leu Asp Met			
405	410	415	
gag gca tcc ccc aat cac ctg cag acc aag gcc tat gtg cgc cag ttt			1831
Glu Ala Ser Pro Asn His Leu Gln Thr Lys Ala Tyr Val Arg Gln Phe			
420	425	430	435
cag gtc atc gac aac cag aac ctc ctc ttc gag ctc tcc tac aag ctg			1879
Gln Val Ile Asp Asn Gln Asn Leu Leu Phe Glu Leu Ser Tyr Lys Leu			
440	445	450	
gag gca aac agt cag tga			1897
Glu Ala Asn Ser Gln *			
455			

&lt;210&gt; 385

&lt;211&gt; 1998

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;222&gt; (200)..(1879)

&lt;220&gt;

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&lt;222&gt; (1)...(1998)

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acaaaggggg ctggaggatt tagccactct gtcctcccct tccggcagtc cagggcctcc 180  
tcccgagcac agcggcgct atg gac tct cca gga tac aac tgc ttc gtg gac 232  
Met Asp Ser Pro Gly Tyr Asn Cys Phe Val Asp  
1 5 10  
aaa gac aag atg gac gct gcc atc cag gac ctg ggg ccc aag gag ctg 280  
Lys Asp Lys Met Asp Ala Ala Ile Gln Asp Leu Gly Pro Lys Glu Leu  
15 20 25  
agc tgc act gaa ctg cag gaa ctg aag cag ctg gcg cgc cag ggc tac 328  
Ser Cys Thr Glu Leu Gln Glu Leu Lys Gln Leu Ala Arg Gln Gly Tyr  
30 35 40  
tgg gcc caa agc cac gcc ctg cgg gga aag gtg tac cag cgc ctg atc 376  
Trp Ala Gln Ser His Ala Leu Arg Gly Lys Val Tyr Gln Arg Leu Ile  
45 50 55  
cgg gac att ccc tgc cgc acg gtc acg cct gac gcc agc gtg tac agc 424  
Arg Asp Ile Pro Cys Arg Thr Val Thr Pro Asp Ala Ser Val Tyr Ser  
60 65 70 75  
gac atc gtg ggc aag atc gtg ggc aag cac agc agc agc tgc ctg ccg 472  
Asp Ile Val Gly Lys Ile Val Gly Lys His Ser Ser Ser Cys Leu Pro  
80 85 90  
ctg ccc gag ttc gtg gac aac acg cag gtg ccc agc tac tgc ctg aat 520  
Leu Pro Glu Phe Val Asp Asn Thr Gln Val Pro Ser Tyr Cys Leu Asn  
95 100 105  
gca cgc ggc gag ggg gcc gtg cgc aag atc ctc ctg tgc ctg gcc aac 568  
Ala Arg Gly Glu Gly Ala Val Arg Lys Ile Leu Leu Cys Leu Ala Asn  
110 115 120  
cag ttc ccc gac atc tcc ttc tgc ccc gcc ctg ccg gcc gtg gtg gcc 616  
Gln Phe Pro Asp Ile Ser Phe Cys Pro Ala Leu Pro Ala Val Val Ala  
125 130 135  
ctg ctg ctg cac tac agc atc gac gag gcc gag tgc ttc gag aag gcc 664  
Leu Leu Leu His Tyr Ser Ile Asp Glu Ala Glu Cys Phe Glu Lys Ala  
140 145 150 155  
tgc cgc atc ctg gcc tgc aat gac ccc ggc agg agg ctg atc gac cag 712  
Cys Arg Ile Leu Ala Cys Asn Asp Pro Gly Arg Arg Leu Ile Asp Gln  
160 165 170  
agc ttc ctg gcc ttt gag tgc tcc tgc atg acg ttt ggg gac ctg gtg 760  
Ser Phe Leu Ala Phe Glu Ser Ser Cys Met Thr Phe Gly Asp Leu Val  
175 180 185  
aac aag tac tgc cag gcg gcc cac aag ctg atg gtg gcc gtg tgc gag 808  
Asn Lys Tyr Cys Gln Ala Ala His Lys Leu Met Val Ala Val Ser Glu  
190 195 200  
gat gtc ctg cag gtc tat gcg gac tgg cag cgc tgg ctg ttt ggg gag 856  
Asp Val Leu Gln Val Tyr Ala Asp Trp Gln Arg Trp Leu Phe Gly Glu  
205 210 215  
ctg ccc ctc tgc tac ttc gcc cgg gtc ttt gac gtc ttc ctg gtg gag 904

973

Ala Asp Arg Leu Ser Pro Phe Leu Ala Ala Arg His Phe Asn Leu Pro  
 480 485 490

tcc aag acc gag tcc atg ttc atg gcg ggg ggc agc gac tgc ctc atc 1720  
 Ser Lys Thr Glu Ser Met Phe Met Ala Gly Gly Ser Asp Cys Leu Ile  
 495 500 505

gtc ggg gga gga ggc ggc cag gcg ctc tac atc gat ggg gac ctg aac 1768  
 Val Gly Gly Gly Gly Gln Ala Leu Tyr Ile Asp Gly Asp Leu Asn  
 510 515 520

cgg ggc cgc aca agc cac tgc gac acc ttc aac aac cag ccc ctc tgc 1816  
 Arg Gly Arg Thr Ser His Cys Asp Thr Phe Asn Asn Gln Pro Leu Cys  
 525 530 535

tcc gag aac ttc ctc att gct gcc gtg aag gcc tgg ggc ttc cag gac 1864  
 Ser Glu Asn Phe Leu Ile Ala Ala Val Lys Ala Trp Gly Phe Gln Asp  
 540 545 550 555

cct gac acc cag tga cggcctgtgc cacggtgact gagccgtggt ggggcggtgg 1919  
 Pro Asp Thr Gln \*  
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cgaacaagg agtgttcgt 1998

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<400> 386

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 Met Pro Gly Ser Asp Thr Ala Leu Thr Val  
 1 5 10

gac cgg acc tac tcg gac ccc ggc cgg cac cac cgc tgc aag agc cgg 159  
 Asp Arg Thr Tyr Ser Asp Pro Gly Arg His His Arg Cys Lys Ser Arg  
 15 20 25

gta gaa cgt cat gac atg aat acc tta agc ctg ccc ctg aac ata cgc 207  
 Val Glu Arg His Asp Met Asn Thr Leu Ser Leu Pro Leu Asn Ile Arg  
 30 35 40

cga ggg ggg tca gac acc aac ctc aac ttt gat gtc ccg gat ggc atc 255  
 Arg Gly Gly Ser Asp Thr Asn Leu Asn Phe Asp Val Pro Asp Gly Ile  
 45 50 55

ctg gac ttc cac aag gtc aaa ctc act gca gac agc ctg aag caa aaa 303  
 Leu Asp Phe His Lys Val Lys Leu Thr Ala Asp Ser Leu Lys Gln Lys  
 60 65 70

att cta aag gta aca gag cag ata aaa att gag caa aca tcg cgc gat 351  
 Ile Leu Lys Val Thr Glu Gln Ile Lys Ile Glu Gln Thr Ser Arg Asp

75	80	85	90	
ggg aat gtt gcg gag tat ctg aaa cta gtg aac aac gcg gac aag cag				399
Gly Asn Val Ala Glu Tyr Leu Lys Leu Val Asn Asn Ala Asp Lys Gln	95	100	105	
cag gcg gga cgt atc aag caa gtc ttt gag aag aag aat cag aaa tca				447
Gln Ala Gly Arg Ile Lys Gln Val Phe Glu Lys Lys Asn Gln Lys Ser	110	115	120	
gct cac tcc atc gcc cag ctg cag aag aag tta gag cag tat cat cga				495
Ala His Ser Ile Ala Gln Leu Gln Lys Lys Leu Glu Gln Tyr His Arg	125	130	135	
aag ctc aga gag atc gag cag aat gga gcc tct agg agc tca aag gac				543
Lys Leu Arg Glu Ile Glu Gln Asn Gly Ala Ser Arg Ser Ser Lys Asp	140	145	150	
att tcc aaa gac cac ctg aag gat ata cat cgc tct ttg aaa gat gcc				591
Ile Ser Lys Asp His Leu Lys Asp Ile His Arg Ser Leu Lys Asp Ala	155	160	165	170
cac gtg aaa tct cga act gcc ccc cat tgc atg gag agc agc aaa tcg				639
His Val Lys Ser Arg Thr Ala Pro His Cys Met Glu Ser Ser Lys Ser	175	180	185	
ggc atg cca ggg gtc tca ctt act cca cct gtg ttc gtt ttc aat aag				687
Gly Met Pro Gly Val Ser Leu Thr Pro Pro Val Phe Val Phe Asn Lys	190	195	200	
tcc aga gag ttt gcc aac ctg atc cgg aat aag ttt ggc agc gcc gac				735
Ser Arg Glu Phe Ala Asn Leu Ile Arg Asn Lys Phe Gly Ser Ala Asp	205	210	215	
aac att gct cac ttg aaa aat tcc tta gag gag ttt agg cca gag gcg				783
Asn Ile Ala His Leu Lys Asn Ser Leu Glu Glu Phe Arg Pro Glu Ala	220	225	230	
agt gcc agg gcc tac ggg ggc agc gct acc atc gtg aac aaa ccc aag				831
Ser Ala Arg Ala Tyr Gly Gly Ser Ala Thr Ile Val Asn Lys Pro Lys	235	240	245	250
tat ggc agt gat gat gaa tgt tcg agt ggc acg tca ggc tcg gcc gac				879
Tyr Gly Ser Asp Asp Glu Cys Ser Ser Gly Thr Ser Gly Ser Ala Asp	255	260	265	
agt aac gga aac cag tcg ttt ggg gct ggt gga gcc agc aca ctg gac				927
Ser Asn Gly Asn Gln Ser Phe Gly Ala Gly Gly Ala Ser Thr Leu Asp	270	275	280	
agc cag ggc aag ctc gcc gtg atc ctg gag gaa ctg agg gag atc aag				975
Ser Gln Gly Lys Leu Ala Val Ile Leu Glu Glu Leu Arg Glu Ile Lys	285	290	295	
gat acc caa gct cag ctg gct gag gac atc gag gca ctg aag gtg cag				1023
Asp Thr Gln Ala Gln Leu Ala Glu Asp Ile Glu Ala Leu Lys Val Gln	300	305	310	
ttt aag aga gaa tat ggt ttt att tct cag acc ctg caa gag gaa aga				1071
Phe Lys Arg Glu Tyr Gly Phe Ile Ser Gln Thr Leu Gln Glu Glu Arg	315	320	325	330
tac agg tat gag cga ctg gag gac cag ctg cat gac ctg acg gac ctg				1119
Tyr Arg Tyr Glu Arg Leu Glu Asp Gln Leu His Asp Leu Thr Asp Leu				

335	340	345	
cat cag cat gag aca gcc aac ctg aag	cag gag ctg gcc agc att gag		1167
His Gln His Glu Thr Ala Asn Leu Lys	Gln Glu Leu Ala Ser Ile Glu		
350	355	360	
gag aag gtg gcc tac cag gcc tac gag	cgc tcg cgg gac atc cag gaa		1215
Glu Lys Val Ala Tyr Gln Ala Tyr Glu	Arg Ser Arg Asp Ile Gln Glu		
365	370	375	
gcc ttg gaa tcc tgc cag act cgc att	tct aag ctg gag ctc cac cag		1263
Ala Leu Glu Ser Cys Gln Thr Arg Ile	Ser Lys Leu Glu Leu His Gln		
380	385	390	
caa gag cag caa gct ctg cag aca gac	acc gtg aat gct aaa gtt ctc		1311
Gln Glu Gln Gln Ala Leu Gln Thr Asp	Thr Val Asn Ala Lys Val Leu		
395	400	405	410
ctg ggg agg tgc atc aac gtg atc ctg	gcc ttc atg act gtc atc tta		1359
Leu Gly Arg Cys Ile Asn Val Ile Leu	Ala Phe Met Thr Val Ile Leu		
415	420	425	
gtg tgt gtg tcc acc atc gcg aag ttc	gtc tca ccc atg atg aag agt		1407
Val Cys Val Ser Thr Ile Ala Lys Phe	Val Ser Pro Met Met Lys Ser		
430	435	440	
cgc tgc cac att ctt ggc acc ttc ttt	gcc gtg act ctt ctt gct ata		1455
Arg Cys His Ile Leu Gly Thr Phe Phe	Ala Val Thr Leu Leu Ala Ile		
445	450	455	
ttt tgt aaa aac tgg gac cat atc ctg	tgt gcc ata gaa agg atg ata		1503
Phe Cys Lys Asn Trp Asp His Ile Leu	Cys Ala Ile Glu Arg Met Ile		
460	465	470	
ata cca aga tga agc cactgggtcc	tgccctcaag ttctttcaag tttttat		1558
Ile Pro Arg *			
475			
aaagaaaact ctgtgcatac taccaaattt	tacagtgaat gattgtgcgg actcgtgtgt		1618
aagaaaaact aggactgtgt ggtgtaaata	actacaattc tcttaactcg gtagcagttg		1678
ccaactcagt ccttgtaact cgtaaacacg	gatctgtttc agagctctcc taccttgctc		1738
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120	
agggcttgcc ggggtccgga ggttgacctc	gccccgcag ccggccttcg aggetgecte
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1700 1705 1710 1715	
aat gcc ctc tcc agt agt cct gct cca aac atc cag aca ggt cga cct	5418
Asn Ala Leu Ser Ser Ser Pro Ala Pro Asn Ile Gln Thr Gly Arg Pro	
1720 1725 1730	
ttg gtc ctt agc tca cga gcc acc cct gtt cag ctt cct tcc cct cct	5466
Leu Val Leu Ser Ser Arg Ala Thr Pro Val Gln Leu Pro Ser Pro Pro	
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Cys Thr Ser Ser Pro Val Val Pro Ser His Pro Pro Val Gln Gln Val	
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aaa gaa ttg aat cca gat gag gct agc cct cag gtg aac acc tca gca	5562
Lys Glu Leu Asn Pro Asp Glu Ala Ser Pro Gln Val Asn Thr Ser Ala	
1765 1770 1775	
gat cag aac act ctt ccc tct tca cag tca acc aca atg gtt tct ccc	5610
Asp Gln Asn Thr Leu Pro Ser Ser Gln Ser Thr Thr Met Val Ser Pro	
1780 1785 1790 1795	
ctt ttg acc aat agt cca ggg tcc tct ggc aac cgg cga agc cca gtc	5658
Leu Leu Thr Asn Ser Pro Gly Ser Ser Gly Asn Arg Arg Ser Pro Val	
1800 1805 1810	
tcg tct agt aag ggc aaa gga aaa gtg gac aaa att ggc caa att ttg	5706
Ser Ser Ser Lys Gly Lys Gly Lys Val Asp Lys Ile Gly Gln Ile Leu	
1815 1820 1825	
ttg acc aag gca tgt aag aaa gtt aca ggc tct ctt gag aaa ggg gaa	5754
Leu Thr Lys Ala Cys Lys Lys Val Thr Gly Ser Leu Glu Lys Gly Glu	
1830 1835 1840	
gaa caa tat ggt gca gat gga gag act gaa ggc caa ggg cta gac acc	5802
Glu Gln Tyr Gly Ala Asp Gly Glu Thr Glu Gly Gln Gly Leu Asp Thr	
1845 1850 1855	
aca gct ccg ggg ctc atg gga aca gag cag tta tcc aca gag ctg gac	5850
Thr Ala Pro Gly Leu Met Gly Thr Glu Gln Leu Ser Thr Glu Leu Asp	
1860 1865 1870 1875	
agt aaa acc cca acg ccc cca gca ccc act ctg cta aaa atg acc tct	5898
Ser Lys Thr Pro Thr Pro Pro Ala Pro Thr Leu Leu Lys Met Thr Ser	
1880 1885 1890	
agc cct gtg ggc ccg ggc act gcc tca gca gga ccc agc tta cct ggc	5946
Ser Pro Val Gly Pro Gly Thr Ala Ser Ala Gly Pro Ser Leu Pro Gly	
1895 1900 1905	
ggt gct ctc ccc acc agt gta cgc tcg ata gta acc act ctg gta ccc	5994
Gly Ala Leu Pro Thr Ser Val Arg Ser Ile Val Thr Thr Leu Val Pro	
1910 1915 1920	
tcc gag ctc atc tcc gcc gta ccg acc aca aaa agc aat cat ggt ggc	6042
Ser Glu Leu Ile Ser Ala Val Pro Thr Thr Lys Ser Asn His Gly Gly	
1925 1930 1935	
ata gca tct gag tca ctt gcg ggt ggc cta gtg gag gag aag gtg gga	6090
Ile Ala Ser Glu Ser Leu Ala Gly Gly Leu Val Glu Glu Lys Val Gly	
1940 1945 1950 1955	

tcc cat cca gaa ctt cta ccc agc ata gcc ccg tcg cag aat tta gtc	6138
Ser His Pro Glu Leu Leu Pro Ser Ile Ala Pro Ser Gln Asn Leu Val	
1960 1965 1970	
tca aag gaa act tca acc aca gca ctg cag gcc tct gtt gcc aga cca	6186
Ser Lys Glu Thr Ser Thr Thr Ala Leu Gln Ala Ser Val Ala Arg Pro	
1975 1980 1985	
gag ctg gag gta aat gct gcc ata gtc tct gga caa agc agt gag ccc	6234
Glu Leu Glu Val Asn Ala Ala Ile Val Ser Gly Gln Ser Ser Glu Pro	
1990 1995 2000	
aaa gag ata gtt gaa aag tcc aaa atc cca ggc cga aga aac tcc cga	6282
Lys Glu Ile Val Glu Lys Ser Lys Ile Pro Gly Arg Arg Asn Ser Arg	
2005 2010 2015	
act gaa gag cca act gtg gcc tct gaa agt gtg gaa aat gga cat cgt	6330
Thr Glu Glu Pro Thr Val Ala Ser Glu Ser Val Glu Asn Gly His Arg	
2020 2025 2030 2035	
aaa cga tct tct cga cct gct tca gcc tcc agc tct act aaa gac ata	6378
Lys Arg Ser Ser Arg Pro Ala Ser Ala Ser Ser Ser Thr Lys Asp Ile	
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acc agt gcg gtg caa tcc aag cga aga aaa tcc aag taa acaagcagga	6427
Thr Ser Ala Val Gln Ser Lys Arg Arg Lys Ser Lys *	
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Met Arg Leu Lys Ile Gly Phe Ile Leu

1

5

cgc agt ttg ctg gtg gtg gga agc ttc ctg ggg cta gtg gtc ctc tgg	161
Arg Ser Leu Leu Val Val Gly Ser Phe Leu Gly Leu Val Val Leu Trp	
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tct tcc ctg acc ccg cgg ccg gac gac cca agc ccg ctg agc agg atg	209
Ser Ser Leu Thr Pro Arg Pro Asp Asp Pro Ser Pro Leu Ser Arg Met	
30 35 40	
agg gaa gac aga gat gtc aat gac ccc atg ccc aac cga ggc ggc aat	257
Arg Glu Asp Arg Asp Val Asn Asp Pro Met Pro Asn Arg Gly Gly Asn	
45 50 55	
gga cta gct cct ggg gag gac aga ttc aaa cct gtg gta cca tgg cct	305
Gly Leu Ala Pro Gly Glu Asp Arg Phe Lys Pro Val Val Pro Trp Pro	
60 65 70	
cat gtt gaa gga gta gaa gtg gac tta gag tct att aga aga ata aac	353
His Val Glu Gly Val Glu Val Asp Leu Glu Ser Ile Arg Arg Ile Asn	
75 80 85	
aag gcc aaa aat gaa caa gag cac cat gct gga gga gat tcc cag aaa	401
Lys Ala Lys Asn Glu Gln Glu His His Ala Gly Gly Asp Ser Gln Lys	
90 95 100 105	
gat atc atg cag agg cag tat ctc aca ttt aag cct cag aca ttc acc	449
Asp Ile Met Gln Arg Gln Tyr Leu Thr Phe Lys Pro Gln Thr Phe Thr	
110 115 120	
tac cat gat cct gtg ctt cgc cca ggg atc ctc ggt aac ttt gaa ccc	497
Tyr His Asp Pro Val Leu Arg Pro Gly Ile Leu Gly Asn Phe Glu Pro	
125 130 135	
aaa gaa cct gag cct cct gga gtg gtt ggt ggc cct ggg aga gaa agc	545
Lys Glu Pro Glu Pro Pro Gly Val Val Gly Gly Pro Gly Arg Glu Ser	
140 145 150	
caa gcc att ggt ttt ggg gcc cag aat tta aac aag caa ttc aag cca	593
Gln Ala Ile Gly Phe Gly Ala Gln Asn Leu Asn Lys Gln Phe Lys Pro	
155 160 165	
gca ttt aaa gag ttt ggg ttt aac atg gtg gca agt gac atg ttc tca	641
Ala Phe Lys Glu Phe Phe Asn Met Val Ala Ser Asp Met Phe Ser	
170 175 180 185	
ctg gac cgc aac gtc aat gac tta cgc caa gaa gaa tgc aag tat tgg	689
Leu Asp Arg Asn Val Asn Asp Leu Arg Gln Glu Glu Cys Lys Tyr Trp	
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cat tat gat gaa aac ttg ctc act tcg agc gtt gtc att gtc ttc cat	737
His Tyr Asp Glu Asn Leu Leu Thr Ser Ser Val Val Ile Val Phe His	
205 210 215	
aat gaa gga tgg tca acc ctc atg aga aca gtc cac agt gta att aaa	785
Asn Glu Gly Trp Ser Thr Leu Met Arg Thr Val His Ser Val Ile Lys	
220 225 230	
agg act cca agg aaa tat tta gca gaa att gtg tta att gac gat ttc	833
Arg Thr Pro Arg Lys Tyr Leu Ala Glu Ile Val Leu Ile Asp Asp Phe	
235 240 245	
agt aat aaa gaa cac tta aaa gaa aaa ctg gat gaa tat att aag ctg	881

Ser Asn Lys Glu His Leu Lys Glu Lys Leu Asp Glu Tyr Ile Lys Leu	
250 255 260 265	
tgg aat ggc cta gtg aag gta ttt cga aat gaa aga agg gaa ggt tta	929
Trp Asn Gly Leu Val Lys Val Phe Arg Asn Glu Arg Arg Glu Gly Leu	
270 275 280	
att caa gca cga agt att ggt gct cag aag gct aaa ctt gga cag gtt	977
Ile Gln Ala Arg Ser Ile Gly Ala Gln Lys Ala Lys Leu Gly Gln Val	
285 290 295	
ttg ata tac ctt gat gcc cac tgt gag gtg gca gtt aac tgg tat gca	1025
Leu Ile Tyr Leu Asp Ala His Cys Glu Val Ala Val Asn Trp Tyr Ala	
300 305 310	
cca ctt gta gct ccc ata tct aag gac aga acc att tgc act gtg ccg	1073
Pro Leu Val Ala Pro Ile Ser Lys Asp Arg Thr Ile Cys Thr Val Pro	
315 320 325	
ctt ata gat gtc ata aat ggc aac aca tat gaa att ata ccc caa ggg	1121
Leu Ile Asp Val Ile Asn Gly Asn Thr Tyr Glu Ile Ile Pro Gln Gly	
330 335 340 345	
ggg ggt gat gaa gat ggg tat gcc cga gga gca tgg gat tgg agt atg	1169
Gly Gly Asp Glu Asp Gly Tyr Ala Arg Gly Ala Trp Asp Trp Ser Met	
350 355 360	
ctc tgg aaa cgg gtg cct ctg acc cct caa gag aag aga ctg aga aag	1217
Leu Trp Lys Arg Val Pro Leu Thr Pro Gln Glu Lys Arg Leu Arg Lys	
365 370 375	
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Thr Lys Thr Glu Pro Tyr Arg Ser Pro Ala Met Ala Gly Gly Leu Cys	
380 385 390	
gcc att gaa cga gag ttc ttc ttt gaa ttg ggt ctc tat gat cca ggt	1313
Ala Ile Glu Arg Glu Phe Phe Phe Glu Leu Gly Leu Tyr Asp Pro Gly	
395 400 405	
ctc cag att tgg ggt ggt gaa aac ttt gag atc tca tac aag ata tgg	1361
Leu Gln Ile Trp Gly Gly Glu Asn Phe Glu Ile Ser Tyr Lys Ile Trp	
410 415 420 425	
cag tgt ggt ggc aaa tta tta ttt gtt cct tgt tct cgt gtt gga cat	1409
Gln Cys Gly Gly Lys Leu Leu Phe Val Pro Cys Ser Arg Val Gly His	
430 435 440	
atc tac cgt ctt gag ggc tgg caa gga aat cct ccg ccc att tat gtt	1457
Ile Tyr Arg Leu Glu Gly Trp Gln Gly Asn Pro Pro Pro Ile Tyr Val	
445 450 455	
ggg tct tct cca act ctg aag aat tat gtt aga gtt gtg gag gtt tgg	1505
Gly Ser Ser Pro Thr Leu Lys Asn Tyr Val Arg Val Val Glu Val Trp	
460 465 470	
tgg gat gaa tat aaa gac tac ttc tat gct agt cgt cct gaa tcg cag	1553
Trp Asp Glu Tyr Lys Asp Tyr Phe Tyr Ala Ser Arg Pro Glu Ser Gln	
475 480 485	
gca tta cca tat ggg gat ata tcg gag ctg aaa aaa ttt cga gaa gat	1601
Ala Leu Pro Tyr Gly Asp Ile Ser Glu Leu Lys Lys Phe Arg Glu Asp	
490 495 500 505	
cac aac tgc aaa agt ttt aag tgg ttc atg gaa gaa ata gct tat gat	1649

His	Asn	Cys	Lys	Ser	Phe	Lys	Trp	Phe	Met	Glu	Glu	Ile	Ala	Tyr	Asp		
				510					515						520		
atc	acc	tca	cac	tac	cct	ttg	cca	ccc	aaa	aat	gtt	gac	tgg	gga	gaa	1697	
Ile	Thr	Ser	His	Tyr	Pro	Leu	Pro	Pro	Lys	Asn	Val	Asp	Trp	Gly	Glu		
			525					530					535				
atc	aga	ggc	ttc	gaa	act	gct	tac	tgc	att	gat	agc	atg	gga	aaa	aca	1745	
Ile	Arg	Gly	Phe	Glu	Thr	Ala	Tyr	Cys	Ile	Asp	Ser	Met	Gly	Lys	Thr		
		540					545					550					
aat	gga	ggc	ttt	gtt	gaa	cta	gga	ccc	tgc	cac	agg	atg	gga	ggg	aat	1793	
Asn	Gly	Gly	Phe	Val	Glu	Leu	Gly	Pro	Cys	His	Arg	Met	Gly	Gly	Asn		
	555					560					565						
cag	ctt	ttc	aga	atc	aat	gaa	gca	aat	caa	ctc	atg	cag	tat	gac	cag	1841	
Gln	Leu	Phe	Arg	Ile	Asn	Glu	Ala	Asn	Gln	Leu	Met	Gln	Tyr	Asp	Gln		
570					575					580					585		
tgt	ttg	aca	aag	gga	gct	gat	gga	tca	aaa	gtt	atg	att	aca	cac	tgt	1889	
Cys	Leu	Thr	Lys	Gly	Ala	Asp	Gly	Ser	Lys	Val	Met	Ile	Thr	His	Cys		
			590					595					600				
aat	cta	aat	gaa	ttt	aag	gaa	tgg	cag	tac	ttc	aag	aac	ctg	cac	aga	1937	
Asn	Leu	Asn	Glu	Phe	Lys	Glu	Trp	Gln	Tyr	Phe	Lys	Asn	Leu	His	Arg		
			605					610					615				
ttt	act	cat	att	cct	tca	gga	aag	tgt	tta	gat	cgc	tca	gag	gtc	ctg	1985	
Phe	Thr	His	Ile	Pro	Ser	Gly	Lys	Cys	Leu	Asp	Arg	Ser	Glu	Val	Leu		
		620					625					630					
cat	caa	gta	ttc	atc	tcc	aat	tgt	gac	tcc	agt	aaa	acg	act	caa	aaa	2033	
His	Gln	Val	Phe	Ile	Ser	Asn	Cys	Asp	Ser	Ser	Lys	Thr	Thr	Gln	Lys		
	635					640					645						
tgg	gaa	atg	aat	aac	atc	cat	agt	gtt	tag	a	gagaaaaaaaa	taaaccaata				2084	
Trp	Glu	Met	Asn	Asn	Ile	His	Ser	Val	*								
650						655											
acctacctac	tgacaagtaa	atttatacag	gactgaaaac	cgcttgaaac	ctgctgcaac											2144	
tattgttatt	aactctgtat	agctccaaac	ctggaacctc	ctgatcagtt	tgaaggacat											2204	
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990

atc atg tgg tgg gaa agc ttg ctt ctc tta aca gct tat ttt tgc tat	1083
Ile Met Trp Trp Glu Ser Leu Leu Leu Leu Thr Ala Tyr Phe Cys Tyr	
220 225 230	
gtg gtt ttc atg aaa ttc aac gtc caa gta gaa aaa tgg gtg aag caa	1131
Val Val Phe Met Lys Phe Asn Val Gln Val Glu Lys Trp Val Lys Gln	
235 240 245	
atg ata aac cgc aat aag gtc gtc aag gtg aca gca cca gaa gcc caa	1179
Met Ile Asn Arg Asn Lys Val Val Lys Val Thr Ala Pro Glu Ala Gln	
250 255 260 265	
gca aag cca tct gca gcc agg gac aag gat gaa cca act cta ccg gct	1227
Ala Lys Pro Ser Ala Ala Arg Asp Lys Asp Glu Pro Thr Leu Pro Ala	
270 275 280	
aag ccg cgt ctc cag cga ggt gga agc tct gcc tcc ctc cac aac agt	1275
Lys Pro Arg Leu Gln Arg Gly Gly Ser Ser Ala Ser Leu His Asn Ser	
285 290 295	
ctc atg agg aat agc atc ttc caa ctc atg ata cac acc ctt gac cca	1323
Leu Met Arg Asn Ser Ile Phe Gln Leu Met Ile His Thr Leu Asp Pro	
300 305 310	
ctc gcc gaa gaa ctt gga tca tat gga aaa cta aaa tat tat gac aca	1371
Leu Ala Glu Glu Leu Gly Ser Tyr Gly Lys Leu Lys Tyr Tyr Asp Thr	
315 320 325	
atg act gaa gaa ggg agg ttc aga gaa aag gct tca att ctc cac aag	1419
Met Thr Glu Glu Gly Arg Phe Arg Glu Lys Ala Ser Ile Leu His Lys	
330 335 340 345	
atc gcc aag aag aaa tgt cat gtg gat gag aac gag cgg cag aat ggg	1467
Ile Ala Lys Lys Lys Cys His Val Asp Glu Asn Glu Arg Gln Asn Gly	
350 355 360	
gct gcc aac cac gtg gaa aaa att gag ctt cca aac agc acc agc aca	1515
Ala Ala Asn His Val Glu Lys Ile Glu Leu Pro Asn Ser Thr Ser Thr	
365 370 375	
gat gtt gaa atg aca cca tcc agt gat gct tca gaa cct gta caa aat	1563
Asp Val Glu Met Thr Pro Ser Ser Asp Ala Ser Glu Pro Val Gln Asn	
380 385 390	
gga aat ctc tcc cac aac att gaa ggt gca gaa gcc cag acc gct gat	1611
Gly Asn Leu Ser His Asn Ile Glu Gly Ala Glu Ala Gln Thr Ala Asp	
395 400 405	
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Glu Glu Glu Asp Gln Pro Leu Ser Leu Ala Trp Pro Ser Glu Thr Arg	
410 415 420 425	
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Lys Gln Val Thr Phe Leu Ile Val Phe Pro Ile Val Phe Pro Leu Trp	
430 435 440	
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Ile Thr Leu Pro Asp Val Arg Lys Pro Ser Ser Arg Lys Phe Phe Pro	
445 450 455	
atc acg ttc ttt ggc tcc att acc tgg att gca gta ttc tct tac ttg	1803
Ile Thr Phe Phe Gly Ser Ile Thr Trp Ile Ala Val Phe Ser Tyr Leu	
460 465 470	

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Met Val Trp Trp Ala His Gln Val Gly Glu Thr Ile Gly Ile Ser Glu
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gag att atg ggc ctg acc atc ttg gct gct ggg acc tcc atc cct gat      1899
Glu Ile Met Gly Leu Thr Ile Leu Ala Ala Gly Thr Ser Ile Pro Asp
490                      495                      500                      505

ctt atc acc agt gtc ata gtg gcc cgg aag ggg cta ggg gac atg gct      1947
Leu Ile Thr Ser Val Ile Val Ala Arg Lys Gly Leu Gly Asp Met Ala
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gtg tcc agc tct gtt gga agc aac att ttt gac atc act gta ggg ctc      1995
Val Ser Ser Ser Val Gly Ser Asn Ile Phe Asp Ile Thr Val Gly Leu
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cca ctg ccc tgg ctc ctg tac acc gtc att cac aga ttc cag cca gtg      2043
Pro Leu Pro Trp Leu Leu Tyr Thr Val Ile His Arg Phe Gln Pro Val
      540                      545                      550

gct gtc agc agc aat ggc ctt ttc tgt gcc atc gtc ctt ctc ttc atc      2091
Ala Val Ser Ser Asn Gly Leu Phe Cys Ala Ile Val Leu Leu Phe Ile
555                      560                      565

atg ctg ctc ttc gtc atc ctc tct atc gcc ctc tgc aag tgg cga atg      2139
Met Leu Leu Phe Val Ile Leu Ser Ile Ala Leu Cys Lys Trp Arg Met
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aac aaa atc ctg ggc ttc atc atg ttt ggc ctc tac ttt gtg ttc ctg      2187
Asn Lys Ile Leu Gly Phe Ile Met Phe Gly Leu Tyr Phe Val Phe Leu
      590                      595                      600

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Val Val Ser Val Leu Leu Glu Asp Arg Ile Leu Thr Cys Pro Val Ser
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Ile *

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agtgtccctc cttggtgaat ttgaggagag atggattcac actgggcca ttcacttcac      2411

aggctgcttc caccctgect actgaaatga cttcatgtaa aagacaaaga gaaccgtcaa      2471

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	atg gtc Met Val 1
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Ile Gly Ser Thr Val Ile Leu Ser Cys Ala Leu Thr Gly Ser Pro Glu	
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ttc acc atc cgc tgg tat cgc aac acg gag ctg gtg ctg cct gac gag	739
Phe Thr Ile Arg Trp Tyr Arg Asn Thr Glu Leu Val Leu Pro Asp Glu	
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Ala Ile Ser Ile Arg Gly Leu Ser Asn Glu Thr Leu Leu Ile Thr Ser	
55 60 65	
gcc cag aag agc cat tcc ggg gcc tac cag tgc ttc gct acc cgc aag	835
Ala Gln Lys Ser His Ser Gly Ala Tyr Gln Cys Phe Ala Thr Arg Lys	
70 75 80	
gcc cag acc gcc cag gac ttt gcc atc att gca ctt gag gat ggc acg	883
Ala Gln Thr Ala Gln Asp Phe Ala Ile Ile Ala Leu Glu Asp Gly Thr	
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ccc cgc atc gtc tcg tcc ttc agc gag aag gtg gtc aac ccc ggg gag	931
Pro Arg Ile Val Ser Ser Phe Ser Glu Lys Val Val Asn Pro Gly Glu	
100 105 110	
cag ttc tca ctg atg tgt gcg gcc aag ggc gcc ccg ccc ccc acg gtc	979
Gln Phe Ser Leu Met Cys Ala Ala Lys Gly Ala Pro Pro Pro Thr Val	
115 120 125 130	
acc tgg gcc ctc gac gat gag ccc atc gtg cgg gat ggc agc cac cgc	1027
Thr Trp Ala Leu Asp Asp Glu Pro Ile Val Arg Asp Gly Ser His Arg	
135 140 145	
acc aac cag tac acc atg tcg gac ggc acc acc atc agc cac atg aac	1075
Thr Asn Gln Tyr Thr Met Ser Asp Gly Thr Thr Ile Ser His Met Asn	
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Val Thr Gly Pro Gln Ile Arg Asp Gly Gly Val Tyr Arg Cys Thr Ala	
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cgg aac ttg gtg ggc agt gct gaa tat cag gcg cga ata aac gta aga	1171

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Gly	Pro	Pro	Ser	Ile	Arg	Ala	Met	Arg	Asn	Ile	Thr	Ala	Val	Ala	Gly		
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cgg	gac	acc	ctt	atc	aac	tgc	agg	gtc	atc	ggc	tat	ccc	tac	tac	tcc	1267	
Arg	Asp	Thr	Leu	Ile	Asn	Cys	Arg	Val	Ile	Gly	Tyr	Pro	Tyr	Tyr	Ser		
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Ile	Lys	Trp	Tyr	Lys	Asp	Ala	Leu	Leu	Leu	Pro	Asp	Asn	His	Arg	Gln		
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Val	Val	Phe	Glu	Asn	Gly	Thr	Leu	Lys	Leu	Thr	Asp	Val	Gln	Lys	Gly		
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Met	Asp	Glu	Gly	Glu	Tyr	Leu	Cys	Ser	Val	Leu	Ile	Gln	Pro	Gln	Leu		
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Ser	Ile	Ser	Gln	Ser	Val	His	Val	Ala	Val	Lys	Val	Pro	Pro	Leu	Ile		
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Gln	Pro	Phe	Glu	Phe	Pro	Pro	Ala	Ser	Ile	Gly	Gln	Leu	Leu	Tyr	Ile		
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Pro	Cys	Val	Val	Ser	Ser	Gly	Asp	Met	Pro	Ile	Arg	Ile	Thr	Trp	Arg		
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Lys	Asp	Gly	Gln	Val	Ile	Ile	Ser	Gly	Ser	Gly	Val	Thr	Ile	Glu	Ser		
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Lys	Glu	Phe	Met	Ser	Ser	Leu	Gln	Ile	Ser	Ser	Val	Ser	Leu	Lys	His		
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Asn	Gly	Asn	Tyr	Thr	Cys	Ile	Ala	Ser	Asn	Ala	Ala	Ala	Thr	Val	Ser		
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cgg	gag	cgc	cag	ctc	atc	gtg	cgt	gtg	ccc	cct	cga	ttt	gtg	gtg	caa	1747	
Arg	Glu	Arg	Gln	Leu	Ile	Val	Arg	Val	Pro	Pro	Arg	Phe	Val	Val	Gln		
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ccc	aac	aac	cag	gat	ggc	atc	tac	ggc	aaa	gct	ggt	gtg	ctc	aac	tgc	1795	
Pro	Asn	Asn	Gln	Asp	Gly	Ile	Tyr	Gly	Lys	Ala	Gly	Val	Leu	Asn	Cys		
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Ser	Val	Asp	Gly	Tyr	Pro	Pro	Pro	Lys	Val	Met	Trp	Lys	His	Ala	Lys		
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Asn	Gly	Val	Ile	Arg	Gly	Tyr	Gln	Ile	Gly	Tyr	Arg	Glu	Asn	Ser	Pro	
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Gly	Ser	Asn	Gly	Gln	Tyr	Ser	Ile	Val	Glu	Met	Lys	Ala	Thr	Gly	Asp	
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Ser	Glu	Val	Tyr	Thr	Leu	Asp	Asn	Leu	Lys	Lys	Phe	Ala	Gln	Tyr	Gly	
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Val	Val	Val	Gln	Ala	Phe	Asn	Arg	Ala	Gly	Thr	Gly	Pro	Ser	Ser	Ser	
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gag	atc	aat	gcc	acc	act	ctg	gag	gat	gtg	ccc	agc	cag	ccc	cct	gag	2947
Glu	Ile	Asn	Ala	Thr	Thr	Leu	Glu	Asp	Val	Pro	Ser	Gln	Pro	Pro	Glu	
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Ser	Glu	Pro	Pro	Arg	Ser	Thr	Leu	Asn	Gly	Val	Leu	Lys	Gly	Tyr	Arg	
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Val	Ile	Phe	Trp	Ser	Leu	Tyr	Val	Asp	Gly	Glu	Trp	Gly	Glu	Met	Gln	
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Asn	Ile	Thr	Thr	Thr	Arg	Glu	Arg	Val	Glu	Leu	Arg	Gly	Met	Glu	Lys	
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Gly	Val	Arg	Ser	Ser	Val	Leu	Tyr	Ile	Gln	Thr	Lys	Glu	Asp	Val	Pro	
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Tyr	Thr	Ile	Phe	Cys	Ser	Ser	Pro	Gly	Ser	Gly	Gln	Pro	Ala	Pro	Ser	
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Glu	Tyr	Glu	Thr	Ser	Pro	Glu	Gln	Leu	Phe	Tyr	Arg	Ile	Ala	His	Leu	
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Asn Arg Gly Gln Gln Tyr Leu Leu Trp Val Ala Ala Val Thr Ser Ala	
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Gly Arg Gly Asn Ser Ser Glu Lys Val Thr Ile Glu Pro Ala Gly Lys	
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Ala Pro Ala Lys Ile Ile Ser Phe Gly Gly Thr Val Thr Thr Pro Trp	
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Met Lys Asp Val Arg Leu Pro Cys Asn Ser Val Gly Asp Pro Ala Pro	
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Ala Val Lys Trp Thr Lys Asp Ser Glu Asp Ser Ala Ile Pro Val Ser	
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Met Asp Gly His Arg Leu Ile His Thr Asn Gly Thr Leu Leu Leu Arg	
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Thr Gly Gly Phe Asp Thr Ile Ile Val Asn Leu Leu Val Gln Val Pro	
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Pro Asp Gln Pro Arg Leu Thr Val Ser Lys Thr Ser Ala Ser Ser Ile	
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Thr Leu Thr Trp Ile Pro Gly Asp Asn Gly Gly Ser Ser Ile Arg Gly	
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Gly Arg Ile Ser Glu Ile Ile Glu Ala Lys Thr His Gly Arg Glu Pro	
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Ser Phe Ser Lys Asp Gln His Leu Phe Thr His Ile Asn Ser Thr His	
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His Ile Asp Ile Pro Arg Val Gln Leu Leu Ile Glu Asp Lys Glu Gly	
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Ile Lys Gln Leu Gly Asp Asp Lys Ala Thr Ile Pro Val Thr Asp Ala	
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Leu His His Pro Thr Leu Ile Gln Ser Thr Gly Pro Leu Ile Asp Met	
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Met Pro Ala Pro Pro Ala Gly Thr Ala Pro Pro Ala Pro Gly Pro Thr	
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 Trp Met Ser Ser Ser Met Glu Pro Ile Thr Gln Asp Lys Arg Val Ser  
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 cag ggc cat aac gga gac cta tac ttc tcc aac gtg atg ctg cag gac 512  
 Gln Gly His Asn Gly Asp Leu Tyr Phe Ser Asn Val Met Leu Gln Asp  
 100 105 110 115  
 atg cag acc gac tac agt tgt aac gcc cgc ttc cac ttc acc cac acc 560  
 Met Gln Thr Asp Tyr Ser Cys Asn Ala Arg Phe His Phe Thr His Thr  
 120 125 130  
 atc cag cag aag aac cct ttc acc ctc aag gtc ctc acc acc cga gga 608  
 Ile Gln Gln Lys Asn Pro Phe Thr Leu Lys Val Leu Thr Thr Arg Gly  
 135 140 145



gtt gca gaa aga aca cca agc ttc atg tat ccc cag ggc acc gcg agc	656
Val Ala Glu Arg Thr Pro Ser Phe Met Tyr Pro Gln Gly Thr Ala Ser	
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Ser Gln Met Val Leu Arg Gly Met Asp Leu Leu Glu Cys Ile Ala	
165 170 175	
tcc ggg gtc cca aca cca gac atc gca tgg tac aag aaa ggt ggg gac	752
Ser Gly Val Pro Thr Pro Asp Ile Ala Trp Tyr Lys Lys Gly Gly Asp	
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ctc cca tct gat aag gcc aag ttt gag aac ttt aat aag gcc ctg cgt	800
Leu Pro Ser Asp Lys Ala Lys Phe Glu Asn Phe Asn Lys Ala Leu Arg	
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Ile Thr Asn Val Ser Glu Glu Asp Ser Gly Glu Tyr Phe Cys Leu Ala	
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Ser Asn Lys Met Gly Ser Ile Arg His Thr Ile Ser Val Arg Val Lys	
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Ala Ala Pro Tyr Trp Leu Asp Glu Pro Lys Asn Leu Ile Leu Ala Pro	
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Gly Glu Asp Gly Arg Leu Val Cys Arg Ala Asn Gly Asn Pro Lys Pro	
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Thr Val Gln Trp Met Val Asn Gly Glu Pro Leu Gln Ser Ala Pro Pro	
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Asn Pro Asn Arg Glu Val Ala Gly Asp Thr Ile Ile Phe Arg Asp Thr	
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Gln Ile Ser Ser Arg Ala Val Tyr Gln Cys Asn Thr Ser Asn Glu His	
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Gly Tyr Leu Leu Ala Asn Ala Phe Val Ser Val Leu Asp Val Pro Pro	
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Arg Trp Phe Lys Asn Gly Gln Gly Ser Asn Leu Asp Gly Gly Asn Tyr	
375 380 385	
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His Val Tyr Glu Asn Gly Ser Leu Glu Ile Lys Met Ile Arg Lys Glu	
390 395 400	

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cga gcc tac tac tgg agg gag agc agc ttg ctg aag aac ctg tgg gtg Arg Ala Tyr Tyr Trp Arg Glu Ser Ser Leu Leu Lys Asn Leu Trp Val 760 765 770	2480
tct cag aag aga cag caa gcc agc ttc cct ggt gac cgc ctc cgt ggc Ser Gln Lys Arg Gln Gln Ala Ser Phe Pro Gly Asp Arg Leu Arg Gly 775 780 785	2528
gtg gtg tcc cgc ctc ttc ccc tac agt aac tac aag ctg gag atg gtt Val Val Ser Arg Leu Phe Pro Tyr Ser Asn Tyr Lys Leu Glu Met Val 790 795 800	2576
gtg gtc aat ggg aga ggt gat ggg cct cgc agt gag acc aag gag ttc Val Val Asn Gly Arg Gly Asp Gly Pro Arg Ser Glu Thr Lys Glu Phe 805 810 815	2624
acc acc ccg gaa gga gta ccc agt gcc cct agg cgt ttc cga gtc cgg Thr Thr Pro Glu Gly Val Pro Ser Ala Pro Arg Arg Phe Arg Val Arg 820 825 830 835	2672
cag ccc aac ctg gag aca atc aac ctg gaa tgg gat cat cct gag cat Gln Pro Asn Leu Glu Thr Ile Asn Leu Glu Trp Asp His Pro Glu His 840 845 850	2720
cca aat ggg atc atg att gga tac act ctc aaa tat gtg gcc ttt aac Pro Asn Gly Ile Met Ile Gly Tyr Thr Leu Lys Tyr Val Ala Phe Asn 855 860 865	2768
ggg acc aaa gta gga aag cag ata gtg gaa aac ttc tct ccc aat cag Gly Thr Lys Val Gly Lys Gln Ile Val Glu Asn Phe Ser Pro Asn Gln 870 875 880	2816
acc aag ttc acg gtg caa aga acg gac ccc gtg tca cgc tac cgc ttt Thr Lys Phe Thr Val Gln Arg Thr Asp Pro Val Ser Arg Tyr Arg Phe 885 890 895	2864
acc ctc agc gcc agg acg cag gtg ggc tct ggg gaa gcc gtc aca gag Thr Leu Ser Ala Arg Thr Gln Val Gly Ser Gly Glu Ala Val Thr Glu 900 905 910 915	2912

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Gly Val Lys Gly Pro Ser *	
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Ser Gln Met Val Leu Arg Gly Met Asp Leu Leu Leu Glu Cys Ile Ala	
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Ser Gly Val Pro Thr Pro Asp Ile Ala Trp Tyr Lys Lys Gly Gly Asp	
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Leu Pro Ser Asp Lys Ala Lys Phe Glu Asn Phe Asn Lys Ala Leu Arg	
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Ile Thr Asn Val Ser Glu Glu Asp Ser Gly Glu Tyr Phe Cys Leu Ala	
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Ser Asn Lys Met Gly Ser Ile Arg His Thr Ile Ser Val Arg Val Lys	
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Asn Pro Asn Arg Glu Val Ala Gly Asp Thr Ile Ile Phe Arg Asp Thr	
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Gln Ile Ser Ser Arg Ala Val Tyr Gln Cys Asn Thr Ser Asn Glu His	
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Gly Tyr Leu Leu Ala Asn Ala Phe Val Ser Val Leu Asp Val Pro Pro	
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His Val Tyr Glu Asn Gly Ser Leu Glu Ile Lys Met Ile Arg Lys Glu	
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Cys Arg Val Lys His Asp Pro Ser Leu Lys Leu Thr Val Ser Trp Leu	
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Leu Ser Ala Arg Thr Gln Val Gly Ser Gly Glu Ala Val Thr Glu Glu	
920 925 930	



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Val Lys Gly Pro Ser *	
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ccgcctctaa agagagcaat cactacaatt atg gct ggg att ttg cgc tta 171
Met Ala Gly Ile Leu Arg Leu
1 5

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gta gtt caa tgg ccc cca ggc aga cta cag acc gtg aca aaa ggt gtg      219
Val Val Gln Trp Pro Pro Gly Arg Leu Gln Thr Val Thr Lys Gly Val
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gag tct ctt att tgt aca gat tgg att cgt cac aaa ttc acc aga tca      267
Glu Ser Leu Ile Cys Thr Asp Trp Ile Arg His Lys Phe Thr Arg Ser
      25                      30                      35

aga att cca gaa aaa gtg ttt cag gcc tca cct gaa gat cat gaa aaa      315
Arg Ile Pro Glu Lys Val Phe Gln Ala Ser Pro Glu Asp His Glu Lys
      40                      45                      50                      55

tac ggt ggg gat cca cag aac cct cat aaa ctg cat att gtt acc aga      363
Tyr Gly Gly Asp Pro Gln Asn Pro His Lys Leu His Ile Val Thr Arg
      60                      65                      70

ata aaa agt aca aga aga cgt cca tat tgg gaa aaa gat ata ata aag      411
Ile Lys Ser Thr Arg Arg Arg Pro Tyr Trp Glu Lys Asp Ile Ile Lys
      75                      80                      85

atg ctt gga tta gaa aaa gca cat acc cct caa gtt cac aag aat atc      459
Met Leu Gly Leu Glu Lys Ala His Thr Pro Gln Val His Lys Asn Ile
      90                      95                      100

cct tca gtg aat gca aaa ttg aaa gta gtt aag cat ttg ata aga atc      507
Pro Ser Val Asn Ala Lys Leu Lys Val Val Lys His Leu Ile Arg Ile
      105                      110                      115

aag ccc ttg aag ttg cca caa gga ctt cca aca gag gag aac atg tct      555
Lys Pro Leu Lys Leu Pro Gln Gly Leu Pro Thr Glu Glu Asn Met Ser
      120                      125                      130                      135

aac acg tgc ctc aaa agc act ggg gag tta gta gtg cag tgg cat ctg      603
Asn Thr Cys Leu Lys Ser Thr Gly Glu Leu Val Val Gln Trp His Leu
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Lys Pro Val Glu Gln Lys Ala His Glu Ser *
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agaacctctg cattctagtt accctttgct tcccttcacc tcttgtaaaa tttggcttgg      834

caacaatgac attgtcatgc ttattgtccc aatatccatc ctgtcgtaga tottaatgtt      894

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 Met Pro Glu Glu Lys Asp Cys Gly Gly Gly Asp Ala  
 1 5 10  
 ctc tcc aat ggc atc aag aaa cac aga aca agt ttg cct tct cct atg 157  
 Leu Ser Asn Gly Ile Lys Lys His Arg Thr Ser Leu Pro Ser Pro Met  
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 Phe Ser Arg Asn Asp Phe Ser Ile Trp Ser Ile Leu Arg Lys Cys Ile  
 30 35 40  
 gga atg gaa cta tcc aag atc acg atg cca gtt ata ttt aat gag cct 253  
 Gly Met Glu Leu Ser Lys Ile Thr Met Pro Val Ile Phe Asn Glu Pro  
 45 50 55 60  
 ctg agc ttc cta cag cgc cta act gaa tac atg gag cat act tac ctc 301  
 Leu Ser Phe Leu Gln Arg Leu Thr Glu Tyr Met Glu His Thr Tyr Leu  
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 atc cac aag gcc agt tca ctc tct gat cct gtg gaa agg atg cag tgt 349  
 Ile His Lys Ala Ser Ser Leu Ser Asp Pro Val Glu Arg Met Gln Cys  
 80 85 90  
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 Val Ala Ala Phe Ala Val Ser Ala Val Ala Ser Gln Trp Glu Arg Thr  
 95 100 105  
 gga aaa cct ttc aac cca ctg ctg gga gag act tat gaa tta gtg cga 445  
 Gly Lys Pro Phe Asn Pro Leu Leu Gly Glu Thr Tyr Glu Leu Val Arg  
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 gat gac ctt gga ttt aga ctc atc tcc gaa cag gtc agc cat cac cca 493  
 Asp Asp Leu Gly Phe Arg Leu Ile Ser Glu Gln Val Ser His His Pro  
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 cca atc agt gca ttt cat gct gaa gga tta aac aat gac ttc atc ttt 541  
 Pro Ile Ser Ala Phe His Ala Glu Gly Leu Asn Asn Asp Phe Ile Phe  
 145 150 155  
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 His Gly Ser Ile Tyr Pro Lys Leu Lys Phe Trp Gly Lys Ser Val Glu  
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 Ala Glu Pro Lys Gly Thr Ile Thr Leu Glu Leu Leu Glu His Asn Glu  
 175 180 185  
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 Ala Tyr Thr Trp Thr Asn Pro Thr Cys Cys Val His Asn Ile Ile Val  
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 Gly Lys Leu Trp Ile Glu Gln Tyr Gly Asn Val Glu Ile Ile Asn His  
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 Lys Thr Gly Asp Lys Cys Val Leu Asn Phe Lys Pro Cys Gly Leu Phe  
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Gly Lys Glu Leu His Lys Val Glu Gly Tyr Ile Gln Asp Lys Ser Lys	
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Lys Lys Leu Cys Ala Leu Tyr Gly Lys Trp Thr Glu Cys Leu Tyr Ser	
255 260 265	
gtt gac cct gcc acg ttt gac gct tac aaa aaa aat gat aag aaa aat	925
Val Asp Pro Ala Thr Phe Asp Ala Tyr Lys Lys Asn Asp Lys Lys Asn	
270 275 280	
aca gaa gag aag aag aac agc aaa cag atg agc acc tct gag gag ttg	973
Thr Glu Glu Lys Lys Asn Ser Lys Gln Met Ser Thr Ser Glu Glu Leu	
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gat gaa atg cca gtg ccg gat tct gaa agt gta ttc att atc cct gga	1021
Asp Glu Met Pro Val Pro Asp Ser Glu Ser Val Phe Ile Ile Pro Gly	
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Ser Val Leu Leu Trp Arg Ile Ala Pro Arg Pro Pro Asn Ser Ala Gln	
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Met Tyr Asn Phe Thr Ser Phe Ala Met Val Leu Asn Glu Val Asp Lys	
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gac atg gag agt gtg att ccc aag aca gac tgc agg tta cgg cct gac	1165
Asp Met Glu Ser Val Ile Pro Lys Thr Asp Cys Arg Leu Arg Pro Asp	
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Ile Arg Ala Met Glu Asn Gly Glu Ile Asp Gln Ala Ser Glu Glu Lys	
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Lys Arg Leu Glu Glu Lys Gln Arg Ala Ala Arg Lys Asn Arg Ser Lys	
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Ser Glu Glu Asp Trp Lys Thr Arg Trp Phe His Gln Gly Pro Asn Pro	
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 tcc ctt agt cga atc aag agc aac gtg gat ggg cgg tac ctg gtg gac 96  
 Ser Leu Ser Arg Ile Lys Ser Asn Val Asp Gly Arg Tyr Leu Val Asp  
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 ggc gtc cct ttc agc tgc tgc aat cct agc tcg cca cgg ccc tgc atc 144  
 Gly Val Pro Phe Ser Cys Cys Asn Pro Ser Ser Pro Arg Pro Cys Ile  
 35 40 45  
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 Gln Tyr Gln Ile Thr Asn Asn Ser Ala His Tyr Ser Tyr Asp His Gln  
 50 55 60  
 acg gag gag ctc aac ctg tgg gtg cgt ggc tgc agg gct gcc ctg ctg 240  
 Thr Glu Glu Leu Asn Leu Trp Val Arg Gly Cys Arg Ala Ala Leu Leu  
 65 70 75 80  
 agc tac tac agc agc ctc atg aac tcc atg ggt gtc gtc acg ctc ctc 288  
 Ser Tyr Tyr Ser Ser Leu Met Asn Ser Met Gly Val Val Thr Leu Leu  
 85 90 95  
 att tgg ctc ttc gag gtg acc att aca att ggg ctg cgc tac cta cag 336  
 Ile Trp Leu Phe Glu Val Thr Ile Thr Ile Gly Leu Arg Tyr Leu Gln  
 100 105 110  
 acg tcg ctg gat ggt gtg tcc aac ccc gag gaa tct gag agc gag agc 384  
 Thr Ser Leu Asp Gly Val Ser Asn Pro Glu Glu Ser Glu Ser Glu Ser  
 115 120 125  
 gag ggc tgg ctg ctg gag aag agc gtg ccg gag acc tgg aag gcc ttt 432  
 Glu Gly Trp Leu Leu Glu Lys Ser Val Pro Glu Thr Trp Lys Ala Phe  
 130 135 140  
 ctg gag agt gtg aag aag ctg ggc aag ggc aac cag gtg act gtg gct 480  
 Leu Glu Ser Val Lys Lys Leu Gly Lys Gly Asn Gln Val Thr Val Ala  
 145 150 155 160  
 att aac aaa aac atc agc tct gac cct ttg cca aga gca gtg gac aat 528  
 Ile Asn Lys Asn Ile Ser Ser Asp Pro Leu Pro Arg Ala Val Asp Asn  
 165 170 175  
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 Glu Phe Glu Thr Val Ala Thr Gln Leu Leu Lys Arg Thr Gln Ala Met  
 180 185 190  
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 Leu Asn Lys Tyr Arg Cys Leu Leu Leu Glu Asp Ala Met Arg Ile Asn  
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 Pro Ser Ala Glu Met Val Met Ile Asp Arg Met Phe Asn Gln Glu Glu

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Gly Phe Gln Ala Asp Phe Cys Cys Ser Phe Lys Leu Asp Lys Ala Ala			
245	250	255	
cat gag aca cag ttt ggc cgg agt gac cag cat ggc agt aaa gca agc			816
His Glu Thr Gln Phe Gly Arg Ser Asp Gln His Gly Ser Lys Ala Ser			
260	265	270	
agc tct ctg caa ccg cca gcc aag gcc caa ggc aga gac cga gcc aaa			864
Ser Ser Leu Gln Pro Pro Ala Lys Ala Gln Gly Arg Asp Arg Ala Lys			
275	280	285	
acc ggt gtg acg gaa ccc atg aat cat gac cag ttt cat cta gtg cct			912
Thr Gly Val Thr Glu Pro Met Asn His Asp Gln Phe His Leu Val Pro			
290	295	300	
aat cac atc gtg gtc tct gca gaa gga aac att tct aaa aaa aca gaa			960
Asn His Ile Val Val Ser Ala Glu Gly Asn Ile Ser Lys Lys Thr Glu			
305	310	315	320
tgc ctt ggc aga gca ctg aaa ttt gac aaa gtg ggc tta gtg cag tac			1008
Cys Leu Gly Arg Ala Leu Lys Phe Asp Lys Val Gly Leu Val Gln Tyr			
325	330	335	
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Gln Ser Thr Ser Glu Glu Lys Ala Ser Arg Arg Glu Pro Leu Lys Ala			
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Ser Asp His Gly Thr Glu Ser Lys Leu Ser Ser Ile Leu Ala Asp Ser			
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Asn Ser Pro Lys Asn Glu Val Leu His Thr Asp Ile Met Lys Gly Ser			
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Gly Glu Pro Gln Pro Asp Leu Gln Leu Thr Lys Ser Leu Glu Thr Thr			
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Phe Lys Asn Ile Leu Glu Leu Lys Lys Ala Gly Arg Gln Pro Gln Ser			
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Asp Pro Thr Val Ser Gly Ser Val Glu Leu Asp Phe Pro Asn Phe Ser			
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cct atg gct tca cag gaa aac tgc ctg gaa aag ttc atc ccg gac cac			1440
Pro Met Ala Ser Gln Glu Asn Cys Leu Glu Lys Phe Ile Pro Asp His			



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Ser Asp Val Val Met Asp Asp Asp Asp Asp Ser Cys Leu Leu Asp Leu				
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Ile Gly Asp Pro Gln Ala Leu Asn Tyr Phe Leu His Gly Pro Ser Asn				
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Lys Ser Ser Asn Asp Asp Leu Thr Asn Ala Gly Tyr Ser Ala Ala Asn				
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Ser Asn Ser Ile Phe Ala Asn Ser Ser Asn Ala Asp Pro Lys Ser Ser				
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Leu Lys Gly Val Ser Asn Gln Leu Gly Glu Gly Pro Ser Asp Gly Leu				
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Pro Leu Ser Ser Ser Leu Gln Phe Leu Glu Asp Glu Leu Glu Ser Ser				
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Pro Leu Pro Asp Leu Thr Glu Asp Gln Pro Phe Asp Ile Leu Gln Lys				
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Ser Leu Gln Glu Ala Asn Ile Thr Glu Gln Thr Leu Ala Glu Glu Ala				
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Tyr Leu Asp Ala Ser Ile Gly Ser Ser Gln Gln Phe Ala Gln Ala Gln				
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Asn Tyr Ser Gly Gln Thr Leu Gln Pro Ile Gly Val Thr His Val Pro				
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Ser Gln Ile Ser Gly Ser Gly Gln Ile Gln Leu Ile Gly Ser Phe Gly				
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atagtgtcac ctaaattcaa ttcactggcc gt 2530

&lt;210&gt; 399

&lt;211&gt; 2595



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (15)..(1172)

&lt;400&gt; 399

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ggtagggatct gaac  atg gcg gcg gtg gta gct gct acg gcg ctg aag ggc      50
Met Ala Ala Val Val Ala Ala Thr Ala Leu Lys Gly
      1              5              10

cgg ggg gcg aga aat gcc cgc gtc ctc cgg ggg att ctc gca gga gcc      98
Arg Gly Ala Arg Asn Ala Arg Val Leu Arg Gly Ile Leu Ala Gly Ala
      15              20              25

aca gct aac aag gct tct cat aac agg acc cgg gcc ctg caa agc cac      146
Thr Ala Asn Lys Ala Ser His Asn Arg Thr Arg Ala Leu Gln Ser His
      30              35              40

agc tcc cca gag ggc aag gag gaa cct gaa ccc cta tcc ccg gag ctg      194
Ser Ser Pro Glu Gly Lys Glu Glu Pro Glu Pro Leu Ser Pro Glu Leu
      45              50              55              60

gaa tac att ccc aga aag agg ggc aag aac ccc atg aaa gct gtg gga      242
Glu Tyr Ile Pro Arg Lys Arg Gly Lys Asn Pro Met Lys Ala Val Gly
      65              70              75

ctg gcc tgg tac agc ctg tac acc cgc acc tgg ctc ggg tac ctc ttc      290
Leu Ala Trp Tyr Ser Leu Tyr Thr Arg Thr Trp Leu Gly Tyr Leu Phe
      80              85              90

tac cga cag cag ctg cgc agg gct cgg aat cgc tac cct aaa ggc cac      338
Tyr Arg Gln Gln Leu Arg Arg Ala Arg Asn Arg Tyr Pro Lys Gly His
      95              100             105

tcg aaa acc cag ccc cgc ctc ttc aat gga gtg aag gtg ctt ccc atc      386
Ser Lys Thr Gln Pro Arg Leu Phe Asn Gly Val Lys Val Leu Pro Ile
      110             115             120

cct gtc ctc tcg gac aac tac agc tac ctc atc atc gac acc cag gcc      434
Pro Val Leu Ser Asp Asn Tyr Ser Tyr Leu Ile Ile Asp Thr Gln Ala
      125             130             135             140

cag ctg gct gtg gct gtg gac cct tca gac cct cgg gct gtg cag gct      482
Gln Leu Ala Val Ala Val Asp Pro Ser Asp Pro Arg Ala Val Gln Ala
      145             150             155

tcc att gaa aag gaa ggg gtc acc ttg gtc gcc att ctg tgt act cac      530
Ser Ile Glu Lys Glu Gly Val Thr Leu Val Ala Ile Leu Cys Thr His
      160             165             170

aag cac tgg gac cac agt gga ggg aac cgt gac ctc agc cgg cgg cac      578
Lys His Trp Asp His Ser Gly Gly Asn Arg Asp Leu Ser Arg Arg His
      175             180             185

cgg gac tgt cgg gtg tac ggg agc cct cag gac ggc atc ccc tac ctc      626
Arg Asp Cys Arg Val Tyr Gly Ser Pro Gln Asp Gly Ile Pro Tyr Leu
      190             195             200

acc cat ccc ctg tgt cat caa gat gtg gtc agc gtg gga cgg ctt cag      674
Thr His Pro Leu Cys His Gln Asp Val Val Ser Val Gly Arg Leu Gln
      205             210             215             220

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atc cgg gcc ctg gct aca cct ggc cac aca caa ggc cat ctg gtc tac	722
Ile Arg Ala Leu Ala Thr Pro Gly His Thr Gln Gly His Leu Val Tyr	
225 230 235	
cta ctg gat ggg gag ccc tac aag ggt ccc tcc tgc ctc ttc tca ggg	770
Leu Leu Asp Gly Glu Pro Tyr Lys Gly Pro Ser Cys Leu Phe Ser Gly	
240 245 250	
gac ctg ctc ttc ctc tct ggc tgt ggg cgg acc ttt gag ggc aat gca	818
Asp Leu Leu Phe Leu Ser Gly Cys Gly Arg Thr Phe Glu Gly Asn Ala	
255 260 265	
gag acc atg ctg agc tca ctg gac act gtg ctg ggg cta ggg gat gac	866
Glu Thr Met Leu Ser Ser Leu Asp Thr Val Leu Gly Leu Gly Asp Asp	
270 275 280	
acc ctt ctg tgg cct ggt cat gag tat gca gag gag aac ctg ggc ttt	914
Thr Leu Leu Trp Pro Gly His Glu Tyr Ala Glu Glu Asn Leu Gly Phe	
285 290 295 300	
gca ggt gtg gtg gag ccc gag aac ctg gcc cgg gag agg aag atg cag	962
Ala Gly Val Val Glu Pro Glu Asn Leu Ala Arg Glu Arg Lys Met Gln	
305 310 315	
tgg gtg cag cgg cag cgg ctg gag cgc aag ggc acg tgc cca tct acc	1010
Trp Val Gln Arg Gln Arg Leu Glu Arg Lys Gly Thr Cys Pro Ser Thr	
320 325 330	
ctg gga gag gag cgc tcc tac aac ccg ttc ctg aga acc cac tgc ctg	1058
Leu Gly Glu Glu Arg Ser Tyr Asn Pro Phe Leu Arg Thr His Cys Leu	
335 340 345	
gcg cta cag gag gct ctg ggg ccg ggg ccg ggc ccc act ggg gat gat	1106
Ala Leu Gln Glu Ala Leu Gly Pro Gly Pro Gly Pro Thr Gly Asp Asp	
350 355 360	
gac tac tcc cgg gcc cag ctc ctg gaa gag ctc cgc cgg ctg aag gat	1154
Asp Tyr Ser Arg Ala Gln Leu Leu Glu Glu Leu Arg Arg Leu Lys Asp	
365 370 375 380	
atg cac aag agc aag tga tgcccc cagcgcccc agcccagccc actccccgca	1208
Met His Lys Ser Lys *	
385	
tggggaggcc gccaccacca acacctcatc atccttctca tcgctaacac caccaactcc	1268
atcggcacccc aagcgggcat catcccccca cactgctcag gggaggggag ggatcaggcg	1328
atgagactgt gaggccaaaa gaagggggcc tgttgagggc tgggaacccc gcagcgcgag	1388
gctgcctcat caacggcaag aggaaaggag ggggtctcggg acatctccag accctaccaa	1448
ctgggaggggt cccctcctcc ttcctactc ctgggacggc agcaaggaca tgggggctgc	1508
tgtagcttc tccgtcagga ggcctcatct cactgtagcc ctggaaccca ggggtccatct	1568
tgcccttccc ccatccatgg ttgggaaaga agctcagccc ctcacagtgg cctcaagtgt	1628
gatgccttac aaaagcacca ctcatgagg cagctggact ctggtgtcct gagactctgc	1688
cctcttccca cagcctccct gccccacca tccctgcaaa gccatttttc agaagagacc	1748
attcctaaga aactgaagg gctggaatgc tggctggcca ctctctgcct cagtggcctc	1808

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cctacagcct ggaagaagga gggtcctgat tgccaaggaa acctctcctc attgggctaa 1868
ggagacactg gagtctggag tgtggagccc cacagtcttg caggtcacat gctctccttg 1928
cacatctggc ctggttgtag ccactggcct ctgcctctgc cctgggcca aagggcccct 1988
ccttgccagg ggagagacag ccacggctct ctttggccga tgctgtattc tcattttggc 2048
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gcccttttct tctttgagtt agtaaagatt tattctgtaa cctgacactc atctggccct 2168
ttgcagtttg ccagccatat tcccatgtga tttccactg gatccaggcc cccatccggc 2228
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ggctctgctc acctctggtg accctccaag atgccctgc cctcagtttc cctcatgat 2528
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agttaga 2595

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<210> 400  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (142)..(1479)

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<400> 400
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ttatcctatc aattggggcg cgggcctgtg agccagttgg agttgcggcg gcgggaacga 120
ttgggctgag cagaggacga c atg ttg ctt ttc gtg gag cag gta gca tct 171
                        Met Leu Leu Phe Val Glu Gln Val Ala Ser
                        1             5             10

aaa gga act ggt tta aat cct aat gcc aaa gta tgg caa gaa att gct 219
Lys Gly Thr Gly Leu Asn Pro Asn Ala Lys Val Trp Gln Glu Ile Ala
                        15             20             25

cct gga aat act gat gcc acc cca gta act cat gga act gaa agc tct 267
Pro Gly Asn Thr Asp Ala Thr Pro Val Thr His Gly Thr Glu Ser Ser
                        30             35             40

tgg cat gaa ata gca gct aca tca ggt gct cat cct gag ggt aat gca 315
Trp His Glu Ile Ala Ala Thr Ser Gly Ala His Pro Glu Gly Asn Ala
                        45             50             55

gag ctc tca gaa gat ata tgt aaa gaa tat gaa gta atg tat tct tca 363
Glu Leu Ser Glu Asp Ile Cys Lys Glu Tyr Glu Val Met Tyr Ser Ser
                        60             65             70

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tct tgt gaa acc aca aga aat act aca ggc att gaa gaa tca act gat Ser Cys Glu Thr Thr Arg Asn Thr Thr Gly Ile Glu Glu Ser Thr Asp 75 80 85 90	411
ggg atg att tta gga cca gaa gat ctg agt tac caa ata tat gat gtt Gly Met Ile Leu Gly Pro Glu Asp Leu Ser Tyr Gln Ile Tyr Asp Val 95 100 105	459
tcc gga gaa agc aat tca gca gtt tct aca gaa gac cta aaa gaa tgt Ser Gly Glu Ser Asn Ser Ala Val Ser Thr Glu Asp Leu Lys Glu Cys 110 115 120	507
ctg aag aaa caa tta gaa ttc tgt ttt tca cga gaa aat ttt tca aag Leu Lys Lys Gln Leu Glu Phe Cys Phe Ser Arg Glu Asn Phe Ser Lys 125 130 135	555
gat ctt tac ttg ata tct caa atg gat agt gat cag ttc atc cca att Asp Leu Tyr Leu Ile Ser Gln Met Asp Ser Asp Gln Phe Ile Pro Ile 140 145 150	603
tgg aca gtt gcc aac atg gaa gaa ata aaa aag ttg act aca gac cct Trp Thr Val Ala Asn Met Glu Glu Ile Lys Lys Leu Thr Thr Asp Pro 155 160 165 170	651
gat cta att ctt gaa gtg tta aga tct tct ccc atg gta caa gtt gat Asp Leu Ile Leu Glu Val Leu Arg Ser Ser Pro Met Val Gln Val Asp 175 180 185	699
gag aag ggt gag aaa gtg aga cca agt cat aag cgt tgt att gta att Glu Lys Gly Glu Lys Val Arg Pro Ser His Lys Arg Cys Ile Val Ile 190 195 200	747
ctt aga gag att cct gaa aca aca cca ata gag gaa gtg aaa ggt ttg Leu Arg Glu Ile Pro Glu Thr Thr Pro Ile Glu Glu Val Lys Gly Leu 205 210 215	795
ttc aaa agt gaa aac tgc ccc aaa gtg ata agc tgt gag ttt gca cac Phe Lys Ser Glu Asn Cys Pro Lys Val Ile Ser Cys Glu Phe Ala His 220 225 230	843
aat agc aac tgg tat atc act ttc cag tca gac aca gat gca caa cag Asn Ser Asn Trp Tyr Ile Thr Phe Gln Ser Asp Thr Asp Ala Gln Gln 235 240 245 250	891
gct ttt aaa tac tta aga gaa gaa gtt aaa aca ttt cag ggc aag cca Ala Phe Lys Tyr Leu Arg Glu Glu Val Lys Thr Phe Gln Gly Lys Pro 255 260 265	939
att atg gca agg ata aaa gcc atc aat aca ttt ttt gct aag aat ggt Ile Met Ala Arg Ile Lys Ala Ile Asn Thr Phe Phe Ala Lys Asn Gly 270 275 280	987
tat cga tta atg gat tct agt atc tat agt cac ccc att caa act caa Tyr Arg Leu Met Asp Ser Ser Ile Tyr Ser His Pro Ile Gln Thr Gln 285 290 295	1035
gca cag tat gcc tcc cca gtc ttt atg cag cct gta tat aat cct cac Ala Gln Tyr Ala Ser Pro Val Phe Met Gln Pro Val Tyr Asn Pro His 300 305 310	1083
caa cag tac tcg gtc tat agt att gtg cct cag tct tgg tct cca aat Gln Gln Tyr Ser Val Tyr Ser Ile Val Pro Gln Ser Trp Ser Pro Asn 315 320 325 330	1131

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cct aca cct tac ttt gaa aca cca ctg gct ccc ttt ccc aat ggt agt      1179
Pro Thr Pro Tyr Phe Glu Thr Pro Leu Ala Pro Phe Pro Asn Gly Ser
                335                      340                      345

ttt gtg aat ggc ttt aat tcg cca gga tct tat aaa aca aat gct gct      1227
Phe Val Asn Gly Phe Asn Ser Pro Gly Ser Tyr Lys Thr Asn Ala Ala
                350                      355                      360

gct atg aat atg ggt cga cca ttc caa aaa aat cgt gtg aag cct cag      1275
Ala Met Asn Met Gly Arg Pro Phe Gln Lys Asn Arg Val Lys Pro Gln
                365                      370                      375

ttt agg tca tct ggt ggt tca gaa cac tca aca gag ggc tct gta tcc      1323
Phe Arg Ser Ser Gly Gly Ser Glu His Ser Thr Glu Gly Ser Val Ser
                380                      385                      390

ttg ggg gat gga cag ttg aac aga tat agt tca aga aac ttt cca gct      1371
Leu Gly Asp Gly Gln Leu Asn Arg Tyr Ser Ser Arg Asn Phe Pro Ala
                395                      400                      405                      410

gaa cgg cat aac ccc aca gta act ggg cat cag gag caa act tac ctt      1419
Glu Arg His Asn Pro Thr Val Thr Gly His Gln Glu Gln Thr Tyr Leu
                415                      420                      425

cag aag gag act tcc act ttg cag gtg gaa cag aat ggg gac tat ggt      1467
Gln Lys Glu Thr Ser Thr Leu Gln Val Glu Gln Asn Gly Asp Tyr Gly
                430                      435                      440

agg ggc agg taa gaa aataaagtac ctgaaaacct ttgataataa tgtgatcatc      1522
Arg Gly Arg *
                445

ctgaataatt gaagaacgtg atcttcataa taattaaatg agcatttaat tattggtata      1582

tggttatatt aaataaatac gttattttca gaaaaaaaaa aaa                      1625

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<210> 401  
 <211> 895  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (152) .. (724)

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actggacgcc cgcagtaccg gtccgtaatt cccgggtcga cccacgcgtc cgcccacgcg      60

tccggtcgcg accctggtcc ggacctgacc tgaattgcga cccaacctg gactgctccc      120

ctgaccgcaa cccctacccc cgcccaccag c      atg gcc cgg cac gtg ttc cta      172
                Met Ala Arg His Val Phe Leu
                1                      5

acg ggg ccc cca gga gtt gga aaa aca aca ttg atc cat aaa gcc agt      220
Thr Gly Pro Pro Gly Val Gly Lys Thr Thr Leu Ile His Lys Ala Ser
                10                      15                      20

gag gtt tta aaa tcc tct ggt gtg cct gtt gat gga ttt tat acc gaa      268
Glu Val Leu Lys Ser Ser Gly Val Pro Val Asp Gly Phe Tyr Thr Glu

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25	30	35	
gaa gtc aga cag gga ggg aga aga ata gga ttc gat gtc gtc acg ttg			316
Glu Val Arg Gln Gly Gly Arg Arg Ile Gly Phe Asp Val Val Thr Leu			
40	45	50	55
tcc ggc acc cgg ggg cct tta tcg aga gtt ggg tta gag cct cca cct			364
Ser Gly Thr Arg Gly Pro Leu Ser Arg Val Gly Leu Glu Pro Pro Pro			
	60	65	70
gga aaa cgt gaa tgc cga gtt ggg cag tat gtg gtc gac ctg act tct			412
Gly Lys Arg Glu Cys Arg Val Gly Gln Tyr Val Val Asp Leu Thr Ser			
	75	80	85
ttt gag cag ttg gca cta ccc gtc ttg agg aat gcc gac tgc agc agt			460
Phe Glu Gln Leu Ala Leu Pro Val Leu Arg Asn Ala Asp Cys Ser Ser			
	90	95	100
ggc cca ggg caa aga gtg tgc gtc atc gat gag att ggg aag atg gag			508
Gly Pro Gly Gln Arg Val Cys Val Ile Asp Glu Ile Gly Lys Met Glu			
	105	110	115
ctc ttc agt cag ctt ttc att caa gct gtt cgt cag acg ctg tct acc			556
Leu Phe Ser Gln Leu Phe Ile Gln Ala Val Arg Gln Thr Leu Ser Thr			
	120	125	130
cca ggg act ata atc ctt ggc aca atc cca gtt cct aaa gga aag cca			604
Pro Gly Thr Ile Ile Leu Gly Thr Ile Pro Val Pro Lys Gly Lys Pro			
	140	145	150
ctg gct ctt gta gaa gaa atc aga aac aga aag gat gtg aag gtg ttt			652
Leu Ala Leu Val Glu Glu Ile Arg Asn Arg Lys Asp Val Lys Val Phe			
	155	160	165
aat gtc acc aag gaa aac aga aac cac ctt ctg cca gat atc gtg acg			700
Asn Val Thr Lys Glu Asn Arg Asn His Leu Leu Pro Asp Ile Val Thr			
	170	175	180
tgc gtg cag agc agc agg aag tga agacacgtgc attcctgcct tccgtgaagg			754
Cys Val Gln Ser Ser Arg Lys *			
	185	190	
agtgccaggt tcaagaggag cctgatggag ccctgcctgt cgaggctgta tgcctatggg			814
gttatggaac cttgtgggct tttctagaga aaactcaaca gctgtttccc ataaaatgtt			874
taaaagatca aaaaaaaaaa a			895

<210> 402  
 <211> 1301  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (56)..(1267)

<400> 402	
aagctggtac gctgcaggt accggtccgg aattcccggg tcgacgattt cgtga atg	58
	Met
	1

gag ccg gta ggc tgc tgc ggc gag tgc cgc ggc tcc tcc gta gac ccg	106
Glu Pro Val Gly Cys Cys Gly Glu Cys Arg Gly Ser Ser Val Asp Pro	
5 10 15	
cgg agc acc ttc gtg ttg agt aac ctg gcg gag gtg gtg gag cgt gtg	154
Arg Ser Thr Phe Val Leu Ser Asn Leu Ala Glu Val Val Glu Arg Val	
20 25 30	
ctc acc ttc ctg ccc gcc aag gcg ttg ctg cgg gtg gcc tgc gtg tgc	202
Leu Thr Phe Leu Pro Ala Lys Ala Leu Leu Arg Val Ala Cys Val Cys	
35 40 45	
cgc tta tgg agg gag tgt gtg cgc aga gta ttg cgg acc cat cgg agc	250
Arg Leu Trp Arg Glu Cys Val Arg Arg Val Leu Arg Thr His Arg Ser	
50 55 60 65	
gta acc tgg atc tcc gca ggc ctg gcg gag gcc ggc cac ctg gag ggg	298
Val Thr Trp Ile Ser Ala Gly Leu Ala Glu Ala Gly His Leu Glu Gly	
70 75 80	
cat tgc ttg gtt cgc gtg gta gca gag gag ctt gag aat gtt cgc atc	346
His Cys Leu Val Arg Val Val Ala Glu Glu Leu Glu Asn Val Arg Ile	
85 90 95	
tta cca cat aca gtt ctt tac atg gct gat tca gaa act ttc att agt	394
Leu Pro His Thr Val Leu Tyr Met Ala Asp Ser Glu Thr Phe Ile Ser	
100 105 110	
ctg gaa gag tgt cgt ggc cat aag aga gca agg aaa aga act agt atg	442
Leu Glu Glu Cys Arg Gly His Lys Arg Ala Arg Lys Arg Thr Ser Met	
115 120 125	
gaa aca gca ctt gcc ctt gag aag cta ttc ccc aaa caa tgc caa gtc	490
Glu Thr Ala Leu Ala Leu Glu Lys Leu Phe Pro Lys Gln Cys Gln Val	
130 135 140 145	
ctt ggg att gtg acc cca gga att gta gtg act cca atg gga tca ggt	538
Leu Gly Ile Val Thr Pro Gly Ile Val Val Thr Pro Met Gly Ser Gly	
150 155 160	
agc aat cga cct cag gaa ata gaa att gga gaa tct ggt ttt gct tta	586
Ser Asn Arg Pro Gln Glu Ile Glu Ile Gly Glu Ser Gly Phe Ala Leu	
165 170 175	
tta ttc cct caa att gaa gga ata aaa ata caa ccc ttt cat ttt att	634
Leu Phe Pro Gln Ile Glu Gly Ile Lys Ile Gln Pro Phe His Phe Ile	
180 185 190	
aag gat cca aag aat tta aca tta gaa aga cat caa ctc act gaa gta	682
Lys Asp Pro Lys Asn Leu Thr Leu Glu Arg His Gln Leu Thr Glu Val	
195 200 205	
ggt ctt tta gat aac cct gaa ctt cgt gtg gtc ctt gtc ttt ggt tat	730
Gly Leu Leu Asp Asn Pro Glu Leu Arg Val Val Leu Val Phe Gly Tyr	
210 215 220 225	
aat tgc tgt aag gtg gga gcc agt aat tat ctg cag caa gta gtc agc	778
Asn Cys Cys Lys Val Gly Ala Ser Asn Tyr Leu Gln Gln Val Val Ser	
230 235 240	
act ttc agt gat atg aat atc atc ttg gct gga ggc cag gtg gac aac	826
Thr Phe Ser Asp Met Asn Ile Ile Leu Ala Gly Gly Gln Val Asp Asn	
245 250 255	

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ctg tca tca ctg act tct gaa aag aac cct ctg gat att gat gcc tcg      874
Leu Ser Ser Leu Thr Ser Glu Lys Asn Pro Leu Asp Ile Asp Ala Ser
      260                      265                      270

ggt gtg gtt gga ctg tca ttt agt gga cac cga atc cag agt gcc act      922
Gly Val Val Gly Leu Ser Phe Ser Gly His Arg Ile Gln Ser Ala Thr
      275                      280                      285

gtg ctc ctc aac gag gac gtc agt gat gag aag act gct gag gct gcg      970
Val Leu Leu Asn Glu Asp Val Ser Asp Glu Lys Thr Ala Glu Ala Ala
      290                      295                      300                      305

atg cag cgc ctc aaa gcg gcc aac att cca gag cat aac acc att ggc      1018
Met Gln Arg Leu Lys Ala Ala Asn Ile Pro Glu His Asn Thr Ile Gly
      310                      315                      320

ttc atg ttt gca tgc gtt ggc agg ggc ttt cag tat tac aga gcc aag      1066
Phe Met Phe Ala Cys Val Gly Arg Gly Phe Gln Tyr Tyr Arg Ala Lys
      325                      330                      335

ggg aat gtt gag gct gat gca ttt aga aag ttt ttt cct agt gtt ccc      1114
Gly Asn Val Glu Ala Asp Ala Phe Arg Lys Phe Phe Pro Ser Val Pro
      340                      345                      350

tta ttc ggc ttc ttt gga aat gga gaa att gga tgt gat cgg ata gtc      1162
Leu Phe Gly Phe Phe Gly Asn Gly Glu Ile Gly Cys Asp Arg Ile Val
      355                      360                      365

act ggg aac ttt ata ttg agg aaa tgt aat gag gta aaa gat gat gat      1210
Thr Gly Asn Phe Ile Leu Arg Lys Cys Asn Glu Val Lys Asp Asp Asp
      370                      375                      380                      385

ctg ttt cat agc tat aca aca ata atg gca ctc ata cat ctg ggg tca      1258
Leu Phe His Ser Tyr Thr Thr Ile Met Ala Leu Ile His Leu Gly Ser
      390                      395                      400

tct aaa taa taattaaagt ggctttcata ataaaaaaaa aaaa      1301
Ser Lys *

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<210> 403
<211> 932
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (48)..(728)

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<400> 403
ccagtgatgg gcaattcgga cggcagccga cggggcgctg cggaggg atg tgg ccc      56
Met Trp Pro
      1

gga ata ttg gca ggg ggg gcc cgg gag gcg tca tgc agg tac ccc gcg      104
Gly Ile Leu Ala Gly Gly Ala Arg Glu Ala Ser Cys Arg Tyr Pro Ala
      5                      10                      15

ctg ggg cct cgc ctc gcc gct cac ttt cca gcg cag cgg ccg cag      152

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Leu Gly Pro Arg Leu Ala Ala His Phe Pro Ala Gln Arg Pro Pro Gln
20                      25                      30                      35

cgg aca ctc cag aac ggc ctg gcc ctg cag cgg tgc ctg cac gcg acg      200
Arg Thr Leu Gln Asn Gly Leu Ala Leu Gln Arg Cys Leu His Ala Thr
                      40                      45                      50

gcg acc cgg gct ctc ccg ctc att ccc atc gtg gtg gag cag acg ggt      248
Ala Thr Arg Ala Leu Pro Leu Ile Pro Ile Val Val Glu Gln Thr Gly
                      55                      60                      65

cgc ggc gag cgc gcc tat gac atc tac tcg cgg ctg ctg cgg gag cgc      296
Arg Gly Glu Arg Ala Tyr Asp Ile Tyr Ser Arg Leu Leu Arg Glu Arg
                      70                      75                      80

atc gtg tgc gtc atg ggc ccg atc gat gac agc gtt gcc agc ctt gtt      344
Ile Val Cys Val Met Gly Pro Ile Asp Asp Ser Val Ala Ser Leu Val
                      85                      90                      95

atc gca cag ctc ctc ttc ctg ctt ctc gcc gcc ggc acc cca ggc atg      392
Ile Ala Gln Leu Leu Phe Leu Leu Leu Ala Ala Gly Thr Pro Gly Met
100                      105                      110                      115

cgc cac tcg ctc ccc aac tcc cgt atc atg atc cac cag ccc tca gga      440
Arg His Ser Leu Pro Asn Ser Arg Ile Met Ile His Gln Pro Ser Gly
                      120                      125                      130

ggc gcc cgg ggc caa gcc aca gac att gcc atc cag gca gag gag atc      488
Gly Ala Arg Gly Gln Ala Thr Asp Ile Ala Ile Gln Ala Glu Glu Ile
                      135                      140                      145

atg aag ctc aag aag cag ctc tat aac atc tac gcc aag cac acc aaa      536
Met Lys Leu Lys Lys Gln Leu Tyr Asn Ile Tyr Ala Lys His Thr Lys
                      150                      155                      160

cag agc ctg cag gtg atc gag tcc gcc atg gag agg gac cgc tac atg      584
Gln Ser Leu Gln Val Ile Glu Ser Ala Met Glu Arg Asp Arg Tyr Met
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Ser Pro Met Glu Ala Gln Glu Phe Gly Ile Leu Asp Lys Val Leu Val
180                      185                      190                      195

cac cct ccc cag gac ggt gag gat gag ccc acg ctg gtg cag aag gag      680
His Pro Pro Gln Asp Gly Glu Asp Glu Pro Thr Leu Val Gln Lys Glu
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cct gta gaa gca gcg ccg gca gca gaa cct gtc cca gct agc acc tga      728
Pro Val Glu Ala Ala Pro Ala Ala Glu Pro Val Pro Ala Ser Thr *
                      215                      220                      225

gagctgggcc tcctctccag aatcatgtgg aggggccaga ggccctgccag acccccagct      788

gggcoctgct caccoccttgt tgctgggctt ggaggggcct cttgaggaac ttttaatttg      848

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Met Leu Thr Ser Leu Ser Arg Pro  
1 5  
ata act acc atg gct ctc agt gcc ttg gtg tac cct ggg atg tgt ggc 159  
Ile Thr Thr Met Ala Leu Ser Ala Leu Val Tyr Pro Gly Met Cys Gly  
10 15 20  
ctt ctg gcc aag cat ctg tca ttt cat att gtt gga gca ttc ctt ata 207  
Leu Leu Ala Lys His Leu Ser Phe His Ile Val Gly Ala Phe Leu Ile  
25 30 35 40  
acc ctg ggg ttg cag ctc tct gta agt ttg ctg tgg cct gac caa gaa 255  
Thr Leu Gly Leu Gln Leu Ser Val Ser Leu Leu Trp Pro Asp Gln Glu  
45 50 55  
aga agg cat atg cag att tct aca gaa att ata att gaa tta aag aat 303  
Arg Arg His Met Gln Ile Ser Thr Glu Ile Ile Ile Glu Leu Lys Asn  
60 65 70  
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Leu Arg \*  
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tattttctttg ggttgaatta cataaaaagtt tgtcactgta cctgtgttcc tgaactatct 419  
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Met Ser Gly Arg Leu Trp Ser Lys Ala Ile Phe Ala Gly Tyr Lys Arg  
1 5 10 15

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Gly Leu Arg Asn Gln Arg Glu His Thr Ala Leu Leu Lys Ile Glu Gly
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Val Tyr Ala Arg Asp Glu Thr Glu Phe Tyr Leu Gly Lys Arg Cys Ala
      35                      40                      45

tat gta tat aaa gca aag aac aac aca gtc act cct ggc ggc aaa cca      249
Tyr Val Tyr Lys Ala Lys Asn Asn Thr Val Thr Pro Gly Gly Lys Pro
      50                      55                      60

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Asn Lys Thr Arg Val Ile Trp Gly Lys Val Thr Arg Ala His Gly Asn
      65                      70                      75                      80

agt ggc atg gtt cgt gcc aaa ttc cga agc aat ctt cct gct aag gcc      345
Ser Gly Met Val Arg Ala Lys Phe Arg Ser Asn Leu Pro Ala Lys Ala
      85                      90                      95

att gga cac aga atc cga gtg atg ctg tac ccc tca agg att taa act      393
Ile Gly His Arg Ile Arg Val Met Leu Tyr Pro Ser Arg Ile *
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gagcaaaagt tgcacagcta aaccagggggc tcattcccag gacagac  atg cag tta      176
                                   Met Gln Leu
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tgg att ccg aaa gac aag tca agg aca ctg atg aca ttg aaa gtc cta      224
Trp Ile Pro Lys Asp Lys Ser Arg Thr Leu Met Thr Leu Lys Val Leu
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Asn Ala Val Ser Glu Thr Val Ala Thr Ser Thr Ala Gly Ile Pro Ser
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aca gcc tgg att cct ttg gct ctc gct cgt cgg cag acg cct tca cca      368
Thr Ala Trp Ile Pro Leu Ala Leu Ala Arg Arg Gln Thr Pro Ser Pro
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gat gta gtc ctc agg gga agc agc gat ggg aga gga agc gac tct gaa      416

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Asn	Gln	Tyr	Leu	Pro	Asn	Lys	Ser	Asn	Gln	Thr	Ala	Tyr	Val	Pro	Ala		
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Pro	Leu	Arg	Lys	Lys	Lys	Ala	Glu	Arg	Glu	Glu	Tyr	Arg	Lys	Ser	Trp		
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Ile	Ala	Arg	Ala	Ser	Val	Leu	Asp	Thr	Ser	Met	Ser	Ala	Gly	Ser	Gly		
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Ser	Pro	Ser	Lys	Thr	Val	Thr	Pro	Lys	Ala	Val	Pro	Met	Leu	Thr	Pro		
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                                           Met Glu Pro Gly Asn
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Arg Ser Leu Asn Pro His Lys Thr Lys His His Met Glu Cys Arg Val
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Ala Trp Glu Cys Gly Ser Ser Arg Gly Pro Trp Gly Leu Leu Arg Tyr
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Thr Phe Ala Pro Val Arg Ala Ser Arg Pro Trp Ala Cys Leu Pro Lys
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Gly Ser Leu Ser Gln Arg Pro Lys Val Pro Pro Pro Val His Leu Pro
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Pro Lys Ser Ser Cys Pro Pro Arg Ala Gly Gly Gly Gly Ala Gln Gly
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Arg Arg Val Pro Cys Thr Tyr Leu Ser Pro Leu Ser His Ser Pro Lys
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 Met Lys Lys Ser Pro Glu Ile Ile Ser Gly  
 1 5 10  
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 Arg Met Thr Phe Gly Thr Ala Ser Glu Leu Ala Ser Val Cys Met Pro  
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 Arg Asn Lys \*  
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Tyr	Asn	Thr	Cys	Phe	Ser	Asp	Val	Cys	Glu	Arg	Met	Glu	Glu	Leu	Arg	
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Lys	Arg	Arg	Val	Ser	Gln	Asp	Leu	Glu	Val	Glu	Lys	Pro	Asp	Ala	Ser	
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Cys	Ser	Ala	Val	Ser	Thr	Pro	Glu	Val	Glu	Arg	Lys	Asn	Pro	Leu	His	
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Glu	Ala	Gln	His	Arg	Gln	Ser	Ala	Ala	Leu	Asp	Pro	Ala	Asp	Trp	Pro	
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cgc atg gcg att cca agt ggt gga ctc acg gaa atc tgc cga aag ccc	4099
Arg Met Ala Ile Pro Ser Gly Gly Leu Thr Glu Ile Cys Arg Lys Pro	
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gtc tct cct ggg tgc att tcg tct gtg tca gat tgg ctc att tcc atc	4147
Val Ser Pro Gly Cys Ile Ser Ser Val Ser Asp Trp Leu Ile Ser Ile	
1175	1180 1185
ggt ctg ccc atg tac gcc gcc acc ctc tcc acc gcg gcc ttc agc aca	4195
Gly Leu Pro Met Tyr Ala Gly Thr Leu Ser Thr Ala Gly Phe Ser Thr	
1190	1195 1200 1205
ctg agc caa gtg cct tct ctg tct cac act tgc ctt cag gag gcc gcc	4243
Leu Ser Gln Val Pro Ser Leu Ser His Thr Cys Leu Gln Glu Ala Gly	
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atc aca gag gag aga cac ata aga aag ctc cta tct gca gcc aga ctc	4291
Ile Thr Glu Glu Arg His Ile Arg Lys Leu Leu Ser Ala Ala Arg Leu	
1225	1230 1235
ttc aaa ctg ccg cca gcc cct gag gcc atg tag ccaggccc ggaatgggcc	4342
Phe Lys Leu Pro Pro Gly Pro Glu Ala Met *	
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aagaaccaag atgccaactg gctgcgaatg ctctatctcc agtctgtctc tgtgtactgg	4642
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gtctgtcatc ttgcaggatg cccgagggcc agatgggctt agctaggcca aagtaacaga	4762
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 gcacgagcca ggcgtactga caggtggacc agcggactgg tggag atg gcg acg 174  
 Met Ala Thr  
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 ctc tct ctg acc gtg aat tca gga gac cct ccg cta gga gct ttg ctg 222  
 Leu Ser Leu Thr Val Asn Ser Gly Asp Pro Pro Leu Gly Ala Leu Leu  
 5 10 15  
 gca gta gaa cac gtg aaa gac gat gtc agc att tcc gtt gaa gaa ggg 270  
 Ala Val Glu His Val Lys Asp Asp Val Ser Ile Ser Val Glu Glu Gly  
 20 25 30 35  
 aaa gag aat att ctt cat gtt tct gaa aat gtg ata ttc aca gat gtg 318  
 Lys Glu Asn Ile Leu His Val Ser Glu Asn Val Ile Phe Thr Asp Val  
 40 45 50  
 aat tct ata ctt cgc tac ttg gct aga gtt gca act aca gct ggg tta 366  
 Asn Ser Ile Leu Arg Tyr Leu Ala Arg Val Ala Thr Thr Ala Gly Leu  
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 Tyr Gly Ser Asn Leu Met Glu His Thr Glu Ile Asp His Trp Leu Glu  
 70 75 80  
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 Phe Ser Ala Thr Lys Leu Ser Ser Cys Asp Ser Phe Thr Ser Thr Ile  
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 aat gaa ctc aat cat tgc ctg tct ctg aga aca tac tta gtt gga aac 510  
 Asn Glu Leu Asn His Cys Leu Ser Leu Arg Thr Tyr Leu Val Gly Asn  
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 tcc ttg agt tta gca gat tta tgt gtt tgg gcc acc cta aaa gga aat 558  
 Ser Leu Ser Leu Ala Asp Leu Cys Val Trp Ala Thr Leu Lys Gly Asn  
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 gct gcc tgg caa gaa cag ttg aaa cag aag aaa gct cca gtt cat gta 606  
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 Lys Arg Trp Phe Gly Phe Leu Glu Ala Gln Gln Ala Phe Gln Ser Val  
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 Gly Thr Lys Trp Asp Val Ser Thr Thr Lys Ala Arg Val Ala Pro Glu



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Lys Lys Gln Asp Val Gly Lys Phe Val Glu Leu Pro Gly Ala Glu Met			
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gga aag gtt acc gtc aga ttt cct cca gag gcc agt ggt tac tta cac			798
Gly Lys Val Thr Val Arg Phe Pro Pro Glu Ala Ser Gly Tyr Leu His			
200	205		210
att ggg cat gca aaa gct gct ctt ctg aac cag cac tac cag gtt aac			846
Ile Gly His Ala Lys Ala Ala Leu Leu Asn Gln His Tyr Gln Val Asn			
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ttt aaa ggg aaa ctg atc atg aga ttt gat gac aca aat cct gaa aaa			894
Phe Lys Gly Lys Leu Ile Met Arg Phe Asp Asp Thr Asn Pro Glu Lys			
230	235		240
aaa aag gaa gat ttt gag aag gtt atc ttg gaa gat gtt gca atg ttg			942
Lys Lys Glu Asp Phe Glu Lys Val Ile Leu Glu Asp Val Ala Met Leu			
245	250		255
cat atc aaa cca gat caa ttt act tat act tcg gat cat ttt gaa act			990
His Ile Lys Pro Asp Gln Phe Thr Tyr Thr Ser Asp His Phe Glu Thr			
260	265		275
ata atg aag tat gca gag aag cta att caa gaa ggg aag gct tat gtg			1038
Ile Met Lys Tyr Ala Glu Lys Leu Ile Gln Glu Gly Lys Ala Tyr Val			
280	285		290
gat gat act cct gct gaa cag atg aaa gca gaa cgt gag cag agg ata			1086
Asp Asp Thr Pro Ala Glu Gln Met Lys Ala Glu Arg Glu Gln Arg Ile			
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Glu Ser Lys His Arg Lys Asn Pro Ile Glu Lys Asn Leu Gln Met Trp			
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gaa gaa atg aaa aaa ggg agc cag ttt ggt cag tcc tgt tgt ttg cga			1182
Glu Glu Met Lys Lys Gly Ser Gln Phe Gly Gln Ser Cys Cys Leu Arg			
325	330		335
gca aaa att gac atg agt agt aac aat gga tgc atg aga gat cca acc			1230
Ala Lys Ile Asp Met Ser Ser Asn Asn Gly Cys Met Arg Asp Pro Thr			
340	345		355
ctt tat cgc tgc aaa att caa cca cat cca aga act gga aat aaa tac			1278
Leu Tyr Arg Cys Lys Ile Gln Pro His Pro Arg Thr Gly Asn Lys Tyr			
360	365		370
aat gtt tat cca aca tat gat ttt gcc tgc ccc ata gtt gac agc atc			1326
Asn Val Tyr Pro Thr Tyr Asp Phe Ala Cys Pro Ile Val Asp Ser Ile			
375	380		385
gaa ggt gtt aca cat gcc ctg aga aca aca gaa tac cat gac aga gat			1374
Glu Gly Val Thr His Ala Leu Arg Thr Thr Glu Tyr His Asp Arg Asp			
390	395		400
gag cag ttt tac tgg att att gaa gct tta ggc ata aga aaa cca tat			1422
Glu Gln Phe Tyr Trp Ile Ile Glu Ala Leu Gly Ile Arg Lys Pro Tyr			
405	410		415
att tgg gaa tat agt cgg cta aat ctc aac aac aca gtg cta tcc aaa			1470
Ile Trp Glu Tyr Ser Arg Leu Asn Leu Asn Asn Thr Val Leu Ser Lys			

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Arg Lys Leu Thr Trp Phe Val Asn Glu Gly Leu Val Asp Gly Trp Asp				
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Asp Pro Arg Phe Pro Thr Val Arg Gly Val Leu Arg Arg Gly Met Thr				
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Val Glu Gly Leu Lys Gln Phe Ile Ala Ala Gln Gly Ser Ser Arg Ser				
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gtc gtg aac atg gag tgg gac aaa atc tgg gcg ttt aac aaa aag gtt				1662
Val Val Asn Met Glu Trp Asp Lys Ile Trp Ala Phe Asn Lys Lys Val				
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Ile Asp Pro Val Ala Pro Arg Tyr Val Ala Leu Leu Lys Lys Glu Val				
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Ile Pro Val Asn Val Pro Glu Ala Gln Glu Glu Met Lys Glu Val Ala				
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Lys His Pro Lys Asn Pro Glu Val Gly Leu Lys Pro Val Trp Tyr Ser				
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ccc aaa gtt ttc att gaa ggt gct gat gca gag act ttt tcg gag ggt				1854
Pro Lys Val Phe Ile Glu Gly Ala Asp Ala Glu Thr Phe Ser Glu Gly				
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Glu Met Val Thr Phe Ile Asn Trp Gly Asn Leu Asn Ile Thr Lys Ile				
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cac aaa aat gca gat gga aaa atc ata tct ctt gat gca aag ttg aat				1950
His Lys Asn Ala Asp Gly Lys Ile Ile Ser Leu Asp Ala Lys Leu Asn				
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ttg gaa aac aaa gac tac aag aaa acc act aag gtc act tgg ctt gca				1998
Leu Glu Asn Lys Asp Tyr Lys Lys Thr Thr Lys Val Thr Trp Leu Ala				
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gag act aca cat gct ctt cct att cca gta atc tgt gtc act tat gag				2046
Glu Thr Thr His Ala Leu Pro Ile Pro Val Ile Cys Val Thr Tyr Glu				
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cac ttg atc aca aag cca gtg cta gga aaa gac gag gac ttt aag cag				2094
His Leu Ile Thr Lys Pro Val Leu Gly Lys Asp Glu Asp Phe Lys Gln				
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Tyr Val Asn Lys Asn Ser Lys His Glu Glu Leu Met Leu Gly Asp Pro				
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tgc ctt aag gat ttg aaa aaa gga gat att ata caa ctc cag aga aga				2190
Cys Leu Lys Asp Leu Lys Lys Gly Asp Ile Ile Gln Leu Gln Arg Arg				
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Gly Phe Phe Ile Cys Asp Gln Pro Tyr Glu Pro Val Ser Pro Tyr Ser				

680															685															690															
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Ile	Leu	Glu	Ser	Lys	Ser	Leu	Tyr	Asp	Glu	Val	Ala	Ala	Gln	Gly	Glu																														
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Val	Val	Arg	Lys	Leu	Lys	Ala	Glu	Lys	Ser	Pro	Lys	Ala	Lys	Ile	Asn																														
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acc agg ttg ggt ctt gag gca aaa aaa gaa gaa aat ctt gct gat tgg Thr Arg Leu Gly Leu Glu Ala Lys Lys Glu Glu Asn Leu Ala Asp Trp 1015 1020 1025			3246
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gac tat aca act aca ata gaa gca ttt ata tct gct agt gga aga gct Asp Tyr Thr Thr Thr Ile Glu Ala Phe Ile Ser Ala Ser Gly Arg Ala 1220 1225 1230 1235			3870
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caaaccctgg gacatgaaca attttcatgt gtaaggtaga agccttcagt aggtagtaaa	3261
gacttaattgt gcatgacttg atgttatatg tagagatata tatatatata tatatatacc	3321
ataaaagcaa tatgtttctct gatcatatac tctgctgtgg tcatgcccac tctttgggag	3381
tatatccct ttatatatat tgagtattgt accacttgag aaattccttt gttctgttat	3441
acaaaattaa tctttctgct cataatgatt gatgatacca ccagtaaaaa taggatgttt	3501
accccaaaac aagtgtcaat taagaatttg aacacaacca catttttttaa aatgaaactt	3561
ctatcggaag taaattaatt tgttgtaata aagtccagta tttaataaaa tgtacaatgt	3621

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3667

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 <213> Homo sapiens

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 tccactctaa cacctcagag taaagaactg atgggcaggc atcggcttct gctgacaatt 180  
 gccaacccggc atgagattgc tgagctgagg tggactctcc agacactgga actggaactc 240  
 caggcccaat ggctcttgtt aagaatgctg caacgtgaga cccttgagag agactgactt 300  
 gttgaag atg aag aga aaa cca aga gcc tcc agt cca gtt gtt gaa gag 349  
 Met Lys Arg Lys Pro Arg Ala Ser Ser Pro Val Val Glu Glu  
 1 5 10  
 caa cca cga gcc aac acc aag gag aca agg aag aag tcc ttc tct 397  
 Gln Pro Arg Ala Asn Thr Lys Glu Thr Arg Lys Lys Lys Ser Phe Ser  
 15 20 25 30  
 caa ccg atg acc gca agc aca aag aag agt ccc aag ata gcg aag aaa 445  
 Gln Pro Met Thr Ala Ser Thr Lys Lys Ser Pro Lys Ile Ala Lys Lys  
 35 40 45  
 gga aaa taa ctcaagg gagagccagg aagaaaaatg ctccacaaaa atccatggct 501  
 Gly Lys \*  
 ttaagaatac ttgaggaagg gagcaggcca acaccctctg gccacagtga ccagctgaat 561  
 gaggaactct aacagaatga gctgcagttg gagcaacaga ggggacatag ctggaacaac 621  
 agagcgagggg gacacagccg gagcaacaga gtgggaggat gccaacatt tcaactctct 681  
 ccctgagcag cgagtaattt cagggcaagc ccagagacta ggatccatct gagaagtctt 741  
 cagaggtctg acccagagta ctcaacaaca ggatacgtcc catggtgatg aaaataaaat 801  
 gaatcttggtg ttaccggtg tattcctcac gacttaagtt aaaaacctga tgaaaagtgg 861  
 ttaatctcca taatgggtgt tagctccatc gcaggggagca tgaggttgga cagacagagt 921  
 cgggcaaggt tatggagaag acttaatcca tccacaagag gtccgagtat gttgatgaag 981  
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 cgggaa 1047

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 Met Lys Ile Thr Arg Gln Lys His  
 1 5  
 gcc aag aag cat ctt ggc ttc ttc cgc aac aac ttc gga gtc cgc gag 160  
 Ala Lys Lys His Leu Gly Phe Phe Arg Asn Asn Phe Gly Val Arg Glu  
 10 15 20  
 ccg tac cag atc ctg ctg gac ggc acc ttc tgt cag gcg gcg ctg cgg 208  
 Pro Tyr Gln Ile Leu Leu Asp Gly Thr Phe Cys Gln Ala Ala Leu Arg  
 25 30 35 40  
 ggc cgc atc cag ctg cgg gag cag ctg ccc cgc tac ctc atg ggg gag 256  
 Gly Arg Ile Gln Leu Arg Glu Gln Leu Pro Arg Tyr Leu Met Gly Glu  
 45 50 55  
 acg cag ctg tgc acc aca aga tgt gtg tta aaa gag cta gaa aca ttg 304  
 Thr Gln Leu Cys Thr Thr Arg Cys Val Leu Lys Glu Leu Glu Thr Leu  
 60 65 70  
 gga aag gac tta tat ggg gca aaa ctg att gca caa aaa tgc caa gtt 352  
 Gly Lys Asp Leu Tyr Gly Ala Lys Leu Ile Ala Gln Lys Cys Gln Val  
 75 80 85  
 cga aat tgt cct cat ttc aag aat gca gtg agt gga tca gaa tgt ctg 400  
 Arg Asn Cys Pro His Phe Lys Asn Ala Val Ser Gly Ser Glu Cys Leu  
 90 95 100  
 ctt tcc atg gtt gaa gag gga aat cct cat cat tat ttt gtg gca aca 448  
 Leu Ser Met Val Glu Glu Gly Asn Pro His His Tyr Phe Val Ala Thr  
 105 110 115 120  
 cag gat cag aat ttg tct gtg aaa gta aaa aag aag cct gga gtt cct 496  
 Gln Asp Gln Asn Leu Ser Val Lys Val Lys Lys Lys Pro Gly Val Pro  
 125 130 135  
 ctc atg ttt att att cag aac act atg gtt ttg gac aaa cct tct ccc 544  
 Leu Met Phe Ile Ile Gln Asn Thr Met Val Leu Asp Lys Pro Ser Pro  
 140 145 150  
 aaa aca att gcc ttt gta aaa gca gtg gag tca ggt cag ctt gtc tca 592  
 Lys Thr Ile Ala Phe Val Lys Ala Val Glu Ser Gly Gln Leu Val Ser  
 155 160 165  
 gtg cat gag aaa gaa agt atc aaa cat ctc aaa gag gaa cag ggt tta 640  
 Val His Glu Lys Glu Ser Ile Lys His Leu Lys Glu Glu Gln Gly Leu  
 170 175 180  
 gtg aaa aac act gaa cag agt aga aga aaa aag cgc aag aaa ata agt 688  
 Val Lys Asn Thr Glu Gln Ser Arg Arg Lys Lys Arg Lys Lys Ile Ser  
 185 190 195 200



ggt ccc aat cct ctt agt tgt ttg aag aaa aag aaa aag gca ccg gac 736  
 Gly Pro Asn Pro Leu Ser Cys Leu Lys Lys Lys Lys Lys Ala Pro Asp  
 205 210 215  
 aca caa tca tct gct tct gaa aag aaa aga aaa aga aaa aga att cgg 784  
 Thr Gln Ser Ser Ala Ser Glu Lys Lys Arg Lys Arg Lys Arg Ile Arg  
 220 225 230  
 aac aga tct aac cca aaa gta ctt tct gag aag cag aat gca gaa gga 832  
 Asn Arg Ser Asn Pro Lys Val Leu Ser Glu Lys Gln Asn Ala Glu Gly  
 235 240 245  
 gaa tga atcctttgga tactttcaag gacattcaaa tgtgaaaatg aattttttac 888  
 Glu \*  
 250  
 aactagaagt atttataata aaagacccaaa cttatttttg taaatgaacc catatgcttt 948  
 actaaaatta attataaaat aaaaacagtg accagtctag ccagcatgga aaaccccatc 1008  
 tctactaaaa tacaaaaatt agctgggcat gatgggtgcac agttgtaatt ccagctactc 1068  
 aggaggctga ggcagtgagaa tcgcttgaac ctgggaggca gagattgcag tgagcccagt 1128  
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 aaaacagtgat atgggtgtag gtgtgatgga attcacttta cttactaaat ggtttcggga 1248  
 ggttgtttct ccaggtaaaa ttgtcgctc tctgggtcca tccccacctt caaacattat 1308  
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 agcg atg cgg gaa tgc ata tca gtc cac gtg ggc caa gcg gga gtt cag 169  
 Met Arg Glu Cys Ile Ser Val His Val Gly Gln Ala Gly Val Gln  
 1 5 10 15  
 att ggc aat gcc tgc tgg gag ctc ttc tgc ctg gaa cac ggc atc cag 217  
 Ile Gly Asn Ala Cys Trp Glu Leu Phe Cys Leu Glu His Gly Ile Gln  
 20 25 30  
 gca gac ggc act ttt gat gct caa gct agc aag atc aac gat gat gac 265  
 Ala Asp Gly Thr Phe Asp Ala Gln Ala Ser Lys Ile Asn Asp Asp Asp  
 35 40 45  
 tcc ttc acc acc ttt ttc agc gag act ggc aat ggg aag cat gtg ccc 313

Ser	Phe	Thr	Thr	Phe	Phe	Ser	Glu	Thr	Gly	Asn	Gly	Lys	His	Val	Pro	
		50					55					60				
cgg	gcc	gtc	atg	ata	gat	ctg	gag	cct	act	gta	gtg	gat	gag	gtt	cgg	361
Arg	Ala	Val	Met	Ile	Asp	Leu	Glu	Pro	Thr	Val	Val	Asp	Glu	Val	Arg	
	65					70				75						
gca	gga	acc	tac	cgc	cag	ctc	ttc	cat	cca	gag	cag	ctg	atc	aca	gga	409
Ala	Gly	Thr	Tyr	Arg	Gln	Leu	Phe	His	Pro	Glu	Gln	Leu	Ile	Thr	Gly	
	80				85				90						95	
aag	gag	gat	gca	gcc	aac	aac	tat	gcc	cgg	ggc	cac	tac	acg	gtg	ggc	457
Lys	Glu	Asp	Ala	Ala	Asn	Asn	Tyr	Ala	Arg	Gly	His	Tyr	Thr	Val	Gly	
			100					105					110			
aag	gag	agc	att	gac	ctg	gtg	ctg	gac	cgc	ata	cgg	aag	ctg	aca	gat	505
Lys	Glu	Ser	Ile	Asp	Leu	Val	Leu	Asp	Arg	Ile	Arg	Lys	Leu	Thr	Asp	
			115					120					125			
gct	tgc	tct	ggc	ctg	cag	ggc	ttc	ctg	att	ttc	cac	agt	ttt	ggg	ggg	553
Ala	Cys	Ser	Gly	Leu	Gln	Gly	Phe	Leu	Ile	Phe	His	Ser	Phe	Gly	Gly	
		130				135						140				
ggc	act	ggc	tcc	ggc	ttc	act	tct	ctg	ctg	atg	gaa	cgc	ctc	tcc	ctg	601
Gly	Thr	Gly	Ser	Gly	Phe	Thr	Ser	Leu	Leu	Met	Glu	Arg	Leu	Ser	Leu	
	145					150				155						
gat	tat	ggc	aag	aaa	tcc	aag	ctg	gag	ttt	gcc	atc	tac	cca	gcc	ccc	649
Asp	Tyr	Gly	Lys	Lys	Ser	Lys	Leu	Glu	Phe	Ala	Ile	Tyr	Pro	Ala	Pro	
	160				165				170						175	
cag	gtc	tct	act	gca	gtg	gtg	gag	ccc	tac	aac	tcc	atc	ctg	acc	acc	697
Gln	Val	Ser	Thr	Ala	Val	Val	Glu	Pro	Tyr	Asn	Ser	Ile	Leu	Thr	Thr	
				180					185					190		
cac	acc	aca	ctg	gaa	cat	tca	gat	tgt	gct	ttc	atg	gtg	gac	aac	gaa	745
His	Thr	Thr	Leu	Glu	His	Ser	Asp	Cys	Ala	Phe	Met	Val	Asp	Asn	Glu	
			195					200					205			
gcc	atc	tat	gac	atc	tgc	cgc	agg	aac	ctt	gac	att	gag	cgc	cct	acc	793
Ala	Ile	Tyr	Asp	Ile	Cys	Arg	Arg	Asn	Leu	Asp	Ile	Glu	Arg	Pro	Thr	
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tat	acc	aac	ctc	aac	cgc	ctc	atc	agt	cag	att	gtg	tcc	tca	atc	act	841
Tyr	Thr	Asn	Leu	Asn	Arg	Leu	Ile	Ser	Gln	Ile	Val	Ser	Ser	Ile	Thr	
		225				230					235					
gct	tct	ctc	cgc	ttt	gac	ggg	gcc	ctc	aat	gtg	gac	ctc	act	gag	ttc	889
Ala	Ser	Leu	Arg	Phe	Asp	Gly	Ala	Leu	Asn	Val	Asp	Leu	Thr	Glu	Phe	
	240				245				250					255		
cag	acc	aac	ctg	gtg	ccc	tac	ccc	cgc	atc	cac	ttc	ccg	ctg	gtc	acc	937
Gln	Thr	Asn	Leu	Val	Pro	Tyr	Pro	Arg	Ile	His	Phe	Pro	Leu	Val	Thr	
			260					265						270		
tac	gcg	ccc	atc	atc	tct	gcc	gag	aaa	gcc	tat	cac	gaa	cag	ctc	tct	985
Tyr	Ala	Pro	Ile	Ile	Ser	Ala	Glu	Lys	Ala	Tyr	His	Glu	Gln	Leu	Ser	
			275				280						285			
gtg	gcc	gag	ata	acc	agc	tcc	tgc	ttt	gag	ccc	aac	agc	cag	atg	gtg	1033
Val	Ala	Glu	Ile	Thr	Ser	Ser	Cys	Phe	Glu	Pro	Asn	Ser	Gln	Met	Val	
		290					295					300				
aag	tgc	gac	ccg	aga	cat	ggc	aag	tac	atg	gcc	tgc	tgc	atg	ctc	tac	1081

Lys Cys Asp Pro Arg His Gly Lys Tyr Met Ala Cys Cys Met Leu Tyr	
305 310 315	
cgg ggc gac gtg gtg ccc aag gat gtg aat gtc gct att gct gcc atc	1129
Arg Gly Asp Val Val Pro Lys Asp Val Asn Val Ala Ile Ala Ala Ile	
320 325 330 335	
aag acc aag agg acc atc cag ttt gta gac tgg tgt ccc aca ggc ttc	1177
Lys Thr Lys Arg Thr Ile Gln Phe Val Asp Trp Cys Pro Thr Gly Phe	
340 345 350	
aag gtg ggc atc aac tac cag ccc ccg acc gtg gtc ccc ggg gga gac	1225
Lys Val Gly Ile Asn Tyr Gln Pro Pro Thr Val Val Pro Gly Gly Asp	
355 360 365	
ctg gcc aag gtg cag cgg gcc gtc tgc atg ctc agc aac acc acg gcc	1273
Leu Ala Lys Val Gln Arg Ala Val Cys Met Leu Ser Asn Thr Thr Ala	
370 375 380	
att gcg gag gcc tgg gcc cgc ctc gac cac aag ttc gac ctc atg tac	1321
Ile Ala Glu Ala Trp Ala Arg Leu Asp His Lys Phe Asp Leu Met Tyr	
385 390 395	
gcc aag cgg gcc ttt gtg cat tgg tat gtg gga gag ggg atg gaa gaa	1369
Ala Lys Arg Ala Phe Val His Trp Tyr Val Gly Glu Gly Met Glu Glu	
400 405 410 415	
gga gaa ttt tct gag gcc agg gaa gac tta gct gcc ctg gag aag gat	1417
Gly Glu Phe Ser Glu Ala Arg Glu Asp Leu Ala Ala Leu Glu Lys Asp	
420 425 430	
tat gaa gaa gtg ggg act gat tcg ttt gaa gaa gaa aat gaa ggg gag	1465
Tyr Glu Glu Val Gly Thr Asp Ser Phe Glu Glu Glu Asn Glu Gly Glu	
435 440 445	
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Glu Phe *	
450	

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Met Asp Glu	
1	
gat tct tcg ttg aga gat tat act gta agc ttg gac tct gac atg gat	165
Asp Ser Ser Leu Arg Asp Tyr Thr Val Ser Leu Asp Ser Asp Met Asp	
5 10 15	
gat gca tct aaa ttt ctt cag gat tat gat att cga act ggc aac acc	213

Asp	Ala	Ser	Lys	Phe	Leu	Gln	Asp	Tyr	Asp	Ile	Arg	Thr	Gly	Asn	Thr		
20					25					30					35		
agg	gaa	gct	ttg	agt	cct	tgt	cca	agt	act	gta	agt	acc	aag	tct	cag		261
Arg	Glu	Ala	Leu	Ser	Pro	Cys	Pro	Ser	Thr	Val	Ser	Thr	Lys	Ser	Gln		
			40						45					50			
cca	ggc	agc	agt	gct	tct	tct	agt	tct	gga	gtt	aaa	atg	acc	agc	ttt		309
Pro	Gly	Ser	Ser	Ala	Ser	Ser	Ser	Ser	Gly	Val	Lys	Met	Thr	Ser	Phe		
			55					60					65				
gct	gaa	caa	aaa	ttc	agg	aaa	ctg	aat	cat	acc	gat	gga	aaa	agt	agt		357
Ala	Glu	Gln	Lys	Phe	Arg	Lys	Leu	Asn	His	Thr	Asp	Gly	Lys	Ser	Ser		
		70					75					80					
gga	agc	agt	tct	caa	aaa	act	aca	cca	gaa	ggc	tct	gaa	ctt	aat	att		405
Gly	Ser	Ser	Ser	Gln	Lys	Thr	Thr	Pro	Glu	Gly	Ser	Glu	Leu	Asn	Ile		
	85					90					95						
cct	cat	gtg	gtt	gct	tgg	gca	caa	att	cca	gaa	gaa	aca	ggg	ctt	cca		453
Pro	His	Val	Val	Ala	Trp	Ala	Gln	Ile	Pro	Glu	Glu	Thr	Gly	Leu	Pro		
100					105					110				115			
cag	gga	cgg	gac	act	acc	cag	ctg	ttg	gcc	tct	gaa	atg	gtg	cat	ctt		501
Gln	Gly	Arg	Asp	Thr	Thr	Gln	Leu	Leu	Ala	Ser	Glu	Met	Val	His	Leu		
			120						125					130			
agg	atg	aaa	cta	gaa	gaa	aag	agg	cgt	gct	ata	gaa	gcc	cag	aaa	aag		549
Arg	Met	Lys	Leu	Glu	Glu	Lys	Arg	Arg	Ala	Ile	Glu	Ala	Gln	Lys	Lys		
			135					140					145				
aaa	atg	gaa	gct	gct	ttt	acc	aaa	cag	aga	cag	aaa	atg	gga	agg	aca		597
Lys	Met	Glu	Ala	Ala	Phe	Thr	Lys	Gln	Arg	Gln	Lys	Met	Gly	Arg	Thr		
		150					155					160					
gca	ttc	ctt	act	gta	gtg	aaa	aag	aaa	ggg	gat	ggg	ata	tct	cct	cta		645
Ala	Phe	Leu	Thr	Val	Val	Lys	Lys	Lys	Gly	Asp	Gly	Ile	Ser	Pro	Leu		
	165					170					175						
cga	gag	gaa	gcg	gcg	ggt	gca	gaa	gat	gag	aaa	gta	tat	act	gat	cga		693
Arg	Glu	Glu	Ala	Ala	Gly	Ala	Glu	Asp	Glu	Lys	Val	Tyr	Thr	Asp	Arg		
180					185					190				195			
gca	aaa	gaa	aag	gaa	tca	caa	aaa	act	gat	gga	caa	agg	agc	aag	tca		741
Ala	Lys	Glu	Lys	Glu	Ser	Gln	Lys	Thr	Asp	Gly	Gln	Arg	Ser	Lys	Ser		
			200						205					210			
ctg	gca	gat	ata	aaa	gag	agc	atg	gag	aat	cct	caa	gcc	aaa	tgg	cta		789
Leu	Ala	Asp	Ile	Lys	Glu	Ser	Met	Glu	Asn	Pro	Gln	Ala	Lys	Trp	Leu		
			215					220					225				
aag	tct	cca	act	aca	cct	att	gat	cct	gag	aag	cag	tgg	aac	ctg	gca		837
Lys	Ser	Pro	Thr	Thr	Pro	Ile	Asp	Pro	Glu	Lys	Gln	Trp	Asn	Leu	Ala		
		230					235					240					
agc	ccc	tca	gaa	gaa	act	tta	aat	gaa	gga	gag	att	tta	gaa	tat	acc		885
Ser	Pro	Ser	Glu	Glu	Thr	Leu	Asn	Glu	Gly	Glu	Ile	Leu	Glu	Tyr	Thr		
	245					250					255						
aaa	tcc	att	gaa	aag	tta	aat	tca	tcc	ctg	cat	ttt	cta	caa	caa	gaa		933
Lys	Ser	Ile	Glu	Lys	Leu	Asn	Ser	Ser	Leu	His	Phe	Leu	Gln	Gln	Glu		
260					265					270					275		
atg	caa	cgc	ttg	tca	ctt	cag	cag	gag	atg	tta	atg	cag	atg	aga	gag		981

Met Gln Arg Leu Ser Leu Gln Gln Glu Met Leu Met Gln Met Arg Glu	
280 285 290	
caa caa tct tgg gtg att tca cct cca caa ccc tct cca cag aaa cag	1029
Gln Gln Ser Trp Val Ile Ser Pro Pro Gln Pro Ser Pro Gln Lys Gln	
295 300 305	
att cga gat ttt aag cct tct aag cag gca ggc ctg tca tca gcc att	1077
Ile Arg Asp Phe Lys Pro Ser Lys Gln Ala Gly Leu Ser Ser Ala Ile	
310 315 320	
gca cca ttc tcc tca gac tcc cct cgt cct act cac cca tct cca cag	1125
Ala Pro Phe Ser Ser Asp Ser Pro Arg Pro Thr His Pro Ser Pro Gln	
325 330 335	
tct tct aac agg aaa agt gca tct ttt tct gtt aaa agt caa agg act	1173
Ser Ser Asn Arg Lys Ser Ala Ser Phe Ser Val Lys Ser Gln Arg Thr	
340 345 350 355	
cct agg cca aat gag tta aaa ata aca cct ttg aat cga acc ttg aca	1221
Pro Arg Pro Asn Glu Leu Lys Ile Thr Pro Leu Asn Arg Thr Leu Thr	
360 365 370	
cct cct cgg tct gtg gat agc ctt cct cgg tta agg agg ttt tca cca	1269
Pro Pro Arg Ser Val Asp Ser Leu Pro Arg Leu Arg Arg Phe Ser Pro	
375 380 385	
agt caa gtt cct att caa act agg tca ttt gta tgt ttt ggg gat gat	1317
Ser Gln Val Pro Ile Gln Thr Arg Ser Phe Val Cys Phe Gly Asp Asp	
390 395 400	
gga gaa cct cag tta aag gaa tcc aaa cct aaa gag gaa gtt aaa aag	1365
Gly Glu Pro Gln Leu Lys Glu Ser Lys Pro Lys Glu Glu Val Lys Lys	
405 410 415	
gag gaa ttg gaa tcc aaa ggg act ttg gaa cag cgt gga cat aat cca	1413
Glu Glu Leu Glu Ser Lys Gly Thr Leu Glu Gln Arg Gly His Asn Pro	
420 425 430 435	
gaa gaa aag gaa atc aaa cct ttt gag tca aca gtc tct gaa gtc cta	1461
Glu Glu Lys Glu Ile Lys Pro Phe Glu Ser Thr Val Ser Glu Val Leu	
440 445 450	
tca ctg cct gtc aca gag act gta tgt ctg aca cca aat gag gac caa	1509
Ser Leu Pro Val Thr Glu Thr Val Cys Leu Thr Pro Asn Glu Asp Gln	
455 460 465	
ttg aat caa ccc aca gaa ccc cct cct aaa ccc gtt ttc cca ccc act	1557
Leu Asn Gln Pro Thr Glu Pro Pro Lys Pro Val Phe Pro Pro Thr	
470 475 480	
gct cca aaa aat gtt aat ctg att gaa gtt tcc ctc tca gat ttg aaa	1605
Ala Pro Lys Asn Val Asn Leu Ile Glu Val Ser Leu Ser Asp Leu Lys	
485 490 495	
ccc cct gaa aag gct gat gta cct gtt gaa aaa tat gat gga gaa agt	1653
Pro Pro Glu Lys Ala Asp Val Pro Val Glu Lys Tyr Asp Gly Glu Ser	
500 505 510 515	
gat aaa gaa caa ttt gat gat gac cag aaa gta tgc tgt gga ttc ttt	1701
Asp Lys Glu Gln Phe Asp Asp Asp Gln Lys Val Cys Cys Gly Phe Phe	
520 525 530	
ttt aag gat gat caa aaa gca gaa aat gat atg gca atg aaa cgg gca	1749

Phe Lys Asp Asp Gln Lys Ala Glu Asn Asp Met Ala Met Lys Arg Ala	
535 540 545	
gct ttg ttg gag aaa aga tta aga agg gaa aag gaa act cag ctc cgg	1797
Ala Leu Leu Glu Lys Arg Leu Arg Arg Glu Lys Glu Thr Gln Leu Arg	
550 555 560	
aaa caa cag ttg gaa gca gaa atg gag cat aag aag gag gaa aca agg	1845
Lys Gln Gln Leu Glu Ala Glu Met Glu His Lys Lys Glu Glu Thr Arg	
565 570 575	
cgt aaa act gag gaa gaa cgt cag aag aaa gaa gat gag aga gca cgc	1893
Arg Lys Thr Glu Glu Arg Glu Gln Lys Lys Glu Asp Glu Arg Ala Arg	
580 585 590 595	
aga gaa ttt att agg caa gaa tat atg agg cgg aaa caa ctg aaa cta	1941
Arg Glu Phe Ile Arg Gln Glu Tyr Met Arg Arg Lys Gln Leu Lys Leu	
600 605 610	
atg gaa gat atg gat aca gta att aaa ccc cgt cct caa gta gta aaa	1989
Met Glu Asp Met Asp Thr Val Ile Lys Pro Arg Pro Gln Val Val Lys	
615 620 625	
caa aaa aaa cag cga cca aaa tct att cac aga gat cat att gaa tcc	2037
Gln Lys Lys Gln Arg Pro Lys Ser Ile His Arg Asp His Ile Glu Ser	
630 635 640	
ccc aaa aca cca ata aag ggt cct cca gtc tct agc ctt tct ttg gca	2085
Pro Lys Thr Pro Ile Lys Gly Pro Pro Val Ser Ser Leu Ser Ala	
645 650 655	
tcg ctg aac acg ggt gat aac gag agt gta cat tca ggc aag agg acg	2133
Ser Leu Asn Thr Gly Asp Asn Glu Ser Val His Ser Gly Lys Arg Thr	
660 665 670 675	
cca aga tca gag tct gta gaa ggc ttc tta tct cca agt cgt tgt ggc	2181
Pro Arg Ser Glu Ser Val Glu Gly Phe Leu Ser Pro Ser Arg Cys Gly	
680 685 690	
agt cga aat gga gaa aaa gac tgg gag aat gca tca aca act tct tca	2229
Ser Arg Asn Gly Glu Lys Asp Trp Glu Asn Ala Ser Thr Thr Ser Ser	
695 700 705	
gtg gct tct gga aca gaa tat aca gga cca aag ctc tac aaa gaa ccc	2277
Val Ala Ser Gly Thr Glu Tyr Thr Gly Pro Lys Leu Tyr Lys Glu Pro	
710 715 720	
agt gca aaa tcc aat aag cac ata ata caa aat gct tta gct cat tgc	2325
Ser Ala Lys Ser Asn Lys His Ile Ile Gln Asn Ala Leu Ala His Cys	
725 730 735	
tgt ttg gct gga aaa gta aat gaa ggt cag aag aaa aaa ata ctg gag	2373
Cys Leu Ala Gly Lys Val Asn Glu Gly Gln Lys Lys Lys Ile Leu Glu	
740 745 750 755	
gaa atg gag aaa tca gat gcc aac aac ttc tta atc ttg ttc cgg gat	2421
Glu Met Glu Lys Ser Asp Ala Asn Asn Phe Leu Ile Leu Phe Arg Asp	
760 765 770	
tca gga tgc cag ttc aga tct tta tac act tat tgc cca gaa act gaa	2469
Ser Gly Cys Gln Phe Arg Ser Leu Tyr Thr Tyr Cys Pro Glu Thr Glu	
775 780 785	
gaa atc aat aaa ctg act ggg ata ggc cct aaa tct atc act aaa aaa	2517

Glu Ile Asn Lys Leu Thr Gly Ile Gly Pro Lys Ser Ile Thr Lys Lys	
790	795 800
atg att gaa gga ctt tac aaa tat aat tct gac agg aaa cag ttt agc	2565
Met Ile Glu Gly Leu Tyr Lys Tyr Asn Ser Asp Arg Lys Gln Phe Ser	
805 810 815	
cac ata ccc gct aaa act tta tct gcc agt gtt gat gca att acc att	2613
His Ile Pro Ala Lys Thr Leu Ser Ala Ser Val Asp Ala Ile Thr Ile	
820 825 830 835	
cat agc cat tta tgg cag acc aaa aga cca gta aca ccc aaa aaa ctt	2661
His Ser His Leu Trp Gln Thr Lys Arg Pro Val Thr Pro Lys Lys Leu	
840 845 850	
tta ccc act aag gca tag aagttg ggaaatactt gcttcagaac attcatggta	2715
Leu Pro Thr Lys Ala *	
855	
aatttgcaact tcactctttcc tgcctataga aaatctttct aattgccaac aagactttta	2775
ttaattaaaa ctggacatta agctctgttg tcatgaacaa ctggaatgta aaccacagta	2835
ttttggagtg cagaacattc tcaattaagt gataagtcca aatgatgaag gaaatgtttt	2895
aattcacaaa tggagatttg tatgtgttat cagggttcacc tgcttgatat tagatacatt	2955
aaagcactga attttcatgg atattagttg gatttatcat tgaaatatgg ttaagattac	3015
aaattatgtg ttttatttgt tgcttttttt taacctttta atgtatatcc ttgtcttcag	3075
atggtttgct atttttctct cctgggggtt tattctaaga tacctttgta ttttatttca	3135
tgtggagatc atgaaagtag gaaatatacc tttagaagta actcgcacct ttcttatgat	3195
gttaagagaa acactagtgt ttagttttac agtaaccctc atattttaat ggtgttacag	3255
catttgcaaa aattattctg ctaagtattt acaactctat ttattattca ctcaagtatt	3315
aacattctct attaaataag aggaggtgtt gtaaagagct gctagtaggt tcgctttaa	3375
ccacatgagc ttaaccaaga atatgttatg agaagttgct gattaaatca gtgctgtttt	3435
tacaccactt ctggccaact cagaataatt tagattgttc ttttaacaaa aaaggctttc	3495
tatctctttt aaagtaagtc actttataag ttggcagaag tgaatgacac tttgagagta	3555
gtctttcaat ctgaagatgt aagacttctt gaaacaagtt ctcaagaagt ctttacatta	3615
tatttataac tcataataaa atttatatta gaatttttaa acatgtacaa agggctacat	3675
tttaatttta aaatagcttc acattatttt acttatattg gggttttctt cattttaatc	3735
cttttcaagt ggaatggctt agaataagta tacacttgaa atctcctcta catgatcttt	3795
gttctttaac agtgatatcc agagggttag ttggggaaaa acttcattct caggaaaaga	3855
cttgaatgat tatgtgacct tggttatatt cagtgtgttg acaaagtgt aaactagcgg	3915
gggaagacag tattgtatca taaatgagat gcgtagtttg ttttctttca tgggaagtag	3975
agataaaaat atatacatct ctctaattga gttgtttaga gaaagaacta atgtctcata	4035
tgatgtattt acttatttta aaaaaaagaa taggaatgag atgtccctga gctgtacttt	4095

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tctattatta taaggccttt aggcattcagt gcatctgggt tatcaacatt ttctcaaattg 4155
ctgtcaatat tttactgtaa tttatgttct tatatttatg tatatttggt aaaactgtaa 4215
aaaaatttca cagatttttt tccaatacct gtgcaagata catgtgtagc tcaaaactat 4275
ttgtgatcta ctgtttgcat gtaagagacc aggatatgta actcttatat ttttaagtgt 4335
tacatattgt gtatataaca tatggatatt aaaaaatggg aattgcacat ttacctttt 4395
ggacagtaat ttctatcaca gttagaagga aatgatagtc aaatacacgt ttagattaaa 4455
actagtttaa aaaattataa atgaatctaa tcaaaatgtg aatagtagtc aaaaggataa 4515
tttaataagc attttacgtt actaaatttg ttcatttcaa tattaactaa atttccctca 4575
tcaaagcaat ctttgtgata ttacttcgct attaaataaa gaaaattgga tgcaagacaa 4635
tgagagaaact ttaaaactaa acaggaccac cctttattct taaatttggt tgtgtccaac 4695
agttgaattg aatgtctata aggtctaaag gtagaatgtg aatattgcca cagagtccat 4755
tgctctcagt ataagatttt actttattaa tgcagaagga atatggatat atttctttaa 4815
gtctgcagat ttttttatta tgggtcagct tttttttaat tatgttttta aaattatata 4875
gttgaaaaat atgccatttc ataaagtctg aggattttcg tcaaccttac tgaaacacac 4935
tggtgctttc atcatcagag gtcaaattat tatgataact attccattaa gtttgccaaa 4995
catttgctgt ggttaccagt gcagcctgtc aaattctgct atttgacaca gctttggaaa 5055
gatttagttc ttggtttttc cgttttgat tagaatgact gttacagttt tatttggtg 5115
tttaaagcca aattcagcta ttaattatg gtttcatgga cactgttgag caatgtacag 5175
tgtatggtgt gcttacctgt ccactctaga gcattgctta cagggttttt gttttttaag 5235
atgctgtgct gtaaaatact gtcatacttg ctatttcctg gtacagtgtg gtttttcccc 5295
tttcatttga ataaaagcat ggcaccaaatt gactcctttt ctgtttcttg aataaaatgt 5355
agtttttgggt aaaattattt g 5376

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<210> 417
<211> 1180
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (196)..(1077)

```

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<400> 417
ccactttgta caagaaagct gggtagcgt aagcttgggc ccctcgaggt ttactctaga 60
gcggccgcgg gcttgggggc ttgcggggg cggggcggcc ggcgccccg gctgctcccg 120
ccgcccgcgg gacccgcgcc ccgcccgggc agcggtggtg agagccccga ctccccggac 180

```



gccgccgccgcc gtgcc atg ggg ttc ccg gcc gcg gcg ctg ctc tgc gcg ctg 231  
 Met Gly Phe Pro Ala Ala Ala Leu Leu Cys Ala Leu  
 1 5 10

tgc tgc ggc ctc ctg gcc ccg gct gcc cgc gcc ggc tac tcc gag gag 279  
 Cys Cys Gly Leu Leu Ala Pro Ala Ala Arg Ala Gly Tyr Ser Glu Glu  
 15 20 25

cgc tgc agc tgg agg ggc agc ggc ctc acc cag gag ccc ggc agc gtg 327  
 Arg Cys Ser Trp Arg Gly Ser Gly Leu Thr Gln Glu Pro Gly Ser Val  
 30 35 40

ggg cag ctg gcc ctg gcc tgt gcg gag ggc gcg gtt gag tgg ctg tac 375  
 Gly Gln Leu Ala Leu Ala Cys Ala Glu Gly Ala Val Glu Trp Leu Tyr  
 45 50 55 60

ccg gct ggg gcg ctg cgc ctg acc ctg ggc ggc ccc gat ccc aga gcg 423  
 Pro Ala Gly Ala Leu Arg Leu Thr Leu Gly Gly Pro Asp Pro Arg Ala  
 65 70 75

cgg ccc ggc atc gcc tgt ctg cgg ccg gtg cgg ccc ttc gcg ggc gcc 471  
 Arg Pro Gly Ile Ala Cys Leu Arg Pro Val Arg Pro Phe Ala Gly Ala  
 80 85 90

cag gtc ttc gcg gag cgc gca ggg ggc gcc ctg gag ctg ctg ctg gct 519  
 Gln Val Phe Ala Glu Arg Ala Gly Gly Ala Leu Glu Leu Leu Leu Ala  
 95 100 105

gag ggc ccg ggc ccg gca ggg ggc cgc tgc gtg cgc tgg ggt ccc cgc 567  
 Glu Gly Pro Gly Pro Ala Gly Gly Arg Cys Val Arg Trp Gly Pro Arg  
 110 115 120

gag cgc ccg gcc ctc ttc ctg cag gcc acg ccg cac cag gac atc agc 615  
 Glu Arg Arg Ala Leu Phe Leu Gln Ala Thr Pro His Gln Asp Ile Ser  
 125 130 135 140

cgc cgc gtg gcc gcc ttc cgc ttt gag ctg cgc gag gac ggg cgc ccc 663  
 Arg Arg Val Ala Ala Phe Arg Phe Glu Leu Arg Glu Asp Gly Arg Pro  
 145 150 155

gag ctg ccc ccg cag gcc cac ggt ctc ggc gta gac ggt gcc tgc agg 711  
 Glu Leu Pro Pro Gln Ala His Gly Leu Gly Val Asp Gly Ala Cys Arg  
 160 165 170

ccc tgc agc gac gct gag ctg ctc ctg gcc gca tgc acc agc gac ttc 759  
 Pro Cys Ser Asp Ala Glu Leu Leu Leu Ala Ala Cys Thr Ser Asp Phe  
 175 180 185

gta att cac ggg atc atc cat ggg gtc acc cat gac gtg gag ctg cag 807  
 Val Ile His Gly Ile Ile His Gly Val Thr His Asp Val Glu Leu Gln  
 190 195 200

gag tct gtc atc act gtg gtg gcc gcc cgt gtc ctc cgc cag aca ccg 855  
 Glu Ser Val Ile Thr Val Val Ala Ala Arg Val Leu Arg Gln Thr Pro  
 205 210 215 220

ccg ctg ttc cag gcg ggg cga tcc ggg gac cag ggg ctg acc tcc att 903  
 Pro Leu Phe Gln Ala Gly Arg Ser Gly Asp Gln Gly Leu Thr Ser Ile  
 225 230 235

cgt acc cca ctg cgc tgt ggc gtc cac ccg ggc cca ggc acc ttc ctc 951  
 Arg Thr Pro Leu Arg Cys Gly Val His Pro Gly Pro Gly Thr Phe Leu  
 240 245 250

```

ttc atg ggc tgg agc cgc ttt ggg gag gcc cgg ctg ggc tgt gcc cca      999
Phe Met Gly Trp Ser Arg Phe Gly Glu Ala Arg Leu Gly Cys Ala Pro
      255              260              265

cga ttc cag gag ttc cgc cgt gcc tac gag gct gcc cgt gct gcc cac      1047
Arg Phe Gln Glu Phe Arg Arg Ala Tyr Glu Ala Ala Arg Ala Ala His
      270              275              280

ctc cac ccc tgc gag gtg gcg ctg cac tga g gggctgggtg ctggggaggg      1098
Leu His Pro Cys Glu Val Ala Leu His *
      285              290

gctggttagga gggaggggtgg gcccaactgct ttggaggtga tgggactatc aataagaact      1158

ctgttcacgc aaaaaaaaaa aa                                             1180

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```

<210> 418
<211> 1540
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (210)..(1322)

```

```

<220>
<221> misc_feature
<222> (1)...(1540)
<223> n = a,t,c or g

```

```

<400> 418
aggttcccc cnntttgacg actgagagca tgatgatata actatctatt cgatgatgaa      60
gataccccac caaacccaaa aaaagagatc tctcgaggat ccgaattcgc ggccgcgtcg      120
accgacacga ccatcatttg tcgacgccgc tgccaccgcc tgcctgagag aagtcgtcgc      180
ggccgacccc gtcgcctccg ccggctacc atg tcc gcc cag gcg cag atg cgg      233
                        Met Ser Ala Gln Ala Gln Met Arg
                        1              5

gcc ctg ctg gac cag ctc atg ggc acg gct cgg gac gac gaa acc aga      281
Ala Leu Leu Asp Gln Leu Met Gly Thr Ala Arg Asp Asp Glu Thr Arg
      10              15              20

cag agg gtc aag ttt aca gat gac cgt gtc tgc aag agt cac ctt ctg      329
Gln Arg Val Lys Phe Thr Asp Asp Arg Val Cys Lys Ser His Leu Leu
      25              30              35              40

gac tgc tgc ccc cat gac atc ctg gct ggg acg cgc atg gat tta gga      377
Asp Cys Cys Pro His Asp Ile Leu Ala Gly Thr Arg Met Asp Leu Gly
      45              50              55

gaa tgt acc aaa atc cac gac ttg gcc ctc cga gca gat tat gag att      425
Glu Cys Thr Lys Ile His Asp Leu Ala Leu Arg Ala Asp Tyr Glu Ile
      60              65              70

gca agt aaa gaa aga gac ctg ttt ttt gaa tta gat gca atg gat cac      473
Ala Ser Lys Glu Arg Asp Leu Phe Phe Glu Leu Asp Ala Met Asp His
      75              80              85

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ttg gag tcc ttt att gct gaa tgt gat cgg aga act gag ctc gcc aag	521
Leu Glu Ser Phe Ile Ala Glu Cys Asp Arg Arg Thr Glu Leu Ala Lys	
90 95 100	
aag cgg ctg gca gaa aca cag gag gaa atc agt gcg gaa gtt tct gca	569
Lys Arg Leu Ala Glu Thr Gln Glu Glu Ile Ser Ala Glu Val Ser Ala	
105 110 115 120	
aag gca gaa aaa gta cat gag tta aat gaa gaa ata gga aaa ctc ctt	617
Lys Ala Glu Lys Val His Glu Leu Asn Glu Glu Ile Gly Lys Leu Leu	
125 130 135	
gct aaa gcc gaa cag cta ggg gct gaa ggt aat gtg gat gaa tcc cag	665
Ala Lys Ala Glu Gln Leu Gly Ala Glu Gly Asn Val Asp Glu Ser Gln	
140 145 150	
aag att ctt atg gaa gtg gaa aaa gtt cgt gcg aag aaa aaa gaa gct	713
Lys Ile Leu Met Glu Val Glu Lys Val Arg Ala Lys Lys Lys Glu Ala	
155 160 165	
gag gaa gaa tac aga aat tcc atg cct gca tcc agt ttt cag cag caa	761
Glu Glu Glu Tyr Arg Asn Ser Met Pro Ala Ser Ser Phe Gln Gln Gln	
170 175 180	
aag ctg cgt gtc tgc gag gtc tgt tca gcc tac ctt ggt ctc cat gac	809
Lys Leu Arg Val Cys Glu Val Cys Ser Ala Tyr Leu Gly Leu His Asp	
185 190 195 200	
aat gac cgt cgc ctg gca gac cac ttc ggt ggc aag tta cac ttg ggg	857
Asn Asp Arg Arg Leu Ala Asp His Phe Gly Gly Lys Leu His Leu Gly	
205 210 215	
ttc att cag atc cga gag aag ctt gat cag ttg agg aaa act gtc gct	905
Phe Ile Gln Ile Arg Glu Lys Leu Asp Gln Leu Arg Lys Thr Val Ala	
220 225 230	
gaa aag cag gag aag aga aat cag gat cgc ttg agg agg aga gag gag	953
Glu Lys Gln Glu Lys Arg Asn Gln Asp Arg Leu Arg Arg Arg Glu Glu	
235 240 245	
agg gaa cgg gag gag cgt ctg agc agg agg tcg gga tca aga acc aga	1001
Arg Glu Arg Glu Glu Arg Leu Ser Arg Arg Ser Gly Ser Arg Thr Arg	
250 255 260	
gat cgc agg agg tca cgc tcc cgg gat cgg cgt cgg agg cgg tca aga	1049
Asp Arg Arg Arg Ser Arg Ser Arg Asp Arg Arg Arg Arg Ser Arg	
265 270 275 280	
tct acc tcc cga gag cga cgg aaa ttg tcc cgg tcc cgg tcc cga gat	1097
Ser Thr Ser Arg Glu Arg Arg Lys Leu Ser Arg Ser Arg Ser Arg Asp	
285 290 295	
aga cat cgg cgc cac cgc agc cgt tcc cgg agc cac agc cgg gga cat	1145
Arg His Arg Arg His Arg Ser Arg Ser Arg Ser His Ser Arg Gly His	
300 305 310	
cgt cgg gct tcc cgg gac cga agt gcg aaa tac aag ttc tcc aga gag	1193
Arg Arg Ala Ser Arg Asp Arg Ser Ala Lys Tyr Lys Phe Ser Arg Glu	
315 320 325	
cgg gca tcc aga gag gag tcc tgg gag agc ggg cgg agc gag cga ggg	1241
Arg Ala Ser Arg Glu Glu Ser Trp Glu Ser Gly Arg Ser Glu Arg Gly	
330 335 340	

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ccc ccg gac tgg agg ctt gag agc tcc aac ggg aag atg gct tca cgg      1289
Pro Pro Asp Trp Arg Leu Glu Ser Ser Asn Gly Lys Met Ala Ser Arg
345                      350                      355                      360

agg tca gaa gag aag gag gcc ggc gag atc tga acccgtct cccgggtgct      1340
Arg Ser Glu Glu Lys Glu Ala Gly Glu Ile *
                      365                      370

gtaaatagtc tgataaacgt tcacacagtc taaaattacc ctttatatatt gctgaataca      1400

actcatcttt tgtagtttaa aatttctatt gttttggagc tagctgtgag tttctagaag      1460

tgtacagagt tgctcctgtg ttcccgggtc atgttgagta ggaataaata aatctgatgc      1520

tgcctcctga aaaaaaaaaa                                         1540

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```

<210> 419
<211> 1363
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (210) .. (1145)

```

```

<220>
<221> misc_feature
<222> (1) ... (1363)
<223> n = a,t,c or g

```

```

<400> 419
aggttcccc cnntttgacg actgagagca tgatgatata actatctatt cgatgatgaa      60
gataccccac caaacccaaa aaaagagatc tctcgaggat ccgaattcgc ggccgcgtcg      120
accgacacga ccatcatttg tcgacgccgc tgccaccgcc tgcctgagag aagtcgtcgc      180
ggccgacccc gtcgcctccg ccggtctacc atg tcc gcc cag gcg cag atg cgg      233
                               Met Ser Ala Gln Ala Gln Met Arg
                               1                      5

gcc ctg ctg gac cag ctc atg ggc acg gct cgg gac gac gaa acc aga      281
Ala Leu Leu Asp Gln Leu Met Gly Thr Ala Arg Asp Asp Glu Thr Arg
   10                      15                      20

cag agg gtc aag ttt aca gat gac cgt gtc tgc aag agt cac ctt ctg      329
Gln Arg Val Lys Phe Thr Asp Asp Arg Val Cys Lys Ser His Leu Leu
   25                      30                      35                      40

gac tgc tgc ccc cat gac atc ctg gct ggg acg cgc atg gat tta gga      377
Asp Cys Cys Pro His Asp Ile Leu Ala Gly Thr Arg Met Asp Leu Gly
                      45                      50                      55

gaa tgt acc aaa atc cac gac ttg gcc ctc cga gca gat tat gag att      425
Glu Cys Thr Lys Ile His Asp Leu Ala Leu Arg Ala Asp Tyr Glu Ile
                      60                      65                      70

gca agt aaa gaa aga gac ctg ttt ttt gaa tta gat gca atg gat cac      473
Ala Ser Lys Glu Arg Asp Leu Phe Glu Leu Asp Ala Met Asp His
   75                      80                      85

```

ttg gag tcc ttt att gct gaa tgt gat cgg aga act gag ctc gcc aag	521
Leu Glu Ser Phe Ile Ala Glu Cys Asp Arg Arg Thr Glu Leu Ala Lys	
90 95 100	
aag cgg ctg gca gaa aca cag gag gaa atc agt gcg gaa gtt tct gca	569
Lys Arg Leu Ala Glu Thr Gln Glu Glu Ile Ser Ala Glu Val Ser Ala	
105 110 115 120	
aag gca gaa aaa gta cat gag tta aat gaa gaa ata gga aaa ctc ctt	617
Lys Ala Glu Lys Val His Glu Leu Asn Glu Glu Ile Gly Lys Leu Leu	
125 130 135	
gct aaa gcc gaa cag cta ggg gct gaa ggt aat gtg gat gaa tcc cag	665
Ala Lys Ala Glu Gln Leu Gly Ala Glu Gly Asn Val Asp Glu Ser Gln	
140 145 150	
aag att ctt atg gaa gtg gaa aaa gtt cgt gcg aag aaa aaa gaa gct	713
Lys Ile Leu Met Glu Val Glu Lys Val Arg Ala Lys Lys Lys Glu Ala	
155 160 165	
gag aaa act gtc gct gaa aag cag gag aag aga aat cag gat cgc ttg	761
Glu Lys Thr Val Ala Glu Lys Gln Glu Lys Arg Asn Gln Asp Arg Leu	
170 175 180	
agg agg aga gag gag agg gaa cgg gag gag cgt ctg agc agg agg tcg	809
Arg Arg Arg Glu Glu Arg Glu Arg Glu Glu Arg Leu Ser Arg Arg Ser	
185 190 195 200	
gga tca aga acc aga gat cgc agg agg tca cgc tcc cgg gat cgg cgt	857
Gly Ser Arg Thr Arg Asp Arg Arg Arg Ser Arg Ser Arg Asp Arg Arg	
205 210 215	
cgg agg cgg tca aga tct acc tcc cga gag cga cgg aaa ttg tcc cgg	905
Arg Arg Arg Ser Arg Ser Thr Ser Arg Glu Arg Arg Lys Leu Ser Arg	
220 225 230	
tcc cgg tcc cga gat aga cat cgg cgc cac cgc agc cgt tcc cgg agc	953
Ser Arg Ser Arg Asp Arg His Arg Arg His Arg Ser Arg Ser Arg Ser	
235 240 245	
cac agc cgg gga cat cgt cgg gct tcc cgg gac cga agt gcg aaa tac	1001
His Ser Arg Gly His Arg Arg Ala Ser Arg Asp Arg Ser Ala Lys Tyr	
250 255 260	
aag ttc tcc aga gag cgg gca tcc aga gag gag tcc tgg gag agc ggg	1049
Lys Phe Ser Arg Glu Arg Ala Ser Arg Glu Glu Ser Trp Glu Ser Gly	
265 270 275 280	
cgg agc gag cga ggg ccc ccg gac tgg agg ctt gag agc tcc aac ggg	1097
Arg Ser Glu Arg Gly Pro Pro Asp Trp Arg Leu Glu Ser Ser Asn Gly	
285 290 295	
aag atg gct tca cgg agg tca gaa gag aag gag gcc ggc gag atc tga	1145
Lys Met Ala Ser Arg Arg Ser Glu Glu Lys Glu Ala Gly Glu Ile *	
300 305 310	
acccgtctcc cgggtgctgt aaatagtctg ataaacgttc acacagtcta aaattaccct	1205
ttatatattgc tgaatacaac tcattcttttg tagtttaaaa tttctattgt tttggagcta	1265
gctgtgagtt tctagaagtg tacagagttg ctctgtgtt cccgggtcat gttgagtagg	1325
aataaataaa tctgatgctg cctcctgaaa aaaaaaaa	1363

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<220>
<221> CDS
<222> (30) .. (3218)
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1086

gac agc cca tgg gtg aag ccg tct cgg aaa cgg cgc aag cgg gag cct Asp Ser Pro Trp Val Lys Pro Ser Arg Lys Arg Arg Lys Arg Glu Pro 205 210 215	677
ccg cgg gcc aag gag cca cga gga gtg aat ggt gtg ggc tcc tca ggc Pro Arg Ala Lys Glu Pro Arg Gly Val Asn Gly Val Gly Ser Ser Gly 220 225 230	725
ccc agt gag tac atg gag gtc cct ctg ggg tcc ctg gag ctg ccc agc Pro Ser Glu Tyr Met Glu Val Pro Leu Gly Ser Leu Glu Leu Pro Ser 235 240 245	773
gag ggg acc ctc tcc ccc aac cac gct ggg gtg tcc aat gac aca tct Glu Gly Thr Leu Ser Pro Asn His Ala Gly Val Ser Asn Asp Thr Ser 250 255 260	821
tcg ctg gag aca gag cga ggg ttt gag gag ttg ccc ctg tgc agc tgc Ser Leu Glu Thr Glu Arg Gly Phe Glu Glu Leu Pro Leu Cys Ser Cys 265 270 275 280	869
cgc atg gag gca ccc aag att gac cgc atc agc gag agg gcg ggg cac Arg Met Glu Ala Pro Lys Ile Asp Arg Ile Ser Glu Arg Ala Gly His 285 290 295	917
aag tgc atg gcc act gag agt gtg gac gga gag ctg tca ggc tgc aat Lys Cys Met Ala Thr Glu Ser Val Asp Gly Glu Leu Ser Gly Cys Asn 300 305 310	965
gcc gcc atc ctc aag cgg gag acc atg agg cca tcc agc cgt gtg gcc Ala Ala Ile Leu Lys Arg Glu Thr Met Arg Pro Ser Ser Arg Val Ala 315 320 325	1013
ctg atg gtg ctc tgt gag acc cac cgc gcc cgc atg gtc aaa cac cac Leu Met Val Leu Cys Glu Thr His Arg Ala Arg Met Val Lys His His 330 335 340	1061
tgc tgc ccg ggc tgc ggc tac ttc tgc acg gcg ggc acc ttc ctg gag Cys Cys Pro Gly Cys Gly Tyr Phe Cys Thr Ala Gly Thr Phe Leu Glu 345 350 355 360	1109
tgc cac cct gac ttc cgt gtg gcc cac cgc ttc cac aag gcc tgt gtg Cys His Pro Asp Phe Arg Val Ala His Arg Phe His Lys Ala Cys Val 365 370 375	1157
tct cag ctg aat ggg atg gtc ttc tgt ccc cac tgt ggg gag gat gct Ser Gln Leu Asn Gly Met Val Phe Cys Pro His Cys Gly Glu Asp Ala 380 385 390	1205
tct gaa gct caa gag gtg acc atc ccc cgg ggt gac ggg gtg acc cca Ser Glu Ala Gln Glu Val Thr Ile Pro Arg Gly Asp Gly Val Thr Pro 395 400 405	1253
ccg gcc ggc act gca gct cct gca ccc cca ccc ctg tcc cag gat gtc Pro Ala Gly Thr Ala Ala Pro Ala Pro Pro Pro Leu Ser Gln Asp Val 410 415 420	1301
ccc ggg aga gca gac act tct cag ccc agt gcc cgg atg cga ggg cat Pro Gly Arg Ala Asp Thr Ser Gln Pro Ser Ala Arg Met Arg Gly His 425 430 435 440	1349
ggg gaa ccc cgg cgc ccg ccc tgc gat ccc ctg gct gac acc att gac Gly Glu Pro Arg Arg Pro Pro Cys Asp Pro Leu Ala Asp Thr Ile Asp 445 450 455	1397

agc tca ggg ccc tcc ctg acc ctg ccc aat ggg ggc tgc ctt tca gcc Ser Ser Gly Pro Ser Leu Thr Leu Pro Asn Gly Gly Cys Leu Ser Ala 460 465 470	1445
gtg ggg ctg cca ctg ggg cca ggc cgg gag gcc ctg gaa aag gcc ctg Val Gly Leu Pro Leu Gly Pro Gly Arg Glu Ala Leu Glu Lys Ala Leu 475 480 485	1493
gtc atc cag gag tca gag agg cgg aag aag ctc cgt ttc cac cct cgg Val Ile Gln Glu Ser Glu Arg Arg Lys Lys Leu Arg Phe His Pro Arg 490 495 500	1541
cag ttg tac ctg tcc gtg aag cag ggc gag ctg cag aag gtg atc ctg Gln Leu Tyr Leu Ser Val Lys Gln Gly Glu Leu Gln Lys Val Ile Leu 505 510 515 520	1589
atg ctg ttg gac aac ctg gac ccc aac ttc cag agc gac cag cag agc Met Leu Leu Asp Asn Leu Asp Pro Asn Phe Gln Ser Asp Gln Gln Ser 525 530 535	1637
aag cgc acg ccc ctg cat gca gcc gcc cag aag ggc tcc gtg gag atc Lys Arg Thr Pro Leu His Ala Ala Ala Gln Lys Gly Ser Val Glu Ile 540 545 550	1685
tgc cat gtg ctg ctg cag gct gga gcc aac ata aat gca gtg gac aaa Cys His Val Leu Leu Gln Ala Gly Ala Asn Ile Asn Ala Val Asp Lys 555 560 565	1733
cag cag cgg acg cca ctg atg gag gcc gtg gtg aac aac cac ctg gag Gln Gln Arg Thr Pro Leu Met Glu Ala Val Val Asn Asn His Leu Glu 570 575 580	1781
gta gcc cgt tac atg gtg cag cgt ggt ggc tgt gtc tat agc aag gag Val Ala Arg Tyr Met Val Gln Arg Gly Gly Cys Val Tyr Ser Lys Glu 585 590 595 600	1829
gag gac ggt tcc acc tgc ctc cac cac gca gcc aaa atc ggg aac ttg Glu Asp Gly Ser Thr Cys Leu His His Ala Ala Lys Ile Gly Asn Leu 605 610 615	1877
gag atg gtc agc ctg ctg ctg agc aca gga cag gtg gac gtc aac gcc Glu Met Val Ser Leu Leu Leu Ser Thr Gly Gln Val Asp Val Asn Ala 620 625 630	1925
cag gac agt ggg ggg tgg acg ccc atc atc tgg gct gca gag cac aag Gln Asp Ser Gly Gly Trp Thr Pro Ile Ile Trp Ala Ala Glu His Lys 635 640 645	1973
cac atc gag gtg atc cgc atg cta ctg acg cgg ggc gcc gac gtc acc His Ile Glu Val Ile Arg Met Leu Leu Thr Arg Gly Ala Asp Val Thr 650 655 660	2021
ctc act gac aac gag gag aac atc tgc ctg cac tgg gcc tcc ttc acg Leu Thr Asp Asn Glu Glu Asn Ile Cys Leu His Trp Ala Ser Phe Thr 665 670 675 680	2069
ggc agc gcc gcc atc gcc gaa gtc ctt ctg aat gcg cgc tgt gac ctc Gly Ser Ala Ala Ile Ala Glu Val Leu Leu Asn Ala Arg Cys Asp Leu 685 690 695	2117
cat gct gtc aac tac cat ggg gac acc ccc ctg cac atc gca gct cgg His Ala Val Asn Tyr His Gly Asp Thr Pro Leu His Ile Ala Ala Arg 700 705 710	2165



gag agc tac cat gac tgc gtg ctg tta ttc ctg tca cgt ggg gcc aac	2213
Glu Ser Tyr His Asp Cys Val Leu Leu Phe Leu Ser Arg Gly Ala Asn	
715 720 725	
cct gag ctg cgg aac aaa gag ggg gac aca gca tgg gac ctg act ccc	2261
Pro Glu Leu Arg Asn Lys Glu Gly Asp Thr Ala Trp Asp Leu Thr Pro	
730 735 740	
gag cgc tcc gac gtg tgg ttt gcg ctt caa ctc aac cgc aag ctc cga	2309
Glu Arg Ser Asp Val Trp Phe Ala Leu Gln Leu Asn Arg Lys Leu Arg	
745 750 755 760	
ctt ggg gtg gga aat cgg gcc atc cgc aca gag aag atc atc tgc cgg	2357
Leu Gly Val Gly Asn Arg Ala Ile Arg Thr Glu Lys Ile Ile Cys Arg	
765 770 775	
gac gtg gct cgg ggc tat gag aac gtg ccc att ccc tgt gtc aac ggt	2405
Asp Val Ala Arg Gly Tyr Glu Asn Val Pro Ile Pro Cys Val Asn Gly	
780 785 790	
gtg gat ggg gag ccc tgc cct gag gat tac aag tac atc tca gag aac	2453
Val Asp Gly Glu Pro Cys Pro Glu Asp Tyr Lys Tyr Ile Ser Glu Asn	
795 800 805	
tgc gag acg tcc acc atg aac atc gat cgc aac atc acc cac ctg cag	2501
Cys Glu Thr Ser Thr Met Asn Ile Asp Arg Asn Ile Thr His Leu Gln	
810 815 820	
cac tgc acg tgt gtg gac gac tgc tct agc tcc aac tgc ctg tgc ggc	2549
His Cys Thr Cys Val Asp Asp Cys Ser Ser Ser Asn Cys Leu Cys Gly	
825 830 835 840	
cag ctc agc atc cgg tgc tgg tat gac aag gat ggg cga ttg ctc cag	2597
Gln Leu Ser Ile Arg Cys Trp Tyr Asp Lys Asp Gly Arg Leu Leu Gln	
845 850 855	
gaa ttt aac aag att gag cct ccg ctg att ttc gag tgt aac cag gcg	2645
Glu Phe Asn Lys Ile Glu Pro Pro Leu Ile Phe Glu Cys Asn Gln Ala	
860 865 870	
tgc tca tgc tgg aga aac tgc aag aac cgg gtc gta cag agt ggc atc	2693
Cys Ser Cys Trp Arg Asn Cys Lys Asn Arg Val Val Gln Ser Gly Ile	
875 880 885	
aag gtg cgg cta cag ctc tac cga aca gcc aag atg ggc tgg ggg gtc	2741
Lys Val Arg Leu Gln Leu Tyr Arg Thr Ala Lys Met Gly Trp Gly Val	
890 895 900	
cgc gcc ctg cag acc atc cca cag ggg acc ttc atc tgc gag tat gtc	2789
Arg Ala Leu Gln Thr Ile Pro Gln Gly Thr Phe Ile Cys Glu Tyr Val	
905 910 915 920	
ggg gag ctg atc tct gat gct gag gct gat gtg aga gag gat gat tct	2837
Gly Glu Leu Ile Ser Asp Ala Glu Ala Asp Val Arg Glu Asp Asp Ser	
925 930 935	
tac ctc ttc gac tta gac aac aag gat gga gag gtg tac tgc ata gat	2885
Tyr Leu Phe Asp Leu Asp Asn Lys Asp Gly Glu Val Tyr Cys Ile Asp	
940 945 950	
gcc cgt tac tat ggc aac atc agc cgc ctc ctc tgc cac ctg tgt gac	2933
Ala Arg Tyr Tyr Gly Asn Ile Ser Arg Leu Leu Cys His Leu Cys Asp	
955 960 965	

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ccc aac atc att ccc gtc cgg gtc ttc atg ctg cac caa gac ctg cga      2981
Pro Asn Ile Ile Pro Val Arg Val Phe Met Leu His Gln Asp Leu Arg
   970                               975                               980

ttt cca cgc atc gcc ttc ttc agt tcc cga gac atc cgg act ggg gag      3029
Phe Pro Arg Ile Ala Phe Phe Ser Ser Arg Asp Ile Arg Thr Gly Glu
  985                               990                               995                               1000

gag cta ggg ttt gac tat ggc gac cgc ttc tgg gac atc aaa agc aaa      3077
Glu Leu Gly Phe Asp Tyr Gly Asp Arg Phe Trp Asp Ile Lys Ser Lys
      1005                               1010                               1015

tat ttc acc tgc caa tgt ggc tct gag aag tgc aag cac tca gcc gaa      3125
Tyr Phe Thr Cys Gln Cys Gly Ser Glu Lys Cys Lys His Ser Ala Glu
      1020                               1025                               1030

gcc att gcc ctg gag cag agc cgt ctg gcc cgc ctg gac cca cac cct      3173
Ala Ile Ala Leu Glu Gln Ser Arg Leu Ala Arg Leu Asp Pro His Pro
      1035                               1040                               1045

gag ctg ctg ccc gag ctc ggc tcc ctg ccc cct gtc aac aca tga gaa      3221
Glu Leu Leu Pro Glu Leu Gly Ser Leu Pro Pro Val Asn Thr *
      1050                               1055                               1060

cggaccacac cctctctccc cagcatggat ggccacagct cagccgcctc ctctgccacc  3281

agctgctcgc agcccatgcc tgggggtgct gccatcttct ctccccacca ccctttcaca  3341

cattcctgac cagagatccc agccaggccc tggaggctctg acagcccctc cctcccagag  3401

ctggttcctc cctgggaggg caacttcagg gctggccacc ccccggtgtc cccatcctca  3461

gttgaagttt gatgaattga agtcgggcct ctatgccaac tggttccttt tgttctcaat  3521

aaatgttggg tttgtaata aaaaaaaaaa a                                     3552

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<210> 421
<211> 1925
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (510)..(1562)

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<220>
<221> misc_feature
<222> (1)...(1925)
<223> n = a,t,c or g

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```

<400> 421
atttggccct cgaggccaag aattcggcac gaggggagcc gcacgggtccc ctctccttcc      60
ccatcctctc cctccccctc tccgggttcc cccaccacaa ggagccttgg gccgaccact      120
ccccgatgg cctcagccac ggaggacccc gttctggagc gttatttcaa aggccacaaa      180
gctgcatca cctccttggg cctcagcccc aacggcaagc aacttgctac tgcttcttgg      240
gatacctttc tcatgctatg gaatttcaag ccacatgcta gagcttacag atatgtgggt      300

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1091

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Ile Asn Pro Lys Leu Glu Val Ile Asp Leu Gln Ile Ser Thr Pro Pro
      220                      225                      230

gtt atg gat atc ctt tct ttt gat tct acc aca aca aca gaa acc agt      1253
Val Met Asp Ile Leu Ser Phe Asp Ser Thr Thr Thr Thr Glu Thr Ser
      235                      240                      245

ggt agg act ctg cca gac aag ggt gaa gag gcc tgt gga tat ttc ttg      1301
Gly Arg Thr Leu Pro Asp Lys Gly Glu Glu Ala Cys Gly Tyr Phe Leu
      250                      255                      260

aac cct tcc tta atg tca cca gaa tgt ttg cca aca acc acg aaa aag      1349
Asn Pro Ser Leu Met Ser Pro Glu Cys Leu Pro Thr Thr Thr Lys Lys
      265                      270                      275                      280

aaa aca gaa gac atg agt gac ctc ccc tgt gaa agt caa agg agc ata      1397
Lys Thr Glu Asp Met Ser Asp Leu Pro Cys Glu Ser Gln Arg Ser Ile
      285                      290                      295

cct ctc gct gtg act gat gct tta gag cat att atg gaa caa ctc aat      1445
Pro Leu Ala Val Thr Asp Ala Leu Glu His Ile Met Glu Gln Leu Asn
      300                      305                      310

gtt ttg aca cag act gtt tca atc ttg gag cag cga ctg act ttg aca      1493
Val Leu Thr Gln Thr Val Ser Ile Leu Glu Gln Arg Leu Thr Leu Thr
      315                      320                      325

gag gat aag ctg aaa gac tgc ctt gaa aat cag caa aag ctt ttc agt      1541
Glu Asp Lys Leu Lys Asp Cys Leu Glu Asn Gln Gln Lys Leu Phe Ser
      330                      335                      340

gct gtc caa cag aaa agc tga at aaaaaattca ttttcatttg ttgggcagag      1594
Ala Val Gln Gln Lys Ser *
      345                      350

gcccaataaaa tgaacaaatg tacatacact caggaaggta gtacaagata ctccatacaa      1654

cacaaccatg tgctatttat catggcattt cttaaaaggg tgagcaacag aacaaaaggc      1714

agaaaaggga tacctaagga ctaatttaaa cacatatcaa tgtgaaggac taatttaaat      1774

tactatcatt tatgattgca gtaataaagt gataagcatt caagcaactc tgtattttcc      1834

ccatattaat ttaaatgtcc attntcattt ataggccana tcctgccaag aaaagaacct      1894

agatctctgg atttcaactgt taagtcattt a      1925

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<210> 422  
 <211> 956  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (484) .. (837)

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<400> 422
agaggggggg cccttcccgg ccgggtttta ggccttggga aaggatttcg gggccccctc      60

gctccccggg aagcgttttg gccccaccg gaatggtgtc atctggttaa gaagcgcaag      120

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tggcgctttg gagaaaccaa ccaagacccc ggggggggggt tgggccccaa tcctaattac      180
ccttctgtcc ccaacttcca gtagccaaa atataagaa ggcaaactct gtactgttgg      240
caaaaacagc caccctaaaag ttgttaaaaa gcaaaacaaa acacctcaag cttaaatttt      300
tgaaaaacaa tcttcacaca aagatactat caacaaatca cacaccaatt tatcttagaa      360
ggatcaagag atgaaaaaca gcaaaggata ttttcgtaat atgctagaat ctttgaatat      420
aatactgaag ttggcaacca aaagcaattc agaagttcaa cttagaacta atggctgtat      480
ccg  atg gca ctg tct att tta gat att aaa atg tca cca tct tgg tat      528
      Met Ala Leu Ser Ile Leu Asp Ile Lys Met Ser Pro Ser Trp Tyr
        1             5             10             15

ttt cac atg gct ata ggc att ata aac tgg aac act act gcg ggt tta      576
Phe His Met Ala Ile Gly Ile Ile Asn Trp Asn Thr Thr Ala Gly Leu
              20             25             30

tct ggc act ctg tat cca aaa gtc ccc caa aag tac ata ctc ttt gac      624
Ser Gly Thr Leu Tyr Pro Lys Val Pro Gln Lys Tyr Ile Leu Phe Asp
              35             40             45

tct gta att ctg ctt cta ggc atg tta aga aaa ata cgt cag gta tgc      672
Ser Val Ile Leu Leu Leu Gly Met Leu Arg Lys Ile Arg Gln Val Cys
              50             55             60

caa aat gta tac atg aaa ggg tgt tca cca ata aca tta ttt aaa ata      720
Gln Asn Val Tyr Met Lys Gly Cys Ser Pro Ile Thr Leu Phe Lys Ile
              65             70             75

gtt cac tac tgg cca ggc gca gta gct cat gcc tat aat cct agc act      768
Val His Tyr Trp Pro Gly Ala Val Ala His Ala Tyr Asn Pro Ser Thr
              80             85             90             95

ttg gga ggc caa gtt ggg ggc aaa tca cct gag gtc agg agt tcg aga      816
Leu Gly Gly Gln Val Gly Gly Lys Ser Pro Glu Val Arg Ser Ser Arg
              100             105             110

cca gcc tgg act aca tgg tga aa ccccatctct actaaaagaa caaaaattag      869
Pro Ala Trp Thr Thr Trp *
              115

gtcgacgcgg ccgcgaattc ggatcctoga gagatctctt tttttgggtt tgggtgggga      929

tcttcacgtg cgaatcggtta gttatat      956

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<210> 423  
 <211> 1615  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (215)..(1507)

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<400> 423
agttcggaat tcccggcacg acccagcga tcgcggacgc gtgggcccga atgttaccta      60
tgatgaagca ggtggacccc gtgaggetgt cagcaaactt caagaattat gtcacatctat      120

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1094

Val	Ile	Ser	Lys	Lys	Ala	Lys	Val	Lys	Val	Pro	Gln	Lys	Thr	Ala	Gly	
				235					240					245		
aaa	gaa	aat	cat	ttt	gat	atg	cac	aga	gtg	gga	aaa	tgg	cac	caa	gat	1000
Lys	Glu	Asn	His	Phe	Asp	Met	His	Arg	Val	Gly	Lys	Trp	His	Gln	Asp	
			250					255					260			
ttt	cca	gtg	aag	aaa	aga	aag	aaa	ctt	tca	acc	tgg	aaa	caa	gag	ctg	1048
Phe	Pro	Val	Lys	Lys	Arg	Lys	Lys	Leu	Ser	Thr	Trp	Lys	Gln	Glu	Leu	
			265					270					275			
ctc	aaa	ctt	atg	gat	cgt	cac	aag	aaa	gat	tgt	gca	aga	gag	aag	cct	1096
Leu	Lys	Leu	Met	Asp	Arg	His	Lys	Lys	Asp	Cys	Ala	Arg	Glu	Lys	Pro	
			280					285					290			
ttt	aaa	tgt	cag	gaa	tgt	ggg	aaa	acc	ttc	aga	gtt	agc	tct	gac	ctt	1144
Phe	Lys	Cys	Gln	Glu	Cys	Gly	Lys	Thr	Phe	Arg	Val	Ser	Ser	Asp	Leu	
					300					305					310	
att	aag	cac	caa	aga	att	cac	act	gaa	gag	aaa	ccc	tat	aaa	tgt	caa	1192
Ile	Lys	His	Gln	Arg	Ile	His	Thr	Glu	Glu	Lys	Pro	Tyr	Lys	Cys	Gln	
				315						320					325	
cag	tgt	gat	aag	agg	ttt	aga	tgg	agt	tca	gat	ctt	aat	aag	cac	tta	1240
Gln	Cys	Asp	Lys	Arg	Phe	Arg	Trp	Ser	Ser	Asp	Leu	Asn	Lys	His	Leu	
				330				335						340		
aca	aca	cac	caa	gga	ata	aaa	cca	tat	aaa	tgt	tca	tgg	tgt	ggg	aaa	1288
Thr	Thr	His	Gln	Gly	Ile	Lys	Pro	Tyr	Lys	Cys	Ser	Trp	Cys	Gly	Lys	
			345					350						355		
agc	ttc	agt	caa	aat	aca	aat	tta	cat	aca	cac	caa	aga	act	cat	aca	1336
Ser	Phe	Ser	Gln	Asn	Thr	Asn	Leu	His	Thr	His	Gln	Arg	Thr	His	Thr	
			360				365					370				
gga	gaa	aag	ccc	ttc	aca	tgt	cat	gaa	tgt	gga	aaa	aaa	ttc	agt	cag	1384
Gly	Glu	Lys	Pro	Phe	Thr	Cys	His	Glu	Cys	Gly	Lys	Lys	Phe	Ser	Gln	
					380					385					390	
aac	tcc	cac	ctt	att	aaa	cac	cgg	aga	acc	cac	aca	ggt	gag	cag	cca	1432
Asn	Ser	His	Leu	Ile	Lys	His	Arg	Arg	Thr	His	Thr	Gly	Glu	Gln	Pro	
				395						400					405	
tat	act	tgt	agc	ata	tgc	agg	aga	aac	ttc	agc	agg	cgg	tca	agc	ctt	1480
Tyr	Thr	Cys	Ser	Ile	Cys	Arg	Arg	Asn	Phe	Ser	Arg	Arg	Ser	Ser	Leu	
				410					415						420	
ctt	aga	cac	cag	aaa	ctc	cac	ctg	tga	agaga	agctt	gtcca	gtgtcctcat				1532
Leu	Arg	His	Gln	Lys	Leu	His	Leu	*								
				425				430								
tctgaagaca	ttcaccaaat	ggagcttggc	actaaaattt	atgtaaagaa	aaatcacaaa											1592
cctttgaaaa	ttttacatca	gaa														1615

<210> 424  
 <211> 2531  
 <212> DNA  
 <213> Homo sapiens

<220>

&lt;221&gt; CDS

&lt;222&gt; (221) .. (2314)

&lt;400&gt; 424

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aattttccggt tcgacgatcc cgtcccctgg cggagccggc gcgcccgggg tgccgctccc      60
tgccctggcgc gctccgcacc tggaggtgcc ttgcccctct cctgcccacc tcggaatttc      120
cctgtggctc ctttgatcct tcgagtctcc agctcctctc ccttccacct gtttcccca      180
agaaaggcag gatcctggtc cctgctacgt ttctggggcc  atg gct ggt ctg ggc      235
                                         Met Ala Gly Leu Gly
                                         1           5

ccc ggc gta ggc gat tca gag ggg gga ccc cgg ccc ctg ttt tgc aga      283
Pro Gly Val Gly Asp Ser Glu Gly Gly Pro Arg Pro Leu Phe Cys Arg
                        10                        15                        20

aag ggg gct ctg agg cag aag gtg gtc cac gaa gtc aag agc cac aag      331
Lys Gly Ala Leu Arg Gln Lys Val Val His Glu Val Lys Ser His Lys
                        25                        30                        35

ttc acc gct cgc ttc ttc aag cag ccc acc ttc tgc agc cac tgc acc      379
Phe Thr Ala Arg Phe Phe Lys Gln Pro Thr Phe Cys Ser His Cys Thr
                        40                        45                        50

gac ttc atc tgg ggt atc gga aag cag ggc ctg caa tgt caa gtc tgc      427
Asp Phe Ile Trp Gly Ile Gly Lys Gln Gly Leu Gln Cys Gln Val Cys
                        55                        60                        65

agc ttt gtg gtt cat cga cga tgc cac gaa ttt gtg acc ttc gag tgt      475
Ser Phe Val Val His Arg Arg Cys His Glu Phe Val Thr Phe Glu Cys
                        70                        75                        80                        85

cca ggc gct ggg aag ggc ccc cag acg gac gac ccc cgg aac aaa cac      523
Pro Gly Ala Gly Lys Gly Pro Gln Thr Asp Asp Pro Arg Asn Lys His
                        90                        95                        100

aag ttc cgc ctg cat agc tac agc agc ccc acc ttc tgc gac cac tgt      571
Lys Phe Arg Leu His Ser Tyr Ser Ser Pro Thr Phe Cys Asp His Cys
                        105                        110                        115

ggc tcc ctc ctc tac ggg ctt gtg cac cag ggc atg aaa tgc tcc tgc      619
Gly Ser Leu Leu Tyr Gly Leu Val His Gln Gly Met Lys Cys Ser Cys
                        120                        125                        130

tgc gag atg aac gtg cac cgg cgc tgt gtg cgt agc gtg ccc tcc ctg      667
Cys Glu Met Asn Val His Arg Arg Cys Val Arg Ser Val Pro Ser Leu
                        135                        140                        145

tgc ggt gtg gac cac acc gag cgc cgc ggg cgc ctg cag ctg gag atc      715
Cys Gly Val Asp His Thr Glu Arg Arg Gly Arg Leu Gln Leu Glu Ile
                        150                        155                        160                        165

cgg gct ccc aca gca gat gag atc cac gta act gtt ggc gag gcc cgt      763
Arg Ala Pro Thr Ala Asp Glu Ile His Val Thr Val Gly Glu Ala Arg
                        170                        175                        180

aac cta att cct atg gac ccc aat ggt ctc tct gat ccc tat gtg aaa      811
Asn Leu Ile Pro Met Asp Pro Asn Gly Leu Ser Asp Pro Tyr Val Lys
                        185                        190                        195

ctg aag ctc atc cca gac cct cgg aac ctg acg aaa cag aag acc cga      859
Leu Lys Leu Ile Pro Asp Pro Arg Asn Leu Thr Lys Gln Lys Thr Arg

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200	205	210	
acg gtg aaa gcc acg cta aac cct gtg tgg aat gag acc ttt gtg ttc Thr Val Lys Ala Thr Leu Asn Pro Val Trp Asn Glu Thr Phe Val Phe 215 220 225			907
aac ctg aag cca ggg gat gtg gag cgc cgg ctc agc gtg gag gtg tgg Asn Leu Lys Pro Gly Asp Val Glu Arg Arg Leu Ser Val Glu Val Trp 230 235 240 245			955
gac tgg gac cgg acc tcc cgc aac gac ttc atg ggg gcc atg tcc ttt Asp Trp Asp Arg Thr Ser Arg Asn Asp Phe Met Gly Ala Met Ser Phe 250 255 260			1003
ggc gtc tcg gag ctg ctc aag gcg ccc gtg gat ggc tgg tac aag tta Gly Val Ser Glu Leu Leu Lys Ala Pro Val Asp Gly Trp Tyr Lys Leu 265 270 275			1051
ctg aac cag gag gag ggc gag tat tac aat gtg ccg gtg gcc gat gct Leu Asn Gln Glu Glu Gly Glu Tyr Tyr Asn Val Pro Val Ala Asp Ala 280 285 290			1099
gac aac tgc agc ctc ctc cag aag ttt gag gct tgt aac tac ccc ctg Asp Asn Cys Ser Leu Leu Gln Lys Phe Glu Ala Cys Asn Tyr Pro Leu 295 300 305			1147
gaa ttg tat gag cgg gtg cgg atg ggc ccc tct tcc tct ccc atc ccc Glu Leu Tyr Glu Arg Val Arg Met Gly Pro Ser Ser Ser Pro Ile Pro 310 315 320 325			1195
tcc cct tcc cct agt ccc acc gac ccc aag cgc tgc ttc ttc ggg gcg Ser Pro Ser Pro Ser Pro Thr Asp Pro Lys Arg Cys Phe Phe Gly Ala 330 335 340			1243
agt cca gga cgc ctg cac atc tcc gac ttc agc ttc ctc atg gtt cta Ser Pro Gly Arg Leu His Ile Ser Asp Phe Ser Phe Leu Met Val Leu 345 350 355			1291
gga aaa ggc agt ttt ggg aag gtg atg ctg gcc gag cgc agg ggc tct Gly Lys Gly Ser Phe Gly Lys Val Met Leu Ala Glu Arg Arg Gly Ser 360 365 370			1339
gat gag ctc tac gcc atc aag atc ttg aaa aag gac gtg atc gtc cag Asp Glu Leu Tyr Ala Ile Lys Ile Leu Lys Lys Asp Val Ile Val Gln 375 380 385			1387
gac gac gat gtg gac tgc acg ctg gtg gag aaa cgt gtg ctg gcg ctg Asp Asp Asp Val Asp Cys Thr Leu Val Glu Lys Arg Val Leu Ala Leu 390 395 400 405			1435
ggg ggc cgg ggt cct ggc ggc cgg ccc cac ttc ctc acc cag ctc cac Gly Gly Arg Gly Pro Gly Gly Arg Pro His Phe Leu Thr Gln Leu His 410 415 420			1483
tcc acc ttc cag acc ccg gac cgc ctg tat ttc gtg atg gag tac gtc Ser Thr Phe Gln Thr Pro Asp Arg Leu Tyr Phe Val Met Glu Tyr Val 425 430 435			1531
acc ggg gga gac ttg atg tac cac att caa cag ctg ggc aag ttt aag Thr Gly Gly Asp Leu Met Tyr His Ile Gln Gln Leu Gly Lys Phe Lys 440 445 450			1579
gag ccc cat gca gcg ttc tac gcg gca gaa atc gct atc ggc ctc ttc Glu Pro His Ala Ala Phe Tyr Ala Ala Glu Ile Ala Ile Gly Leu Phe			1627

455	460	465	
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Phe Leu His Asn Gln Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn			
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gtg atg ctg gat gct gag gga cac atc aag atc act gac ttt ggc atg			1723
Val Met Leu Asp Ala Glu Gly His Ile Lys Ile Thr Asp Phe Gly Met			
490	495		500
tgt aag gag aac gtc ttc ccc ggg acg aca acc cgc acc ttc tgc ggg			1771
Cys Lys Glu Asn Val Phe Pro Gly Thr Thr Thr Arg Thr Phe Cys Gly			
505	510		515
acc ccg gac tac ata gcc ccg gag atc att gcc tac cag ccc tat ggg			1819
Thr Pro Asp Tyr Ile Ala Pro Glu Ile Ile Ala Tyr Gln Pro Tyr Gly			
520	525		530
aag tct gtc gat tgg tgg tcc ttt gga gtt ctg ctg tat gag atg ttg			1867
Lys Ser Val Asp Trp Trp Ser Phe Gly Val Leu Leu Tyr Glu Met Leu			
535	540		545
gca gga cag cct ccc ttc gat ggg gag gac gag gag gag ctg ttt cag			1915
Ala Gly Gln Pro Pro Phe Asp Gly Glu Asp Glu Glu Glu Leu Phe Gln			
550	555		560
gcc atc atg gaa caa act gtc acc tac ccc aag tcg ctt tcc cgg gaa			1963
Ala Ile Met Glu Gln Thr Val Thr Tyr Pro Lys Ser Leu Ser Arg Glu			
570	575		580
gcc gtg gcc atc tgc aag ggg ttc ctg acc aag cac cca ggg aag cgc			2011
Ala Val Ala Ile Cys Lys Gly Phe Leu Thr Lys His Pro Gly Lys Arg			
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Leu Gly Ser Gly Pro Asp Gly Glu Pro Thr Ile Arg Ala His Gly Phe			
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Phe Arg Trp Ile Asp Trp Glu Arg Leu Glu Arg Leu Glu Ile Pro Pro			
615	620		625
cct ttc aga ccc cgc ccg tgt ggc cgc agc ggc gag aac ttt gac aag			2155
Pro Phe Arg Pro Arg Pro Cys Gly Arg Ser Gly Glu Asn Phe Asp Lys			
630	635		640
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Phe Phe Thr Arg Ala Ala Pro Ala Leu Thr Pro Pro Asp Arg Leu Val			
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ctg gcc agc atc gac cag gcc gat ttc cag ggc ttc acc tac gtg aac			2251
Leu Ala Ser Ile Asp Gln Ala Asp Phe Gln Gly Phe Thr Tyr Val Asn			
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ccc gac ttc gtg cac ccg gat gcc cgc agc ccc acc agc cca gtg cct			2299
Pro Asp Phe Val His Pro Asp Ala Arg Ser Pro Thr Ser Pro Val Pro			
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Val Pro Val Met *			
695			
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Leu Trp Gly Phe Ser Val Phe Arg Arg Ser Trp Ile Leu Asn Cys Trp	
5 10 15	
cta agt tcc agt caa gta gga atc agt gca gcc tgt aag ttc tcc aca	4654
Leu Ser Ser Ser Gln Val Gly Ile Ser Ala Ala Cys Lys Phe Ser Thr	
20 25 30	
ttg aca cac aca cac aca cac aca cac aca cga cat gct cct	4702
Leu Thr His Thr His Thr His Thr His Thr Arg His Ala Pro	
35 40 45	
ttc tgt ggc aca tgc ctg tat tac tga aagct aaatcctcaa aacctagtaa	4754
Phe Cys Gly Thr Cys Leu Tyr Tyr *	
50 55	
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aaccacaggag gagcgtgggg aaaggggctg tgggcctctc ggggagcgag ctgcgggtag 180  
cgccgcactg ggtacaggcg cgcgcttggc tgtcgctctc gccgctgtgt ttgggaggac 240  
tcgaactggc gccaggaaat attaggaagc tgtgattttc aaagctaatt atg aaa 296  
Met Lys  
1  
aca ttt atc att gga atc agt ggt gtg aca aac agt ggc aaa aca aca 344  
Thr Phe Ile Ile Gly Ile Ser Gly Val Thr Asn Ser Gly Lys Thr Thr  
5 10 15  
ctg gct aag aat ttg cag aaa cac ctc cca aat tgc agt gtc ata tct 392  
Leu Ala Lys Asn Leu Gln Lys His Leu Pro Asn Cys Ser Val Ile Ser  
20 25 30  
cag gat gat ttc ttc aag cca gag tct gag ata gag aca gat aaa aat 440  
Gln Asp Asp Phe Phe Lys Pro Glu Ser Glu Ile Glu Thr Asp Lys Asn  
35 40 45 50  
gga ttt ttg cag tac gat gtg ctt gaa gca ctt aac atg gaa aaa atg 488  
Gly Phe Leu Gln Tyr Asp Val Leu Glu Ala Leu Asn Met Glu Lys Met  
55 60 65  
atg tca gcc att tcc tgc tgg atg gaa agc gca aga cac tct gtg gta 536  
Met Ser Ala Ile Ser Cys Trp Met Glu Ser Ala Arg His Ser Val Val  
70 75 80  
tca aca gac cag gaa agt gct gag gaa att ccc att tta atc atc gaa 584  
Ser Thr Asp Gln Glu Ser Ala Glu Glu Ile Pro Ile Leu Ile Ile Glu

85	90	95	
ggt ttt ctt ctt ttt aat tat aag ccc ctt gac act ata tgg aat aga			632
Gly Phe Leu Leu Phe Asn Tyr Lys Pro Leu Asp Thr Ile Trp Asn Arg			
100	105	110	
agc tat ttc ctg act att cca tat gaa gaa tgt aaa agg agg agg agt			680
Ser Tyr Phe Leu Thr Ile Pro Tyr Glu Glu Cys Lys Arg Arg Arg Ser			
115	120	125	130
aca agg gtc tat cag cct cca gac tct ccg gga tac ttt gat ggc cat			728
Thr Arg Val Tyr Gln Pro Pro Asp Ser Pro Gly Tyr Phe Asp Gly His			
	135	140	145
gtg tgg ccc atg tat cta aag tac aga caa gaa atg cag gac atc aca			776
Val Trp Pro Met Tyr Leu Lys Tyr Arg Gln Glu Met Gln Asp Ile Thr			
	150	155	160
tgg gaa gtt gtg tac ctg gat gga aca aaa tct gaa gag gac ctc ttt			824
Trp Glu Val Val Tyr Leu Asp Gly Thr Lys Ser Glu Glu Asp Leu Phe			
	165	170	175
ttg caa gta tat gaa gat cta ata caa gaa cta gca aag caa aag tgt			872
Leu Gln Val Tyr Glu Asp Leu Ile Gln Glu Leu Ala Lys Gln Lys Cys			
	180	185	190
ttg caa gtg aca gca taa agacgg aacacaacaa atccttctctg aagtgaatta			926
Leu Gln Val Thr Ala *			
195	200		
ggaaactcca aggagtaatt taagaacctt caccaagata caatgtatac tgtggtacaa			986
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tcgaactggc gccaggaaat attaggaagc tgtgattttc aaagctaatt atg aaa	296

Met Lys

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 Thr Phe Ile Ile Gly Ile Ser Gly Val Thr Asn Ser Gly Lys Thr Thr  
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ctg gct aag aat ttg cag aaa cac ctc cca aat tgc agt gtc ata tct 392  
 Leu Ala Lys Asn Leu Gln Lys His Leu Pro Asn Cys Ser Val Ile Ser  
           20                  25                  30

cag gat gat ttc ttc aag cca gag tct gag ata gag aca gat aaa aat 440  
 Gln Asp Asp Phe Phe Lys Pro Glu Ser Glu Ile Glu Thr Asp Lys Asn  
           35                  40                  45                  50

gga ttt ttg cag tac gat gtg ctt gaa gca ctt aac atg gaa aaa atg 488  
 Gly Phe Leu Gln Tyr Asp Val Leu Glu Ala Leu Asn Met Glu Lys Met  
                           55                  60                  65

atg tca gcc att tcc tgc tgg atg gaa agc gca aga cac tct gtg gta 536  
 Met Ser Ala Ile Ser Cys Trp Met Glu Ser Ala Arg His Ser Val Val  
                   70                  75                  80

tca aca gac cag gaa agt gct gag gaa att ccc att tta atc atc gaa 584  
 Ser Thr Asp Gln Glu Ser Ala Glu Glu Ile Pro Ile Leu Ile Ile Glu  
           85                  90                  95

ggt ttt ctt ctt ttt aat tat aat aca agg gtc tat cag cct cca gac 632  
 Gly Phe Leu Leu Phe Asn Tyr Asn Thr Arg Val Tyr Gln Pro Pro Asp  
           100                  105                  110

tct ccg gga tac ttt gat ggc cat gtg tgg ccc atg tat cta aag tac 680  
 Ser Pro Gly Tyr Phe Asp Gly His Val Trp Pro Met Tyr Leu Lys Tyr  
           115                  120                  125                  130

aga caa gaa atg cag gac atc aca tgg gaa gtt gtg tac ctg gat gga 728  
 Arg Gln Glu Met Gln Asp Ile Thr Trp Glu Val Val Tyr Leu Asp Gly  
                   135                  140                  145

aca aaa tct gaa gag gac ctc ttt ttg caa gta tat gaa gat cta ata 776  
 Thr Lys Ser Glu Glu Asp Leu Phe Leu Gln Val Tyr Glu Asp Leu Ile  
                   150                  155                  160

caa gaa cta gca aag caa aag tgt ttg caa gtg aca gca taa agacgga 825  
 Gln Glu Leu Ala Lys Gln Lys Cys Leu Gln Val Thr Ala \*  
           165                  170                  175

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           Met Ser Ser Ala Ile Glu Arg Lys Ser Leu Asp Pro Ser Glu  
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 Glu Pro Val Asp Glu Val Leu Gln Ile Pro Pro Ser Leu Leu Thr Cys  
           15                          20                          25                          30  
 ggc ggc tgc cag cag aac atc ggg gac cgc tac ttc ctg aag gcc atc 806  
 Gly Gly Cys Gln Gln Asn Ile Gly Asp Arg Tyr Phe Leu Lys Ala Ile  
                           35                          40                          45  
 gac cag tac tgg cac gag gac tgc ctg agc tgc gac ctc tgt ggc tgc 854  
 Asp Gln Tyr Trp His Glu Asp Cys Leu Ser Cys Asp Leu Cys Gly Cys  
                           50                          55                          60  
 cgg ctg ggt gag gtg ggg cgg cgc ctc tac tac aaa ctg ggc cgg aag 902  
 Arg Leu Gly Glu Val Gly Arg Arg Leu Tyr Tyr Lys Leu Gly Arg Lys  
                           65                          70                          75  
 ctc tgc cgg aga gac tat ctc agg ctt ttt ggg caa gac ggt ctc tgc 950  
 Leu Cys Arg Arg Asp Tyr Leu Arg Leu Phe Gly Gln Asp Gly Leu Cys  
                           80                          85                          90  
 gca tcc tgt gac aag cgg att cgt gcc tat gag atg aca atg cgg gtg 998  
 Ala Ser Cys Asp Lys Arg Ile Arg Ala Tyr Glu Met Thr Met Arg Val  
                           95                          100                          105                          110  
 aaa gac aaa gtg tat cac ctg gaa tgt ttc aag tgc gcc gcc tgt cag 1046  
 Lys Asp Lys Val Tyr His Leu Glu Cys Phe Lys Cys Ala Ala Cys Gln  
                           115                          120                          125  
 aag cat ttc tgt gta ggt gac aga tac ctc ctc atc aac tct gac ata 1094  
 Lys His Phe Cys Val Gly Asp Arg Tyr Leu Leu Ile Asn Ser Asp Ile

130	135	140	
gtg tgc gaa cag gac atc tac gag tgg act aag atc aat ggg atg ata			1142
Val Cys Glu Gln Asp Ile Tyr Glu Trp Thr Lys Ile Asn Gly Met Ile			
145	150	155	
tagggcccgag tccccgggca tctttgggga ggtgttcaact gaagacgccg tctccatggc			1202
atcttcgtct tcaactcttag gcactttggg ggtttgaggg tggggtaagg gatttcttag			1262
gggatggttag acctttattg ggtatcaaga catagcatcc aagtggcata attcaggggc			1322
tgacacttca aggtgacaga aggaccagcc cttgagggag aacttatggc cacagcccat			1382
ccatagtaac tgacatgatt agcagaagaa aggaacattt aggggcaagc aggcgctgtg			1442
ctatcatgat ggaatttcat atctacagat agagagttgt tgtgtacaga cttgttgtga			1502
ctttgacgct tgcgaactag agatgtgcaa ttgatttctt ttcttcctgg ctttttaact			1562
cccctgtttc aatcactgtc ctccacacaa gggaaggaca gaaaggagag tggccattct			1622
ttttttcttg gcccccttcc caaggcctta agctttggac ccaaggaaaa ctgcatggag			1682
acgcatttcg gttgagaatg gaaaccacaa cttttaacca aacaattatt taaagcaatg			1742
ctgatgaatc actgttttta gacaccttca ttttgagggg aggagttcca cagattgttt			1802
ctatacaaat ataaatctta aaaagttggt caactatttt attatcctag attatatcaa			1862
agtatttgtc gtgtgtagaa aaaaaaaca gctctgcagg ctttaataaaa atgacagact			1922
gaaaaaaaaa aaaaaaa			1939

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 <212> DNA  
 <213> Homo sapiens

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 <222> (134)..(517)

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gccacctttg cctacagatg gtgttcaactt tgtttttgtg ggtcacagc ttgacttttg	120
ggggccccag gag atg ttg acc cag cag ggc atg gcg ctg cag aac tac	169
Met Leu Thr Gln Gln Gly Met Ala Leu Gln Asn Tyr	
1 5 10	
gac aac aag ctg gtc aaa tgc ata gag gag cta tgc cag aag cag gag	217
Asp Asn Lys Leu Val Lys Cys Ile Glu Glu Leu Cys Gln Lys Gln Glu	
15 20 25	

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gag ctg tgc tgg cag atc cag cag gag gag gac aag aaa cag cgg ctg      265
Glu Leu Cys Trp Gln Ile Gln Gln Glu Glu Asp Lys Lys Gln Arg Leu
      30                      35                      40

cag aat gag gtg agg cag ctg aca gag aag ctg gcc tgc gtc aac gag      313
Gln Asn Glu Val Arg Gln Leu Thr Glu Lys Leu Ala Cys Val Asn Glu
      45                      50                      55                      60

aag ctg gcc cgc gtc aac gag aac ctg gca cgc aag att gcc tct tgc      361
Lys Leu Ala Arg Val Asn Glu Asn Leu Ala Arg Lys Ile Ala Ser Cys
                        65                      70                      75

agt aag ttc tac cag acc atc gcg gag acg gag gcc gcc tac ctc aag      409
Ser Lys Phe Tyr Gln Thr Ile Ala Glu Thr Glu Ala Ala Tyr Leu Lys
                        80                      85                      90

atc ctg gag agc tcc cag act ttg ctc agc gtt ctc aag agg gaa gct      457
Ile Leu Glu Ser Ser Gln Thr Leu Leu Ser Val Leu Lys Arg Glu Ala
      95                      100                      105

ggg aac ctg acc aag gct aca gcc cca gac cag aaa agt agc ggc ggc      505
Gly Asn Leu Thr Lys Ala Thr Ala Pro Asp Gln Lys Ser Ser Gly Gly
      110                      115                      120

agg gac agc tga cca gaccacaggc agggcctgcc tccgtgtgcc cctcagctca      560
Arg Asp Ser *
      125

gccccagcaa gtgtgtgctc agagcatctt tgttcttcac ggcagcagct accttcctc      620

actgtctcag gtgccgagag gggcagggtgc cagcctccac tggcatcagt gacaagccca      680

gggcacagcc caccgggggg tcctcgcttc atgctcacac aggtatggg gatggtgggc      740

tccaggtcag ctctgcaagg ggcttgtctc tgtggcacc acactcctgc cctgccaggg      800

aggctctggt tgtctgagca ccatgggggc cccctcacct tgtccctcct cagccagcag      860

aggcccaggg caagggacag gaggacaggg gttctccttc accacagaac ccaaacctca      920

ggtctcacc ctgtggcctg tgattatgaa taaagattat ctttgtaaag atcaaaaaaa      980

aaaaa                                                                985

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tggcggaccg tggcggcgtg ggtgaagccg cagctgttg agcgtctcct gcatctgtcc      120
ctggcctaaa cccgacgcta ggctggaggg agcgactgcg ggccgggctg gcggggactg      180
gggcctcggt gtggttcgtg gcggggctgg ggctgcttta cgccctgagg atccctttga      240

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1108

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caattcatag agctgtggaa tttaatcctc atgttccaaa atatttatta gagatgaaaa 1364
gtttaatttt acctccagaa cacattctga aacgggggtga tagtgaagca attgcctatg 1424
ctttctttca tcttcagcac tggaaacgaa tagaagggtgc tcttaatctg ttacagtgtg 1484
catgggaagg cactttttaga atgattccat acccggttaga gaaaggacat ctattttacc 1544
cttatcccgag ctgcacagag acggctgata gagagctatt acctaccttt catcatgttt 1604
ctgcttacc acaaaaggag cttcctttgt tcatccattt cacagcagga ttttgccttt 1664
ttacagcaat gatagccatt ctactcacc agtttctga aatcatgggt atttttgcta 1724
aagctg 1730

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<210> 431
<211> 2896
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (324) .. (2318)

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ctgaaatact ctctggtgcc aacctccaaa ttctcgtctg tcacttcaga cccccactag 120
ttgacagagc agcagaattt caactccagt agacttgaat gtgcctctgg gcaaagaagc 180
agagctaacg aggaaaggga tttaaagagt ttttcttggg tgtttgtcaa acttttattc 240
cctgtctgtg tgcagagggg attcaacttc aatttttctg cagtggctct ggtccagcc 300
ccttacttaa agatctggaa agc atg aag act ggg ctt ttt ttc cta tgt 350
                               Met Lys Thr Gly Leu Phe Phe Leu Cys
                               1 5

ctc ttg gga act gca gct gca atc ccg aca aat gca aga tta tta tct 398
Leu Leu Gly Thr Ala Ala Ala Ile Pro Thr Asn Ala Arg Leu Leu Ser
10 15 20 25

gat cat tcc aaa cca act gct gaa acg gta gca cct gac aac act gca 446
Asp His Ser Lys Pro Thr Ala Glu Thr Val Ala Pro Asp Asn Thr Ala
30 35 40

atc ccc agt tta agg gct gaa gct gaa gaa aat gaa aaa gaa aca gca 494
Ile Pro Ser Leu Arg Ala Glu Ala Glu Glu Asn Glu Lys Glu Thr Ala
45 50 55

gta tcc aca gaa gac gat tcc cac cat aag gct gaa aaa tca tca gta 542
Val Ser Thr Glu Asp Asp Ser His His Lys Ala Glu Lys Ser Ser Val
60 65 70

cta aag tca aaa gag gaa agc cat gaa cag tca gca gaa cag ggc aag 590
Leu Lys Ser Lys Glu Glu Ser His Glu Gln Ser Ala Glu Gln Gly Lys
75 80 85

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agt tct agc caa gag ctg gga ttg aag gat caa gag gac agt gat ggt	638
Ser Ser Ser Gln Glu Leu Gly Leu Lys Asp Gln Glu Asp Ser Asp Gly	
90 95 100 105	
cac tta agt gtg aat ttg gag tat gca cca act gaa ggt aca ttg gac	686
His Leu Ser Val Asn Leu Glu Tyr Ala Pro Thr Glu Gly Thr Leu Asp	
110 115 120	
ata aaa gaa gat atg agt gag cct cag gag aaa aaa ctc tca gag aac	734
Ile Lys Glu Asp Met Ser Glu Pro Gln Glu Lys Lys Leu Ser Glu Asn	
125 130 135	
act gat ttt ttg gct cct ggt gtt agt tcc ttc aca gat tct aac caa	782
Thr Asp Phe Leu Ala Pro Gly Val Ser Ser Phe Thr Asp Ser Asn Gln	
140 145 150	
caa gaa agt atc aca aag aga gag gaa aac caa gaa caa cct aga aat	830
Gln Glu Ser Ile Thr Lys Arg Glu Glu Asn Gln Glu Gln Pro Arg Asn	
155 160 165	
tat tca cat cat cag ttg aac agg agc agt aaa cat agc caa ggc cta	878
Tyr Ser His His Gln Leu Asn Arg Ser Ser Lys His Ser Gln Gly Leu	
170 175 180 185	
agg gat caa gga aac caa gag cag gat cca aat att tcc aat gga gaa	926
Arg Asp Gln Gly Asn Gln Glu Gln Asp Pro Asn Ile Ser Asn Gly Glu	
190 195 200	
gag gaa gaa gaa aaa gag cca ggt gaa gtt ggt acc cac aat gat aac	974
Glu Glu Glu Glu Lys Glu Pro Gly Glu Val Gly Thr His Asn Asp Asn	
205 210 215	
caa gaa aga aag aca gaa ttg ccc agg gag cat gct aac agc aag cag	1022
Gln Glu Arg Lys Thr Glu Leu Pro Arg Glu His Ala Asn Ser Lys Gln	
220 225 230	
gag gaa gac aat acc caa tct gat gat att ttg gaa gag tct gat caa	1070
Glu Glu Asp Asn Thr Gln Ser Asp Asp Ile Leu Glu Glu Ser Asp Gln	
235 240 245	
cca act caa gta agc aag atg cag gag gat gaa ttt gat cag ggt aac	1118
Pro Thr Gln Val Ser Lys Met Gln Glu Asp Glu Phe Asp Gln Gly Asn	
250 255 260 265	
caa gaa caa gaa gat aac tcc aat gca gaa atg gaa gag gaa aat gca	1166
Gln Glu Gln Glu Asp Asn Ser Asn Ala Glu Met Glu Glu Glu Asn Ala	
270 275 280	
tcg aac gtc aat aag cac att caa gaa act gaa tgg cag agt caa gag	1214
Ser Asn Val Asn Lys His Ile Gln Glu Thr Glu Trp Gln Ser Gln Glu	
285 290 295	
ggt aaa act ggc cta gaa gct atc agc aac cac aaa gag aca gaa gaa	1262
Gly Lys Thr Gly Leu Glu Ala Ile Ser Asn His Lys Glu Thr Glu Glu	
300 305 310	
aag act gtt tct gag gct ctg ctc atg gaa cct act gat gat ggt aat	1310
Lys Thr Val Ser Glu Ala Leu Leu Met Glu Pro Thr Asp Asp Gly Asn	
315 320 325	
acc acg ccc aga aat cat gga gtt gat gat gat ggc gat gat gat ggc	1358
Thr Thr Pro Arg Asn His Gly Val Asp Asp Gly Asp Asp Asp Gly	
330 335 340 345	

gat gat ggc ggc act gat ggc ccc agg cac agt gca agt gat gac tac	1406
Asp Asp Gly Gly Thr Asp Gly Pro Arg His Ser Ala Ser Asp Asp Tyr	
350 355 360	
ttc atc cca agc cag gcc ttt ctg gag gcc gag aga gct caa tcc att	1454
Phe Ile Pro Ser Gln Ala Phe Leu Glu Ala Glu Arg Ala Gln Ser Ile	
365 370 375	
gcc tat cac ctc aaa att gag gag caa aga gaa aaa gta cat gaa aat	1502
Ala Tyr His Leu Lys Ile Glu Glu Gln Arg Glu Lys Val His Glu Asn	
380 385 390	
gaa aat ata ggt acc act gag cct gga gag cac caa gag gcc aag aaa	1550
Glu Asn Ile Gly Thr Thr Glu Pro Gly Glu His Gln Glu Ala Lys Lys	
395 400 405	
gca gag aac tca tca aat gag gag gaa acg tca agt gaa ggc aac atg	1598
Ala Glu Asn Ser Ser Asn Glu Glu Glu Thr Ser Ser Glu Gly Asn Met	
410 415 420 425	
agg gtg cat gct gtg gat tct tgc atg agc ttc cag tgt aaa aga ggc	1646
Arg Val His Ala Val Asp Ser Cys Met Ser Phe Gln Cys Lys Arg Gly	
430 435 440	
cac atc tgt aag gca gac caa cag gga aaa cct cac tgt gtc tgc cag	1694
His Ile Cys Lys Ala Asp Gln Gln Gly Lys Pro His Cys Val Cys Gln	
445 450 455	
gat cca gtg act tgt cct cca aca aaa ccc ctt gat caa gtt tgt ggc	1742
Asp Pro Val Thr Cys Pro Pro Thr Lys Pro Leu Asp Gln Val Cys Gly	
460 465 470	
act gac aat cag acc tat gct agt tcc tgt cat cta ttc gct act aaa	1790
Thr Asp Asn Gln Thr Tyr Ala Ser Ser Cys His Leu Phe Ala Thr Lys	
475 480 485	
tgc aga ctg gag ggg acc aaa aag ggg cat caa ctc cag ctg gat tat	1838
Cys Arg Leu Glu Gly Thr Lys Lys Gly His Gln Leu Gln Leu Asp Tyr	
490 495 500 505	
ttt gga gcc tgc aaa tct att cct act tgt acg gac ttt gaa gtg att	1886
Phe Gly Ala Cys Lys Ser Ile Pro Thr Cys Thr Asp Phe Glu Val Ile	
510 515 520	
cag ttt cct cta cgg atg aga gac tgg ctc aag aat atc ctc atg cag	1934
Gln Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Ile Leu Met Gln	
525 530 535	
ctt tat gaa gcc aac tct gaa cac gct ggt tat cta aat gag aag cag	1982
Leu Tyr Glu Ala Asn Ser Glu His Ala Gly Tyr Leu Asn Glu Lys Gln	
540 545 550	
aga aat aaa gtc aag aaa att tac ctg gat gaa aag agg ctt ttg gct	2030
Arg Asn Lys Val Lys Lys Ile Tyr Leu Asp Glu Lys Arg Leu Leu Ala	
555 560 565	
ggg gac cat ccc att gat ctt ctc tta agg gac ttt aag aaa aac tac	2078
Gly Asp His Pro Ile Asp Leu Leu Leu Arg Asp Phe Lys Lys Asn Tyr	
570 575 580 585	
cac atg tat gtg tat cct gtg cac tgg cag ttt agt gaa ctt gac caa	2126
His Met Tyr Val Tyr Pro Val His Trp Gln Phe Ser Glu Leu Asp Gln	
590 595 600	

cac cct atg gat aga gtc ttg aca cat tct gaa ctt gct cct ctg cga 2174  
 His Pro Met Asp Arg Val Leu Thr His Ser Glu Leu Ala Pro Leu Arg  
 605 610 615  
  
 gca tct ctg gtg ccc atg gaa cac tgc ata acc cgt ttc ttt gag gag 2222  
 Ala Ser Leu Val Pro Met Glu His Cys Ile Thr Arg Phe Phe Glu Glu  
 620 625 630  
  
 tgt gac ccc aac aag gat aag cac atc acc ctg aag gag tgg ggc cac 2270  
 Cys Asp Pro Asn Lys Asp Lys His Ile Thr Leu Lys Glu Trp Gly His  
 635 640 645  
  
 tgc ttt gga att aaa gaa gag gac ata gat gaa aat ctc ttg ttt tga 2318  
 Cys Phe Gly Ile Lys Glu Asp Ile Asp Glu Asn Leu Leu Phe \*  
 650 655 660 665  
  
 acgaagattt taaagaactc aactttccag catcctcctc tgttotaacc acttcagaaa 2378  
 tatatgcagc tgtgatactt gtagatttat atttagcaaa atgttagcat gtatgacaag 2438  
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 aacaaaaatg tacaattaag taaagtcaac atatgcaaaa tactgtacat tgtgaacaga 2558  
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 <212> DNA  
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 <222> (1087) .. (3273)

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 ctatgcttca gtaattccca taagctggcg gtcgcctctg ggtctaaact cccaaggcct 180  
 ccattgggca ctgagcacat tcggttattt ccagaaacgc tccgcggtct tggggatcag 240  
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 gttcggtac ttccggaac actcgggtgc ccccttacct caggctccgc ctcggcctcg 480



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caggtcggcg tcctcagctg gccgagcatg gtggcagcct gcacccttggt ctcccttgctc	720
tggtgcagcc agcagagccg ccagccttggt gcgcccattg ccctccgtgt gagggcggtga	780
gcggcctgcc ccagcctcac ctgctgatgg aggactcaat ggcccagtga cctgacacca	840
caccaccaac tccctccac cagctgacga atggtggacc cagtgcgag tggcccttgt	900
aagggtcagt gaataatttg aagcgaggca tgagcggccc ctgtggtcgc ctgtgactgc	960
tggagataga ggtcccagca cccaagcca acccagcgga ccctcccagc cctgcttcaa	1020
ccaatggggc cagtggggct ccaagcagcc acctaaccat ccagacccca cccactcac	1080
gcggcc atg gcg ggc cct gag ggc ttc cag tac cgc gct ctg tac ccg	1128
Met Ala Gly Pro Glu Gly Phe Gln Tyr Arg Ala Leu Tyr Pro	
1 5 10	
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Phe Arg Arg Glu Arg Pro Glu Asp Leu Glu Leu Leu Pro Gly Asp Val	
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ctg gta gtg agc cgg gcg gcc ttg cag gcg ctg ggc gtg gcc gag ggt	1224
Leu Val Val Ser Arg Ala Ala Leu Gln Ala Leu Gly Val Ala Glu Gly	
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ggc gag cgc tgc cca cag agc gtg ggc tgg atg ccc ggc ctc aac gag	1272
Gly Glu Arg Cys Pro Gln Ser Val Gly Trp Met Pro Gly Leu Asn Glu	
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cgc aca cgg cag cga ggt gac ttc cct ggc acc tat gtg gag ttc ctg	1320
Arg Thr Arg Gln Arg Gly Asp Phe Pro Gly Thr Tyr Val Glu Phe Leu	
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Gly Pro Val Ala Leu Ala Arg Pro Gly Pro Arg Pro Arg Gly Pro Arg	
80 85 90	
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Pro Leu Pro Ala Arg Pro Arg Asp Gly Ala Pro Glu Pro Gly Leu Thr	
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ctc ccc gac ttg ccc gag cag ttc tcc cca cct gat gtg gct ccc cct	1464
Leu Pro Asp Leu Pro Glu Gln Phe Ser Pro Pro Asp Val Ala Pro Pro	
115 120 125	
ctt ctg gtg aag ctt gtg gag gcc att gaa agg aca ggg ctg gac agc	1512
Leu Leu Val Lys Leu Val Glu Ala Ile Glu Arg Thr Gly Leu Asp Ser	
130 135 140	
gaa tct cac tac cgc ccg gag ctg ccc gca ccg cgt aca gac tgg tcc	1560
Glu Ser His Tyr Arg Pro Glu Leu Pro Ala Pro Arg Thr Asp Trp Ser	
145 150 155	
ctg agc gac gtg gat cag tgg gac acg gca gcc ctg gct gac ggc att	1608
Leu Ser Asp Val Asp Gln Trp Asp Thr Ala Ala Leu Ala Asp Gly Ile	
160 165 170	

aag agc ttc ctg ctg gca ctg ccc gcg ccg ctc gtg acc ccc gag gcc	1656
Lys Ser Phe Leu Leu Ala Leu Pro Ala Pro Leu Val Thr Pro Glu Ala	
175 180 185 190	
tcg gcc gag gcg cgc cgg gcc ctg cgg gag gcc gcg ggg ccc gtg ggg	1704
Ser Ala Glu Ala Arg Arg Ala Leu Arg Glu Ala Ala Gly Pro Val Gly	
195 200 205	
ccg gcg ctg gag cca ccg acg ctg ccg ctg cac cgc gcg ctc acg ctg	1752
Pro Ala Leu Glu Pro Pro Thr Leu Pro Leu His Arg Ala Leu Thr Leu	
210 215 220	
cgc ttc ctg ctc cag cac ctg ggc cgc gtg gcc agc cgc gcc ccg gcc	1800
Arg Phe Leu Leu Gln His Leu Gly Arg Val Ala Ser Arg Ala Pro Ala	
225 230 235	
ctg ggt ccc gcg gtc cgg gcc ctg ggc gcc acc ttt ggg ccg ctg ctg	1848
Leu Gly Pro Ala Val Arg Ala Leu Gly Ala Thr Phe Gly Pro Leu Leu	
240 245 250	
ctg cgc gcg ccg ccg ccg ccg tcc tcg ccg ccg cca ggg ggc gct ccc	1896
Leu Arg Ala Pro Pro Pro Pro Ser Ser Pro Pro Pro Gly Gly Ala Pro	
255 260 265 270	
gac ggg agt gag ccc agc cct gac ttc ccg gcg ctg ctg gtg gag aag	1944
Asp Gly Ser Glu Pro Ser Pro Asp Phe Pro Ala Leu Leu Val Glu Lys	
275 280 285	
ctg ctt cag gaa cac ttg gaa gag cag gag gtt gcg ccc cca gcg ctg	1992
Leu Leu Gln Glu His Leu Glu Glu Gln Glu Val Ala Pro Pro Ala Leu	
290 295 300	
ccg cct aaa ccc ccc aag gca aag ccg gcc tcc aca gtc ctg gcc aat	2040
Pro Pro Lys Pro Pro Lys Ala Lys Pro Ala Ser Thr Val Leu Ala Asn	
305 310 315	
gga ggg agc cca ccc tcc ctg cag gat gct gag tgg tac tgg ggg gac	2088
Gly Gly Ser Pro Pro Ser Leu Gln Asp Ala Glu Trp Tyr Trp Gly Asp	
320 325 330	
att tca agg gag gag gtg aac gag aaa ctc ccg gac act ccc gat ggc	2136
Ile Ser Arg Glu Glu Val Asn Glu Lys Leu Arg Asp Thr Pro Asp Gly	
335 340 345 350	
acc ttc cta gtc cga gat gct tct agc aag atc cag ggc gag tac acg	2184
Thr Phe Leu Val Arg Asp Ala Ser Ser Lys Ile Gln Gly Glu Tyr Thr	
355 360 365	
ctg acc ctc agg aaa ggc ggg aac aat aag ctg atc aag gtc ttc cac	2232
Leu Thr Leu Arg Lys Gly Gly Asn Asn Lys Leu Ile Lys Val Phe His	
370 375 380	
cga gat ggg cac tat ggc ttc tca gag cca ctc acc ttc tgc tcc gtt	2280
Arg Asp Gly His Tyr Gly Phe Ser Glu Pro Leu Thr Phe Cys Ser Val	
385 390 395	
gtg gac ctc atc aat cac tac cgc cac gag tct ctg gcc cag tac aat	2328
Val Asp Leu Ile Asn His Tyr Arg His Glu Ser Leu Ala Gln Tyr Asn	
400 405 410	
gcc aag ctg gac aca cgg ctc ctc tac cct gtg tcc aaa tac cag cag	2376
Ala Lys Leu Asp Thr Arg Leu Leu Tyr Pro Val Ser Lys Tyr Gln Gln	
415 420 425 430	

gac cag att gtc aag gag gac agc gtg gag gca gtg ggc gcc cag ctt Asp Gln Ile Val Lys Glu Asp Ser Val Glu Ala Val Gly Ala Gln Leu 435 440 445	2424
aag gtc tat cac cag cag tac cag gac aag agc cgc gag tat gac cag Lys Val Tyr His Gln Gln Tyr Gln Asp Lys Ser Arg Glu Tyr Asp Gln 450 455 460	2472
ctt tat gaa gag tac aca cgg acc tcc cag gag ctg cag atg aag cgt Leu Tyr Glu Glu Tyr Thr Arg Thr Ser Gln Glu Leu Gln Met Lys Arg 465 470 475	2520
act gca att gag gcc ttc aat gag act atc aag atc ttt gaa gag cag Thr Ala Ile Glu Ala Phe Asn Glu Thr Ile Lys Ile Phe Glu Glu Gln 480 485 490	2568
agc cag act caa gag aaa tgc agc aag gaa tac ctg gag cgc ttc cgg Ser Gln Thr Gln Glu Lys Cys Ser Lys Glu Tyr Leu Glu Arg Phe Arg 495 500 505 510	2616
cgt gag ggc aac gag aaa gag atg caa agg atc ctg ctg aac tcc gag Arg Glu Gly Asn Glu Lys Glu Met Gln Arg Ile Leu Leu Asn Ser Glu 515 520 525	2664
cgg ctc aag tcc cgc att gcc gag atc cat gag agc cgc acg aag ctg Arg Leu Lys Ser Arg Ile Ala Glu Ile His Glu Ser Arg Thr Lys Leu 530 535 540	2712
gag cag cag ctg cgg gcc cag gcc tcg gac aac aga gag atc gac aag Glu Gln Gln Leu Arg Ala Gln Ala Ser Asp Asn Arg Glu Ile Asp Lys 545 550 555	2760
cgc atg aac agc ctc aag ccg gac ctc atg cag ctg cgc aag atc cga Arg Met Asn Ser Leu Lys Pro Asp Leu Met Gln Leu Arg Lys Ile Arg 560 565 570	2808
gac cag tac ctc gtg tgg ctc acc cag aaa ggc gcc cgg cag aag aaa Asp Gln Tyr Leu Val Trp Leu Thr Gln Lys Gly Ala Arg Gln Lys Lys 575 580 585 590	2856
atc aac gag tgg ctg ggg att aaa aat gag act gag gac cag tac gca Ile Asn Glu Trp Leu Gly Ile Lys Asn Glu Thr Glu Asp Gln Tyr Ala 595 600 605	2904
ctc atg gag gac gag gac gat ctc ccg cac cac gag gaa cgc act tgg Leu Met Glu Asp Glu Asp Asp Leu Pro His His Glu Glu Arg Thr Trp 610 615 620	2952
tac gtg ggc aag atc aac cgc acg cag gca gag gag atg ctg agt ggc Tyr Val Gly Lys Ile Asn Arg Thr Gln Ala Glu Glu Met Leu Ser Gly 625 630 635	3000
aag cgg gat ggc acc ttc ctc atc cgc gag agc agc cag cgg ggc tgc Lys Arg Asp Gly Thr Phe Leu Ile Arg Glu Ser Ser Gln Arg Gly Cys 640 645 650	3048
tac gcc tgc tcc gtg gta gtg gac ggc gac acc aag cac tgc gtc atc Tyr Ala Cys Ser Val Val Val Asp Gly Asp Thr Lys His Cys Val Ile 655 660 665 670	3096
tac cgc acg gcc acc ggc ttc ggc ttc gcg gag ccc tac aac ctg tac Tyr Arg Thr Ala Thr Gly Phe Gly Phe Ala Glu Pro Tyr Asn Leu Tyr 675 680 685	3144

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ggg tcg ctg aag gag ctg gtg ctg cac tac cag cac gcc tcg ctg gtg      3192
Gly Ser Leu Lys Glu Leu Val Leu His Tyr Gln His Ala Ser Leu Val
      690                      695                      700

cag cac aac gac gcg ctc acc gtc acc ctg gcg cac cca gtg cgc gcc      3240
Gln His Asn Asp Ala Leu Thr Val Thr Leu Ala His Pro Val Arg Ala
      705                      710                      715

ccg ggc ccc ggc ccg ccg cct gcc gcc cgc tga gcaccgag gacccgcccc      3291
Pro Gly Pro Gly Pro Pro Pro Ala Ala Arg *
      720                      725

aagcagagcc gccctgggc ccgtctgcgc cggaggctgc ggcggcgga gccacggacc      3351

agaccagcca catccagggg tcctcatttc tccggtcttg gctcttggtt ggggttctct      3411

caccctcttt ctctttcctt ccctccccc ttctccagat ctccctctgt ctctttttct      3471

ctgtctttct tggccctgt ctctctccat gttgggggtc ctaactcccc caccocatat      3531

ctacgtgtcc tccgggcatt gccctctcca tggctctggt caccctgacc ctctgccctg      3591

cccaccgcag gtcccccggt gtcccggaag ccccttctgg ctgcaoctgc catgtttaca      3651

gagggccctt gggctgcgcg gccccagcct gggcaccttg atttttaagc catagacctg      3711

gggtcagggc aggaaggaac ttactctgc tgettccgag aacctcggcc gtgacattcg      3771

gggcggggcg ggaccgccc cacagactcc aacttccct ccaaaccg aagtgaacc      3831

cgccaccggg ttacccccac aagggggcg ctgcgagaag ttcaccacc cccgaaaaa      3891

taattaaact cgcaggccag gcacggtggc tcatgcctgt aatcccagca ctttgggagg      3951

ccaagacggg cggatctttt gaggtcgga gttggaggcc agcctggcca aaatggcaaa      4011

acccgcgcatc tactaaaata caaaaattag ccgggcgtgg tggcggcgc tctagagtat      4071

ccctcgaggg gcccaagctt acgcgtacct agctttcttg tacaaagtgg      4121

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<210> 433  
 <211> 2570  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (259) .. (2373)

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<400> 433
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tggaagaac tttgttcaa tcattacaac aaggaaacta caaactgcta ccgtacaaca      120
aggaaatgga caaactacaa aataattttt ctaggacctt tcagagaact gaggtcacag      180
ggcaaccaag taatcttaaa tctggggaaa gaaagatgcc agctgagaga aacaggactc      240
aagctttact tacctggg atg gac tct gcc aga cac cat ata agc cac tct      291
Met Asp Ser Ala Arg His His Ile Ser His Ser

```

1

5

10

act tct gca ggc ccc atc cct tcc cag aaa gaa gag gaa atg act gag	339
Thr Ser Ala Gly Pro Ile Pro Ser Gln Lys Glu Glu Glu Met Thr Glu	
15 20 25	
tcc cag gga aca gta aca ttc aaa gat gtg gct atc gac ttc act cag	387
Ser Gln Gly Thr Val Thr Phe Lys Asp Val Ala Ile Asp Phe Thr Gln	
30 35 40	
gag gag tgg aag aga ttg gat cct gct cag aga aaa ctg tac cgg aat	435
Glu Glu Trp Lys Arg Leu Asp Pro Ala Gln Arg Lys Leu Tyr Arg Asn	
45 50 55	
gtg atg cta gaa aac tat aac aac tta atc aca gta ggc tat ccg ttc	483
Val Met Leu Glu Asn Tyr Asn Asn Leu Ile Thr Val Gly Tyr Pro Phe	
60 65 70 75	
acc aaa cct gat gtg att ttc aaa ttg gag caa gaa gaa gaa cca tgg	531
Thr Lys Pro Asp Val Ile Phe Lys Leu Glu Gln Glu Glu Glu Pro Trp	
80 85 90	
gtg atg gag gaa gaa gta tta agg aga cac tgg caa gga gaa ata tgg	579
Val Met Glu Glu Glu Val Leu Arg Arg His Trp Gln Gly Glu Ile Trp	
95 100 105	
gga gtt gat gag cat cag aaa aac cag gac aga ctt ttg aga caa gtt	627
Gly Val Asp Glu His Gln Lys Asn Gln Asp Arg Leu Leu Arg Gln Val	
110 115 120	
gaa gtt aaa ttc cag aaa aca ctg act gaa gaa aaa ggc aat gaa tgt	675
Glu Val Lys Phe Gln Lys Thr Leu Thr Glu Glu Lys Gly Asn Glu Cys	
125 130 135	
caa aag aaa ttt gca aat gta ttt cct ctg aac tct gat ttt ttc cct	723
Gln Lys Lys Phe Ala Asn Val Phe Pro Leu Asn Ser Asp Phe Phe Pro	
140 145 150 155	
tcc aga cac aat ctc tat gag tat gac tta ttt gga aag tgt tta gaa	771
Ser Arg His Asn Leu Tyr Glu Tyr Asp Leu Phe Gly Lys Cys Leu Glu	
160 165 170	
cat aat ttt gac tgt cat aat aat gtg aaa tgc ctt atg aga aag gag	819
His Asn Phe Asp Cys His Asn Asn Val Lys Cys Leu Met Arg Lys Glu	
175 180 185	
cat tgt gaa tat aat gaa cct gtg aaa tca tat ggt aat agc tca tcc	867
His Cys Glu Tyr Asn Glu Pro Val Lys Ser Tyr Gly Asn Ser Ser Ser	
190 195 200	
cat ttt gtc att acc ccc ttt aag tgt aat cat tgt gga aaa ggc ttc	915
His Phe Val Ile Thr Pro Phe Lys Cys Asn His Cys Gly Lys Gly Phe	
205 210 215	
aat cag act ttg gac ctc atc aga cat ctg aga att cat act gga gag	963
Asn Gln Thr Leu Asp Leu Ile Arg His Leu Arg Ile His Thr Gly Glu	
220 225 230 235	
aag ccc tat gaa tgt agt aac tgt aga aaa gcc ttc agt cac aag gaa	1011
Lys Pro Tyr Glu Cys Ser Asn Cys Arg Lys Ala Phe Ser His Lys Glu	
240 245 250	
aaa ctt att aaa cat tat aaa att cac agt agg gag cag tct tac aaa	1059
Lys Leu Ile Lys His Tyr Lys Ile His Ser Arg Glu Gln Ser Tyr Lys	

255	260	265	
tgt aat gaa tgt ggt aaa gct ttc att aaa atg tca aat ctc att aga Cys Asn Glu Cys Gly Lys Ala Phe Ile Lys Met Ser Asn Leu Ile Arg 270 275 280			1107
cat caa aga att cat act gga gag aag ccc tat gca tgt aag gaa tgt His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Ala Cys Lys Glu Cys 285 290 295			1155
gag aag tcc ttc agc cag aaa tca aat ctt att gat cat gaa aaa att Glu Lys Ser Phe Ser Gln Lys Ser Asn Leu Ile Asp His Glu Lys Ile 300 305 310 315			1203
cat act gga gag aaa cct tat gaa tgt aat gag tgt gga aaa gca ttc His Thr Gly Glu Lys Pro Tyr Glu Cys Asn Glu Cys Gly Lys Ala Phe 320 325 330			1251
agc cag aag caa agc ctc att gca cat cag aaa gtt cat act ggg gag Ser Gln Lys Gln Ser Leu Ile Ala His Gln Lys Val His Thr Gly Glu 335 340 345			1299
aaa cct tat gca tgt aat gaa tgt ggt aaa gcc ttc cct cga att gca Lys Pro Tyr Ala Cys Asn Glu Cys Gly Lys Ala Phe Pro Arg Ile Ala 350 355 360			1347
tcc ctt gct ctt cat atg aga agt cat aca gga gaa aaa cct tat aaa Ser Leu Ala Leu His Met Arg Ser His Thr Gly Glu Lys Pro Tyr Lys 365 370 375			1395
tgt gat aaa tgt ggt aaa gcc ttc tct cag ttt tcc atg ctt att ata Cys Asp Lys Cys Gly Lys Ala Phe Ser Gln Phe Ser Met Leu Ile Ile 380 385 390 395			1443
cat gtt aga att cat aca ggt gaa aaa ccc tat gaa tgt aat gag tgt His Val Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Asn Glu Cys 400 405 410			1491
gga aaa gcc ttc tct caa agc tca gcc ctt act gta cat atg aga agt Gly Lys Ala Phe Ser Gln Ser Ser Ala Leu Thr Val His Met Arg Ser 415 420 425			1539
cac act ggt gag aaa ccc tat gaa tgt aag gaa tgc aga aaa gcc ttc His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Arg Lys Ala Phe 430 435 440			1587
agc cac aag aaa aac ttc att aca cac cag aaa att cat act aga gag Ser His Lys Lys Asn Phe Ile Thr His Gln Lys Ile His Thr Arg Glu 445 450 455			1635
aaa cct tat gag tgt aat gaa tgt ggg aaa gct ttt ata cag atg tca Lys Pro Tyr Glu Cys Asn Glu Cys Gly Lys Ala Phe Ile Gln Met Ser 460 465 470 475			1683
aat ctt gtt aga cac cag aga att cat act ggg gaa aaa ccc tat ata Asn Leu Val Arg His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Ile 480 485 490			1731
tgt aag gaa tgt ggg aaa gcc ttt agc cag aat tca aat ctc att gct Cys Lys Glu Cys Gly Lys Ala Phe Ser Gln Asn Ser Asn Leu Ile Ala 495 500 505			1779
cat gaa aaa att cat tct gga gag aaa ccc tat gaa tgc aat gaa tgt His Glu Lys Ile His Ser Gly Glu Lys Pro Tyr Glu Cys Asn Glu Cys			1827

510	515	520	
ggt aaa gcc ttc agc caa aag	caa aac ttc att aca cat	caa aaa gtt	1875
Gly Lys Ala Phe Ser Gln Lys	Gln Asn Phe Ile Thr His	Gln Lys Val	
525	530	535	
cat act gga gag aaa cct tat	gat tgt aat gaa tgt ggt	aaa gcc ttc	1923
His Thr Gly Glu Lys Pro Tyr	Asp Cys Asn Glu Cys Gly	Lys Ala Phe	
540	545	550	555
tct caa att gca tcc ctt acc	ctt cat ttg aga agt cat	aca ggg gaa	1971
Ser Gln Ile Ala Ser Leu Thr	Leu His Leu Arg Ser His	Thr Gly Glu	
560	565	570	
aag cct tat gaa tgt gat aaa	tgt ggt aaa gcc ttc tct	cag tgc tca	2019
Lys Pro Tyr Glu Cys Asp Lys	Cys Gly Lys Ala Phe Ser	Gln Cys Ser	
575	580	585	
ctg ctt aat tta cat atg aga	agt cac aca ggt gag aag	ccc tat gta	2067
Leu Leu Asn Leu His Met Arg	Ser His Thr Gly Glu Lys	Pro Tyr Val	
590	595	600	
tgt aat gaa tgt ggg aaa gcc	ttc tct caa aga act tcc	ctt att gtg	2115
Cys Asn Glu Cys Gly Lys Ala	Phe Ser Gln Arg Thr Ser	Leu Ile Val	
605	610	615	
cac atg aga ggc cat aca ggt	gaa aaa ccc tat gaa tgt	aat aaa tgt	2163
His Met Arg Gly His Thr Gly	Glu Lys Pro Tyr Glu Cys	Asn Lys Cys	
620	625	630	635
gga aaa gcc ttc tcc caa agc	tca tcc ctt act ata cat	ata cga gga	2211
Gly Lys Ala Phe Ser Gln Ser	Ser Ser Leu Thr Ile His	Ile Arg Gly	
640	645	650	
cat aca ggt gag aaa ccc tat	gaa tgt aag gaa tgc aga	aaa gcc ttc	2259
His Thr Gly Glu Lys Pro Tyr	Glu Cys Lys Glu Cys Arg	Lys Ala Phe	
655	660	665	
agc cac aag aaa aac ttc att	aca cac cag aaa att cat	act aga gag	2307
Ser His Lys Lys Asn Phe Ile	Thr His Gln Lys Ile His	Thr Arg Glu	
670	675	680	
aaa cct tta agt gta atc att	gtg gaa aag gct tca atc	aga ctt tgg	2355
Lys Pro Leu Ser Val Ile Ile	Val Glu Lys Ala Ser Ile	Arg Leu Trp	
685	690	695	
acc tca tca gac atc tga	gaattc atactggaga gaagccctat	gaatgtagta	2409
Thr Ser Ser Asp Ile *			
700	705		
actgtagaaa agccttcagt	cacaaggaaa aacttattaa	acattataaa gtcgacgcgg	2469
ccgcgaattc ggatcctcga	gagatctctt tttttgggtt	tggtggggta ttttcatcat	2529
cgaatagata gttatgccat	cagcattcag aggggggctg	t	2570

<210> 434  
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 <212> DNA  
 <213> Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (419) .. (1195)

&lt;400&gt; 434

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tttaaagggg ccttcggcac ccagggtcggg tcgccgccgg gactgctgac ggggagggct      120
aggtagccct gggagtcggg atctagaagg tagaggagaa gcggggctgt ctgacccccg      180
gaggtgacaa ggggagaggg gctgtgtgaa taccctccat gggcagtaat gggatgacta      240
tccccagggg gcattgcgaa ggagagaggg ggctgagggg ctgcactttc tggggccccc      300
cgggagagtc agagggcagt taagagggat cacaggcccc gcttggtact gtcaactcccc      360

ttcccaactcc ctgctctcag cattctgtca cctccctacc ccgtcgcggt gccagacc      418
atg gcc aga cct ccc gtg ccc ggt tcg gtg gtt gtc cca aac tgg cac      466
Met Ala Arg Pro Pro Val Pro Gly Ser Val Val Val Pro Asn Trp His
  1             5             10             15

gag agt gcc gag ggc aag gag tac ctg gct tgc att ctg cgc aag aac      514
Glu Ser Ala Glu Gly Lys Glu Tyr Leu Ala Cys Ile Leu Arg Lys Asn
             20             25             30

cgc cgg cgg gtg ttt ggg ctg ctt gag cgg cca gtg ctg ctg ccg cct      562
Arg Arg Arg Val Phe Gly Leu Leu Glu Arg Pro Val Leu Leu Pro Pro
             35             40             45

gtg tcc att gac act gcc agc tac aag atc ttt gtg tcc ggg aag agt      610
Val Ser Ile Asp Thr Ala Ser Tyr Lys Ile Phe Val Ser Gly Lys Ser
             50             55             60

ggg gtg ggc aag acg gcg ctg gtg gcc aag ctg gct ggc ctg gag gtg      658
Gly Val Gly Lys Thr Ala Leu Val Ala Lys Leu Ala Gly Leu Glu Val
             65             70             75             80

cct gtg gtg cac cac gag acc acc ggc atc cag acc acc gtg gta ttt      706
Pro Val Val His His Glu Thr Thr Gly Ile Gln Thr Thr Val Val Phe
             85             90             95

tgg cca gcc aag ctg cag gcc agc agc cgt gtc gtc atg ttt cgt ttt      754
Trp Pro Ala Lys Leu Gln Ala Ser Ser Arg Val Val Met Phe Arg Phe
             100             105             110

gag ttc tgg gac tgt gga gag tct gca ctc aaa aag ttc gat cat atg      802
Glu Phe Trp Asp Cys Gly Glu Ser Ala Leu Lys Lys Phe Asp His Met
             115             120             125

ctg ctg gct tgc atg gag aac aca gat gcc ttc ctc ttc ctc ttc tcc      850
Leu Leu Ala Cys Met Glu Asn Thr Asp Ala Phe Leu Phe Leu Phe Ser
             130             135             140

ttc act gac cgt gcc tcc ttt gaa gac ctc cct gga cag ctg gcc cgc      898
Phe Thr Asp Arg Ala Ser Phe Glu Asp Leu Pro Gly Gln Leu Ala Arg
             145             150             155             160

ata gca ggt gag gcc cct ggt gtc gtc agg atg gtc atc ggc tcc aaa      946
Ile Ala Gly Glu Ala Pro Gly Val Val Arg Met Val Ile Gly Ser Lys
             165             170             175

ttt gac cag tac atg cac acg gac gtg ccc gag cgg gac ctc aca gcc      994
Phe Asp Gln Tyr Met His Thr Asp Val Pro Glu Arg Asp Leu Thr Ala

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180	185	190	
ttc cgg cag gcc tgg gag ctg ccc ctg cta cgg gtg aag agt gtg ccg			1042
Phe Arg Gln Ala Trp Glu Leu Pro Leu Leu Arg Val Lys Ser Val Pro			
195	200	205	
ggg cgg cgg ctg gct gat ggg cgc aca ctg gac ggg cgg gct ggg ctg			1090
Gly Arg Arg Leu Ala Asp Gly Arg Thr Leu Asp Gly Arg Ala Gly Leu			
210	215	220	
gcc gac gtt gcc cac ata ctc aat ggc ctt gct gag cag ctg tgg cac			1138
Ala Asp Val Ala His Ile Leu Asn Gly Leu Ala Glu Gln Leu Trp His			
225	230	235	240
cag gac cag gtg gcg gct ggc ctg ctt ccc aac ccc cca gag agt gct			1186
Gln Asp Gln Val Ala Ala Gly Leu Leu Pro Asn Pro Pro Glu Ser Ala			
245	250	255	
cct gaa tga gtcacga gtggttgctt gtgatccac ccccaaccct caggtctcga			1242
Pro Glu *			
catagggctg gaggtgagg caggaacatg gatcctatct ggaggactgg ccagcatggc			1302
ctgatcaggg aggatgtggc cagagaaggc ccacccgcga gcagcgcttt ccttgacagaa			1362
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agtgggcgtg gggctctgct ccaggcgctc ctgcagagac ccagccccag agaccctacc			1662
ctgcccagtt gccctagggt gtcagcaccg agtcag			1698

&lt;210&gt; 435

&lt;211&gt; 2188

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (349) .. (1425)

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (2188)

&lt;223&gt; n = a, t, c or g

&lt;400&gt; 435

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gaattggcat ctgctggctg tgtggccctt gcttgcccta gtgagttacc atttctctgt	180
ccctacggng gagcctttgg gggtattgtg agttcatggg aggagcgtgt aagcaccggc	240

acagcatcag cccatgagag tgctcctggc ctgagaggggt aagggtcagg gcagctcagg 300

agaccctaga cctgcatagt gatcccccca ccaggaaggc cccacaag atg ctc acc 357  
Met Leu Thr  
1

tgc cct ccc tat ccc tgt ccc cag ctg gag gag cac cgg aat tca cag 405  
Cys Pro Pro Tyr Pro Cys Pro Gln Leu Glu Glu His Arg Asn Ser Gln  
5 10 15

aag cag atg aag ctc cta cag aaa aag cag agc cag ctg gtg caa gag 453  
Lys Gln Met Lys Leu Leu Gln Lys Lys Gln Ser Gln Leu Val Gln Glu  
20 25 30 35

aag gac cac ctg cgc ggt gag cac agc aag gcc gtc ctg gcc cgc agc 501  
Lys Asp His Leu Arg Gly Glu His Ser Lys Ala Val Leu Ala Arg Ser  
40 45 50

aag ctt gag agc cta tgc cgt gag ctg cag cgg cac aac cgc tcc ctc 549  
Lys Leu Glu Ser Leu Cys Arg Glu Leu Gln Arg His Asn Arg Ser Leu  
55 60 65

aag gaa gaa ggt gtg cag cgg gcc cgg gag gag gag gag aag cgc aag 597  
Lys Glu Glu Gly Val Gln Arg Ala Arg Glu Glu Glu Glu Lys Arg Lys  
70 75 80

gag gtg acc tcg cac ttc cag gtg aca ctg aat gac att cag ctg cag 645  
Glu Val Thr Ser His Phe Gln Val Thr Leu Asn Asp Ile Gln Leu Gln  
85 90 95

atg gaa cag cac aat gag cgc aac tcc aag ctg cgc caa gag aac atg 693  
Met Glu Gln His Asn Glu Arg Asn Ser Lys Leu Arg Gln Glu Asn Met  
100 105 110 115

gag ctg gct gag agg ctc aag aag ctg att gag cag tat gag ctg cgc 741  
Glu Leu Ala Glu Arg Leu Lys Lys Leu Ile Glu Gln Tyr Glu Leu Arg  
120 125 130

gag gag cat atc gac aaa gtc ttc aaa cac aag gac cta caa cag cag 789  
Glu Glu His Ile Asp Lys Val Phe Lys His Lys Asp Leu Gln Gln Gln  
135 140 145

ctg gtg gat gcc aag ctc cag cag gcc cag gag atg cta aag gag gca 837  
Leu Val Asp Ala Lys Leu Gln Gln Ala Gln Glu Met Leu Lys Glu Ala  
150 155 160

gaa gag cgg cac cag cgg gag aag gat ttt ctc ctg aaa gag gca gta 885  
Glu Glu Arg His Gln Arg Glu Lys Asp Phe Leu Leu Lys Glu Ala Val  
165 170 175

gag tcc cag agg atg tgt gag ctg atg aag cag caa gag acc cac ctg 933  
Glu Ser Gln Arg Met Cys Glu Leu Met Lys Gln Gln Glu Thr His Leu  
180 185 190 195

aag caa cag ctt gcc cta tac aca gag aag ttt gag gag ttc cag aac 981  
Lys Gln Gln Leu Ala Leu Tyr Thr Glu Lys Phe Glu Glu Phe Gln Asn  
200 205 210

aca ctt tcc aaa agc agc gag gta ttc acc aca ttc aag cag gag atg 1029  
Thr Leu Ser Lys Ser Ser Glu Val Phe Thr Thr Phe Lys Gln Glu Met  
215 220 225

gaa aag atg act aag aag atc aag aag ctg gag aaa gaa acc acc atg 1077  
Glu Lys Met Thr Lys Lys Ile Lys Lys Leu Glu Lys Glu Thr Thr Met

230	235	240	
tac cgg tcc cgg tgg gag agc agc aac aag gcc	ctg ctt gag atg gct	1125	
Tyr Arg Ser Arg Trp Glu Ser Ser Asn Lys Ala	Leu Leu Glu Met Ala		
245	250	255	
gag gag aaa aca gtc cgg gat aaa gaa ctg gag ggc ctg cag gta aaa		1173	
Glu Glu Lys Thr Val Arg Asp Lys Glu Leu Glu Gly Leu Gln Val Lys			
260	265	270	
atc caa cgg ctg gag aag ctg tgc cgg gca ctg cag aca gag cgc aat		1221	
Ile Gln Arg Leu Glu Lys Leu Cys Arg Ala Leu Gln Thr Glu Arg Asn			
280	285	290	
gac ctg aac aag agg gta cag gac ctg agt gct ggt ggc cag ggc tcc		1269	
Asp Leu Asn Lys Arg Val Gln Asp Leu Ser Ala Gly Gly Gln Gly Ser			
295	300	305	
ctc act gac agt ggc cct gag agg agg cca gag ggg cct ggg gct caa		1317	
Leu Thr Asp Ser Gly Pro Glu Arg Arg Pro Glu Gly Pro Gly Ala Gln			
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gca ccc agc tcc ccc agg gtc aca gaa gcg cct tgc tac cca gga gca		1365	
Ala Pro Ser Ser Pro Arg Val Thr Glu Ala Pro Cys Tyr Pro Gly Ala			
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ccg agc aca gaa gca tca ggc cag act ggg cct caa gag ccc acc tcc		1413	
Pro Ser Thr Glu Ala Ser Gly Gln Thr Gly Pro Gln Glu Pro Thr Ser			
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gcc agg gcc tag aga gcctggtgtt gggtcatgct gggaaggag cggcagccca		1468	
Ala Arg Ala *			
gccaggcctg gcccataaaa ggctcccatg ctgagcagcc cattgctgaa gccaggatgt		1528	
tctgacctgg ctggcatctg gcacttgcaa ttttggattt tgtgggtcag ttttacgtac		1588	
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gcaccaggt cttgactgca tttgtcttgt gagcagggt tgcttggtca gctcaggccc		1888	
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tggtagtgcc aggaccaggc caatgatgct tctcagtagc cttatcattc acaggtgcct		2128	
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&lt;211&gt; 2903

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

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&lt;400&gt; 436

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atg ggg gac aag aaa gat gac aag gac tca ccc aag aag aac aag ggc      165
Met Gly Asp Lys Lys Asp Asp Lys Asp Ser Pro Lys Lys Asn Lys Gly
  1             5             10             15

aag gag cgc cgg gac ctg gat gac ctc aag aag gag gtg gct atg aca      213
Lys Glu Arg Arg Asp Leu Asp Asp Leu Lys Lys Glu Val Ala Met Thr
             20             25             30

gag cac aag atg tca gtg gaa gag gtc tgc cgg aaa tac aac aca gac      261
Glu His Lys Met Ser Val Glu Glu Val Cys Arg Lys Tyr Asn Thr Asp
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tgt gtg cag ggt ttg acc cac agc aaa gcc cag gag atc ctg gcc cgg      309
Cys Val Gln Gly Leu Thr His Ser Lys Ala Gln Glu Ile Leu Ala Arg
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gat ggg cct aac gca ctc acg cca ccg cct acc acc cca gag tgg gtc      357
Asp Gly Pro Asn Ala Leu Thr Pro Pro Pro Thr Thr Pro Glu Trp Val
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aag ttt tgc cgg cag ctc ttc ggg ggc ttc tcc atc ctg ctg tgg atc      405
Lys Phe Cys Arg Gln Leu Phe Gly Gly Phe Ser Ile Leu Leu Trp Ile
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ggg gct atc ctc tgc ttc ctg gcc tac ggt atc cag gcg ggc acc gag      453
Gly Ala Ile Leu Cys Phe Leu Ala Tyr Gly Ile Gln Ala Gly Thr Glu
             100             105             110

gac gac ccc tct ggt gac aac ctg tac ctg ggc atc gtg ctg gcg gcc      501
Asp Asp Pro Ser Gly Asp Asn Leu Tyr Leu Gly Ile Val Leu Ala Ala
             115             120             125

gtg gtg atc atc act ggc tgc ttc tcc tac tac cag gag gcc aag agc      549
Val Val Ile Ile Thr Gly Cys Phe Ser Tyr Tyr Gln Glu Ala Lys Ser
             130             135             140

tcc aag atc atg gag tcc ttc aag aac atg gtg ccc cag caa gcc ctg      597
Ser Lys Ile Met Glu Ser Phe Lys Asn Met Val Pro Gln Gln Ala Leu
             145             150             155             160

gtg atc cgg gaa ggt gag aag atg cag gtg aac gct gag gag gtg gtg      645
Val Ile Arg Glu Gly Glu Lys Met Gln Val Asn Ala Glu Glu Val Val
             165             170             175

gtc ggg gac ctg gtg gag atc aag ggt gga gac cga gtg cca gct gac      693
Val Gly Asp Leu Val Glu Ile Lys Gly Gly Asp Arg Val Pro Ala Asp
             180             185             190

ctg cgg atc atc tca gcc cac ggc tgc aag gtg gac aac tcc tcc ctg      741
Leu Arg Ile Ile Ser Ala His Gly Cys Lys Val Asp Asn Ser Ser Leu
             195             200             205

act ggc gaa tcc gag ccc cag act cgc tct ccc gac tgc act cac gac      789
Thr Gly Glu Ser Glu Pro Gln Thr Arg Ser Pro Asp Cys Thr His Asp

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210											215											220											
aac ccc ttg gag act	cgg aac atc acc ttc ttt tcc acc aac tgt gtg	837																															
Asn Pro Leu Glu Thr	Arg Asn Ile Thr Phe Phe Ser Thr Asn Cys Val																																
225	230	235	240																														
gaa ggc acg gct cgg ggc gtg gtg gtg gcc acg ggc gac cgc act gtc	885																																
Glu Gly Thr Ala Arg Gly Val Val Val Ala Thr Gly Asp Arg Thr Val																																	
245	250	255																															
atg ggc cgt atc gcc acc ctg gca tca ggg ctg gag gtg ggc aag acg	933																																
Met Gly Arg Ile Ala Thr Leu Ala Ser Gly Leu Glu Val Gly Lys Thr																																	
260	265	270																															
ccc atc gcc atc gag att gag cac ttc atc cag ctc atc acc ggc gtg	981																																
Pro Ile Ala Ile Glu Ile Glu His Phe Ile Gln Leu Ile Thr Gly Val																																	
275	280	285																															
gct gtc ttc ctg ggt gtc tcc ttc ttc atc ctc tcc ctc att ctc gga	1029																																
Ala Val Phe Leu Gly Val Ser Phe Phe Ile Leu Ser Leu Ile Leu Gly																																	
290	295	300																															
tac acc tgg ctt gag gct gtc atc ttc ctc atc ggc atc atc gtg gcc	1077																																
Tyr Thr Trp Leu Glu Ala Val Ile Phe Leu Ile Gly Ile Ile Val Ala																																	
305	310	315	320																														
aat gtc cca gag ggt ctg ctg gcc act gtc act gtg tgt ctg acg ctg	1125																																
Asn Val Pro Glu Gly Leu Leu Ala Thr Val Thr Val Cys Leu Thr Leu																																	
325	330	335																															
acc gcc aag cgc atg gcc cgg aag aac tgc ctg gtg aag aac ctg gag	1173																																
Thr Ala Lys Arg Met Ala Arg Lys Asn Cys Leu Val Lys Asn Leu Glu																																	
340	345	350																															
gct gta gaa acc ctg ggc tcc acg tcc acc atc tgc tca gat aag aca	1221																																
Ala Val Glu Thr Leu Gly Ser Thr Ser Thr Ile Cys Ser Asp Lys Thr																																	
355	360	365																															
ggg acc ctc act cag aac cgc atg aca gtc gcc cac atg tgg ttt gac	1269																																
Gly Thr Leu Thr Gln Asn Arg Met Thr Val Ala His Met Trp Phe Asp																																	
370	375	380																															
aac cag atc cac gag gct gac acc act gag gac cag tca ggg acc tca	1317																																
Asn Gln Ile His Glu Ala Asp Thr Thr Glu Asp Gln Ser Gly Thr Ser																																	
385	390	395	400																														
ttt gac aag agt tcg cac acc tgg gtg gcc ctg tct cac atc gct ggg	1365																																
Phe Asp Lys Ser Ser His Thr Trp Val Ala Leu Ser His Ile Ala Gly																																	
405	410	415																															
ctc tgc aat cgc gct gtc ttc aag ggt ggt cag gac aac atc cct gtg	1413																																
Leu Cys Asn Arg Ala Val Phe Lys Gly Gly Gln Asp Asn Ile Pro Val																																	
420	425	430																															
ctc aag agg gat gtg gct ggg gat gcg tct gag tct gcc ctg ctc aag	1461																																
Leu Lys Arg Asp Val Ala Gly Asp Ala Ser Glu Ser Ala Leu Leu Lys																																	
435	440	445																															
tgc atc gag ctg tcc tct ggc tcc gtg aag ctg atg cgt gaa cgc aac	1509																																
Cys Ile Glu Leu Ser Ser Gly Ser Val Lys Leu Met Arg Glu Arg Asn																																	
450	455	460																															
aag aaa gtg gct gag att ccc ttc aat tcc acc aac aaa tac cag ctc	1557																																
Lys Lys Val Ala Glu Ile Pro Phe Asn Ser Thr Asn Lys Tyr Gln Leu																																	

465	470	475	480	
tcc atc cat gag acc gag gac ccc aac gac aac cga tac ctg ctg gtg				1605
Ser Ile His Glu Thr Glu Asp Pro Asn Asp Asn Arg Tyr Leu Leu Val	485	490	495	
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Met Lys Gly Ala Pro Glu Arg Ile Leu Asp Arg Cys Ser Thr Ile Leu	500	505	510	
cta cag ggc aag gag cag cct ctg gac gag gaa atg aag gag gcc ttc				1701
Leu Gln Gly Lys Glu Gln Pro Leu Asp Glu Glu Met Lys Glu Ala Phe	515	520	525	
cag aat gcc tac ctt gag ctc ggt ggc ctg ggc gag cgc gtg ctt ggt				1749
Gln Asn Ala Tyr Leu Glu Leu Gly Gly Leu Gly Glu Arg Val Leu Gly	530	535	540	
ttc tgc cat tat tac ctg ccc gag gag cag ttc ccc aag ggc ttt gcc				1797
Phe Cys His Tyr Tyr Leu Pro Glu Glu Gln Phe Pro Lys Gly Phe Ala	545	550	555	560
ttc gac tgt gat gac gtg aac ttc acc acg gac aac ctc tgc ttt gtg				1845
Phe Asp Cys Asp Asp Val Asn Phe Thr Thr Asp Asn Leu Cys Phe Val	565	570	575	
ggc ctc atg tcc atg atc gac cca ccc cgg gca gcc gtc cct gac gcg				1893
Gly Leu Met Ser Met Ile Asp Pro Pro Arg Ala Ala Val Pro Asp Ala	580	585	590	
gtg ggc aag tgt cgc agc gca ggc atc aag gtc atc atg gtc acc ggc				1941
Val Gly Lys Cys Arg Ser Ala Gly Ile Lys Val Ile Met Val Thr Gly	595	600	605	
gat cac ccc atc acg gcc aag gcc att gcc aag ggt gtg ggc atc atc				1989
Asp His Pro Ile Thr Ala Lys Ala Ile Ala Lys Gly Val Gly Ile Ile	610	615	620	
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Phe Glu Gly Asn Glu Thr Val Glu Asp Ile Ala Ala Arg Leu Asn Ile	625	630	635	640
ccc gtc agc cag gtt aac ccc cgg gat gcc aag gcc tgc gtg atc cac				2085
Pro Val Ser Gln Val Asn Pro Arg Asp Ala Lys Ala Cys Val Ile His	645	650	655	
ggc acc gac ctc aag gac ttc acc tcc gag caa atc gac gag atc ctg				2133
Gly Thr Asp Leu Lys Asp Phe Thr Ser Glu Gln Ile Asp Glu Ile Leu	660	665	670	
cag aat cac acc gag atc gtc ttc gcc cgc aca tcc ccc cag cag aag				2181
Gln Asn His Thr Glu Ile Val Phe Ala Arg Thr Ser Pro Gln Gln Lys	675	680	685	
ctc atc att gtg gag ggc tgt cag aga cag ggt gca att gtg gct gtg				2229
Leu Ile Ile Val Glu Gly Cys Gln Arg Gln Gly Ala Ile Val Ala Val	690	695	700	
acc ggg gat ggt gtg aac gac tcc ccc gct ctg aag aag gcc gac att				2277
Thr Gly Asp Gly Val Asn Asp Ser Pro Ala Leu Lys Lys Ala Asp Ile	705	710	715	720
ggg gtg gcc atg ggc atc gct ggc tct gac gtc tcc aag cag gca gct				2325
Gly Val Ala Met Gly Ile Ala Gly Ser Asp Val Ser Lys Gln Ala Ala				

725	730	735	
gac atg atc ctg ctg gac gac aac ttt gcc tcc atc gtc aca ggg gtg			2373
Asp Met Ile Leu Leu Asp Asp Asn Phe Ala Ser Ile Val Thr Gly Val			
740	745	750	
gag gag ggc cgc ctg atc ttc gac aac cta aag aag tcc att gcc tac			2421
Glu Glu Gly Arg Leu Ile Phe Asp Asn Leu Lys Lys Ser Ile Ala Tyr			
755	760	765	
acc ctg acc agc aat atc ccg gag atc acg ccc ttc ctg ctg ttc atc			2469
Thr Leu Thr Ser Asn Ile Pro Glu Ile Thr Pro Phe Leu Leu Phe Ile			
770	775	780	
atg gcc aac atc ccg ctg ccc ctg ggc acc atc acc atc ctc tgc atc			2517
Met Ala Asn Ile Pro Leu Pro Leu Gly Thr Ile Thr Ile Leu Cys Ile			
785	790	795	800
gat ctg ggc act gac atg gtc cct gcc atc tca ctg gcg tac gag gct			2565
Asp Leu Gly Thr Asp Met Val Pro Ala Ile Ser Leu Ala Tyr Glu Ala			
805	810	815	
gcc gaa agc gac atc atg aag aga cag ccc agg aac ccg cgg acg gac			2613
Ala Glu Ser Asp Ile Met Lys Arg Gln Pro Arg Asn Pro Arg Thr Asp			
820	825	830	
aaa ttg gct gag gag cca atg ggg cga agc tac cat ctg tgg gat tat			2661
Lys Leu Ala Glu Glu Pro Met Gly Arg Ser Tyr His Leu Trp Asp Tyr			
835	840	845	
gac tga acgcctctaa gtcagaatcc cgcccaggcg gaacgatacg gcagcgccgc			2717
Asp *			
850			
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ccccctccac gcgccccgcg cgcgcgggag ggcgcgtgcc ccgccgcgcg ccgggaccgg			2837
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cggaattcaa aacggacctg gagg atg ttg atc tcc aag aac atg ccc tgg	171
Met Leu Ile Ser Lys Asn Met Pro Trp	
1	5
cgg cgg ctg cag ggc att tcc ttc ggg atg tat tcg gct gaa gag ctc	219

Arg	Arg	Leu	Gln	Gly	Ile	Ser	Phe	Gly	Met	Tyr	Ser	Ala	Glu	Glu	Leu	
10					15					20					25	
aag	aaa	tta	agt	gtt	aaa	tcc	att	acg	aac	cct	cga	tac	ctg	gac	agc	267
Lys	Lys	Leu	Ser	Val	Lys	Ser	Ile	Thr	Asn	Pro	Arg	Tyr	Leu	Asp	Ser	
				30					35					40		
ctg	ggg	aac	cca	tcg	gca	aac	ggc	ctg	tac	gat	tta	gct	ttg	ggc	cct	315
Leu	Gly	Asn	Pro	Ser	Ala	Asn	Gly	Leu	Tyr	Asp	Leu	Ala	Leu	Gly	Pro	
				45				50					55			
gca	gat	tcc	aaa	gag	gtg	tgc	tcc	acc	tgc	gtg	cag	gac	ttc	agc	aac	363
Ala	Asp	Ser	Lys	Glu	Val	Cys	Ser	Thr	Cys	Val	Gln	Asp	Phe	Ser	Asn	
		60					65				70					
tgt	tct	ggg	cac	ctg	ggc	cac	att	gag	ctc	cca	ctc	aca	gtg	tat	aac	411
Cys	Ser	Gly	His	Leu	Gly	His	Ile	Glu	Leu	Pro	Leu	Thr	Val	Tyr	Asn	
	75					80					85					
cct	ctc	ctc	ttc	gat	aag	ctg	tac	ctg	ctg	ctt	cgg	ggc	tct	tgt	tta	459
Pro	Leu	Leu	Phe	Asp	Lys	Leu	Tyr	Leu	Leu	Arg	Gly	Ser	Cys	Leu		
90					95					100				105		
aac	tgc	cac	atg	ctg	act	tgt	ccc	cgg	gcc	gtg	att	cac	ctc	tta	ctc	507
Asn	Cys	His	Met	Leu	Thr	Cys	Pro	Arg	Ala	Val	Ile	His	Leu	Leu	Leu	
				110					115					120		
tgc	cag	ctg	agg	gtt	ctg	gaa	gtc	ggg	gcc	cta	caa	gca	gtc	tac	gag	555
Cys	Gln	Leu	Arg	Val	Leu	Glu	Val	Gly	Ala	Leu	Gln	Ala	Val	Tyr	Glu	
			125					130					135			
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Leu	Glu	Arg	Ile	Leu	Asn	Arg	Phe	Leu	Glu	Glu	Asn	Ala	Asp	Pro	Ser	
		140					145					150				
gcc	tct	gaa	att	cgg	gag	gaa	tta	gaa	caa	tac	aca	act	gaa	att	gtg	651
Ala	Ser	Glu	Ile	Arg	Glu	Glu	Leu	Glu	Gln	Tyr	Thr	Thr	Glu	Ile	Val	
	155					160					165					
cag	aac	aac	ctc	ctg	ggg	tcc	cag	ggc	gca	cat	gta	aag	aac	gtg	tgt	699
Gln	Asn	Asn	Leu	Leu	Gly	Ser	Gln	Gly	Ala	His	Val	Lys	Asn	Val	Cys	
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Glu	Ser	Lys	Ser	Lys	Leu	Ile	Ala	Leu	Phe	Trp	Lys	Ala	His	Met	Asn	
				190					195					200		
gct	aag	cgc	tgt	ccc	cac	tgc	aag	acc	ggg	cga	tcc	gtt	gtc	cga	aag	795
Ala	Lys	Arg	Cys	Pro	His	Cys	Lys	Thr	Gly	Arg	Ser	Val	Val	Arg	Lys	
			205					210					215			
gaa	cac	aac	agc	aag	ttg	act	atc	aca	ttt	cca	gcc	atg	gtg	cac	agg	843
Glu	His	Asn	Ser	Lys	Leu	Thr	Ile	Thr	Phe	Pro	Ala	Met	Val	His	Arg	
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Thr	Ala	Gly	Gln	Lys	Asp	Ser	Glu	Pro	Leu	Gly	Ile	Glu	Glu	Ala	Gln	
	235						240				245					
ata	gga	aaa	cga	gga	tac	tta	aca	ccc	acc	agt	gcc	cgc	gaa	cac	ctt	939
Ile	Gly	Lys	Arg	Gly	Tyr	Leu	Thr	Pro	Thr	Ser	Ala	Arg	Glu	His	Leu	
250					255					260					265	
tct	gcc	ctg	tgg	aag	aat	gaa	gga	ttc	ttt	ctg	aac	tac	ctt	ttt	tcg	987



Ser	Ala	Leu	Trp	Lys	Asn	Glu	Gly	Phe	Phe	Leu	Asn	Tyr	Leu	Phe	Ser		
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Gly	Met	Asp	Asp	Asp	Gly	Met	Glu	Ser	Arg	Phe	Asn	Pro	Ser	Val	Phe		
			285					290					295				
ttt	cta	gat	ttc	ttg	gtg	gtg	ccg	ccc	tca	agg	tat	cgc	cca	gtc	agt		1083
Phe	Leu	Asp	Phe	Leu	Val	Val	Pro	Pro	Ser	Arg	Tyr	Arg	Pro	Val	Ser		
		300					305					310					
cgc	cta	gga	gac	cag	atg	ttt	act	aat	ggc	cag	acg	gtg	aac	ttg	cag		1131
Arg	Leu	Gly	Asp	Gln	Met	Phe	Thr	Asn	Gly	Gln	Thr	Val	Asn	Leu	Gln		
	315				320						325						
gct	gtc	atg	aag	gat	gta	gtt	ctg	att	cga	aaa	ctt	ctg	gca	ttg	atg		1179
Ala	Val	Met	Lys	Asp	Val	Val	Leu	Ile	Arg	Lys	Leu	Leu	Ala	Leu	Met		
330					335				340					345			
gcc	caa	gaa	cag	aag	ttg	cca	gag	gaa	gtg	gcc	aca	ccc	act	aca	gat		1227
Ala	Gln	Glu	Gln	Lys	Leu	Pro	Glu	Glu	Val	Ala	Thr	Pro	Thr	Thr	Asp		
			350					355						360			
gag	gaa	aaa	gac	tct	ttg	att	gct	att	gac	cga	tcc	ttt	ttg	agt	aca		1275
Glu	Glu	Lys	Asp	Ser	Leu	Ile	Ala	Ile	Asp	Arg	Ser	Phe	Leu	Ser	Thr		
		365					370						375				
ctt	cca	ggc	cag	tcc	ctc	ata	gac	aaa	ctt	tac	aac	att	tgg	att	cgc		1323
Leu	Pro	Gly	Gln	Ser	Leu	Ile	Asp	Lys	Leu	Tyr	Asn	Ile	Trp	Ile	Arg		
		380					385					390					
ctt	cag	agc	cac	gtc	aat	att	gtg	ttt	gat	agc	gag	atg	gac	aaa	cta		1371
Leu	Gln	Ser	His	Val	Asn	Ile	Val	Phe	Asp	Ser	Glu	Met	Asp	Lys	Leu		
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atg	atg	gac	aag	tac	cca	ggc	att	agg	cag	atc	ctg	gag	aag	aaa	gaa		1419
Met	Met	Asp	Lys	Tyr	Pro	Gly	Ile	Arg	Gln	Ile	Leu	Glu	Lys	Lys	Glu		
410					415				420					425			
ggc	ctg	ttc	cga	aaa	cac	atg	atg	gga	aag	cga	gtg	gac	tac	gct	gcg		1467
Gly	Leu	Phe	Arg	Lys	His	Met	Met	Gly	Lys	Arg	Val	Asp	Tyr	Ala	Ala		
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cgc	tca	gtc	atc	tgc	cca	gac	atg	tac	atc	aac	acc	aac	gaa	att	gga		1515
Arg	Ser	Val	Ile	Cys	Pro	Asp	Met	Tyr	Ile	Asn	Thr	Asn	Glu	Ile	Gly		
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att	ccc	atg	gtg	ttt	gcc	aca	aaa	ctg	acc	tac	cca	cag	cca	gtt	acc		1563
Ile	Pro	Met	Val	Phe	Ala	Thr	Lys	Leu	Thr	Tyr	Pro	Gln	Pro	Val	Thr		
	460						465					470					
cca	tgg	aat	gtt	cag	gaa	ctt	agg	caa	gcg	gtc	atc	aac	ggc	cct	aat		1611
Pro	Trp	Asn	Val	Gln	Glu	Leu	Arg	Gln	Ala	Val	Ile	Asn	Gly	Pro	Asn		
	475					480					485						
gtg	cac	cca	gga	gcc	tcc	atg	gtc	atc	aat	gag	gac	ggc	agc	cgc	aca		1659
Val	His	Pro	Gly	Ala	Ser	Met	Val	Ile	Asn	Glu	Asp	Gly	Ser	Arg	Thr		
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Pro	Thr	Leu	His	Arg	Pro	Ser	Ile	Gln	Ala	His	Arg	Ala	Arg	Ile	Leu		
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Tyr	Leu	Val	Pro	Lys	Asp	Gly	Gln	Pro	Leu	Ala	Gly	Leu	Ile	Gln	Asp		
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cgg	gag	cac	tat	atg	gag	ctg	gtg	tac	cga	gga	ctc	acg	gac	aaa	gtg	2139	
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Lys	Ala	Trp	Val	Lys	Glu	Thr	Pro	Arg	Ser	Val	Pro	Gly	Phe	Asn	Pro		
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gac	tgc	atg	tgc	gag	tcc	cag	gtg	atc	atc	agg	gaa	ggg	gag	ctg	ctc	2379	
Asp	Ser	Met	Cys	Glu	Ser	Gln	Val	Ile	Ile	Arg	Glu	Gly	Glu	Leu	Leu		
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Cys	Gly	Val	Leu	Asp	Lys	Ala	His	Tyr	Gly	Ser	Ser	Ala	Tyr	Gly	Leu		
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Val	His	Cys	Cys	Tyr	Glu	Ile	Tyr	Gly	Gly	Glu	Thr	Ser	Gly	Lys	Val		
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Ala	Val	Arg	Ala	Ala	Leu	Asn	Leu	Pro	Glu	Ala	Ala	Ser	Tyr	Asp	Glu	
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gag gaa agc cga agg aaa tac cag aag aag gcg gcc gct tgt cct gac Glu Glu Ser Arg Arg Lys Tyr Gln Lys Lys Ala Ala Ala Cys Pro Asp 1130	1135	1140	1145 3579
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agg acc ttg ctg cag ctg aag tgg cag cgc tca ctg tgt gag ccg ggc Arg Thr Leu Leu Gln Leu Lys Trp Gln Arg Ser Leu Cys Glu Pro Gly 1195	1200	1205	3771
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1133

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Glu Val Leu Asp Leu Arg Arg Leu Tyr Ser Asn Asp Ile His Ala Ile	
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Ile Lys Asp Val Phe Ala Val Tyr Gly Ile Ala Val Asp Pro Arg His	
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Leu Ser Leu Val Ala Asp Tyr Met Cys Phe Glu Gly Val Tyr Lys Pro	
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Leu Asn Arg Phe Gly Ile Arg Ser Asn Ser Ser Pro Leu Gln Gln Met	
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cct gcc aag aag aaa cca cca cca cca cca ccg cag gac ggg cct ggt Pro Ala Lys Lys Lys Pro Pro Pro Pro Pro Gln Asp Gly Pro Gly 605 610 615			1877
tca cgg acg act cca gac aaa gcc ccc aag aag acc tgg ggc cag gat Ser Arg Thr Thr Pro Asp Lys Ala Pro Lys Lys Thr Trp Gly Gln Asp 620 625 630			1925
gca ggc agt ggc aag ggg ggt caa ggg cca cct acc agg aag cca cca Ala Gly Ser Gly Lys Gly Gly Gln Gly Pro Pro Thr Arg Lys Pro Pro 630 635 640			1973

635	640	645	
cgt cgg aca tct tct cac ttg ccg tcc agc cct gca gcc ggg gac tgt			2021
Arg Arg Thr Ser Ser His Leu Pro Ser Ser Pro Ala Ala Gly Asp Cys			
650	655	660	665
ccc atc cta gcc acc cct gaa agc ccc ccg cca ctg gcc cct gag acc			2069
Pro Ile Leu Ala Thr Pro Glu Ser Pro Pro Pro Leu Ala Pro Glu Thr			
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ccg gac gag gca gcc tca gta gct gct gac tca gat gtc caa gtg cct			2117
Pro Asp Glu Ala Ala Ser Val Ala Ala Asp Ser Asp Val Gln Val Pro			
	685	690	695
ggc cct gca gca agc cct aag cct ttg ggc ccg ctc ccg cca ccc cgc			2165
Gly Pro Ala Ala Ser Pro Lys Pro Leu Gly Arg Leu Arg Pro Pro Arg			
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gag agc aag gta acc ccg aga ttg ccg ggt gcc agg cct gat gct ggg			2213
Glu Ser Lys Val Thr Arg Arg Leu Pro Gly Ala Arg Pro Asp Ala Gly			
	715	720	725
atg gga cca cct tca gct gtg gct gag agg ccc aag gtc agc ctg cat			2261
Met Gly Pro Pro Ser Ala Val Ala Glu Arg Pro Lys Val Ser Leu His			
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Phe Asp Thr Glu Thr Asp Gly Tyr Phe Ser Asp Gly Glu Met Ser Asp			
	750	755	760
tca gat gta gag gcc gag gac ggt ggg gtg cag ccg ggt ccc ccg gag			2357
Ser Asp Val Glu Ala Glu Asp Gly Gly Val Gln Arg Gly Pro Arg Glu			
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gca ggg gca gag gag gtg gtc cgc atg ggc gta ctg gcc tcc taa ctc			2405
Ala Gly Ala Glu Glu Val Val Arg Met Gly Val Leu Ala Ser *			
	780	785	790
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gttttctgtg 6315

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<212> DNA
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<222> (990) .. (1340)

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ttcactttct tcacctcaag gtaaggacca tgttctctgt tccatcattc cctgtccttc 180
tcctgtctgt ggtgacagct tcctgtcca aaacaaaagc ctgtgcagat acccagaaga 240
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 aagagagttc aagtgaagga aggaggaggt tcctggatgt ggatgtcatc atttctggga 180  
 acactcttaa atggagactc agatttctta gccaaaattt agggaggatc cagaagaaac 240  
 caaagacgaa gcacccagcgt tcttgggtat ttcctgaaac agaagaaa atg aca aag 297  
 Met Thr Lys  
 1  
 gcc cag gaa tca ctg acc ctg gag gat gtg gct gtg gac ttc acc tgg 345  
 Ala Gln Glu Ser Leu Thr Leu Glu Asp Val Ala Val Asp Phe Thr Trp  
 5 10 15  
 gag gag tgg cag ttc ctg agc cct gct cag aag gac ctg tac cgg gat 393  
 Glu Glu Trp Gln Phe Leu Ser Pro Ala Gln Lys Asp Leu Tyr Arg Asp  
 20 25 30 35  
 gtg atg ttg gag aac tac agc aac ctt gtg tca gtg ggg tat caa gcc 441  
 Val Met Leu Glu Asn Tyr Ser Asn Leu Val Ser Val Gly Tyr Gln Ala  
 40 45 50  
 ggc aaa cct gat gcc ctc acc aag ttg gaa caa gga gaa cca cta tgg 489  
 Gly Lys Pro Asp Ala Leu Thr Lys Leu Glu Gln Gly Glu Pro Leu Trp  
 55 60 65  
 aca cta gaa gat gaa atc cac agt cca gcc cac cca gaa att gag aaa 537  
 Thr Leu Glu Asp Glu Ile His Ser Pro Ala His Pro Glu Ile Glu Lys  
 70 75 80  
 gct gat gat cat ctg cag cag ccc ttg caa aac caa aaa ata ctg aag 585  
 Ala Asp Asp His Leu Gln Gln Pro Leu Gln Asn Gln Lys Ile Leu Lys  
 85 90 95  
 agg acg gga caa cgc tat gaa cac gga aga act ttg aaa tca tat tta 633  
 Arg Thr Gly Gln Arg Tyr Glu His Gly Arg Thr Leu Lys Ser Tyr Leu  
 100 105 110 115  
 ggt tta acc aac cag agc aga aga tac aac aga aag gag cct gct gag 681  
 Gly Leu Thr Asn Gln Ser Arg Arg Tyr Asn Arg Lys Glu Pro Ala Glu  
 120 125 130  
 ttt aat gga gat gga gct ttt ctc cat gat aat cat gaa caa atg cct 729  
 Phe Asn Gly Asp Gly Ala Phe Leu His Asp Asn His Glu Gln Met Pro  
 135 140 145  
 acg gaa att gaa ttc cct gaa agt aga aaa ccc atc agc acc aag tca 777  
 Thr Glu Ile Glu Phe Pro Glu Ser Arg Lys Pro Ile Ser Thr Lys Ser  
 150 155 160  
 caa ttc ctt aaa cat cag caa aca cac aac ata gag aaa gcc cat gaa 825  
 Gln Phe Leu Lys His Gln Gln Thr His Asn Ile Glu Lys Ala His Glu  
 165 170 175

tgc act gac tgt ggg aaa gct ttc ctc aag aag tct cag ctc act gag Cys Thr Asp Cys Gly Lys Ala Phe Leu Lys Lys Ser Gln Leu Thr Glu 180 185 190 195	873
cat aag aga att cat aca gga aag aaa ccc cac gtg tgt agc ttg tgt His Lys Arg Ile His Thr Gly Lys Lys Pro His Val Cys Ser Leu Cys 200 205 210	921
ggg aaa gcc ttc tac aag aag tac agg ctc act gaa cac gag aga gct Gly Lys Ala Phe Tyr Lys Lys Tyr Arg Leu Thr Glu His Glu Arg Ala 215 220 225	969
cac aga gga gag aaa ccc cac ggg tgt agc ttg tgt ggg aaa gcc ttc His Arg Gly Glu Lys Pro His Gly Cys Ser Leu Cys Gly Lys Ala Phe 230 235 240	1017
tac aag agg tac agg ctc act gaa cac gag aga gct cac aaa gga gag Tyr Lys Arg Tyr Arg Leu Thr Glu His Glu Arg Ala His Lys Gly Glu 245 250 255	1065
aaa cca tac ggg tgc agt gaa tgt ggg aaa gcc ttc ccc agg aaa tct Lys Pro Tyr Gly Cys Ser Glu Cys Gly Lys Ala Phe Pro Arg Lys Ser 260 265 270 275	1113
gag ctt act gaa cat caa agg att cac acg gga att aag ccc cat caa Glu Leu Thr Glu His Gln Arg Ile His Thr Gly Ile Lys Pro His Gln 280 285 290	1161
tgc agc gaa tgt ggg aga gct ttc tcc aga aaa tca cta ctc gtt gta Cys Ser Glu Cys Gly Arg Ala Phe Ser Arg Lys Ser Leu Leu Val Val 295 300 305	1209
cat cag cga act cat aca gga gag aag cct cat aca tgc agt gaa tgt His Gln Arg Thr His Thr Gly Glu Lys Pro His Thr Cys Ser Glu Cys 310 315 320	1257
gga aaa ggc ttc att cag aag ggc aat ctc aac ata cat caa cga act Gly Lys Gly Phe Ile Gln Lys Gly Asn Leu Asn Ile His Gln Arg Thr 325 330 335	1305
cac act gga gag aaa cct tat gga tgc att gac tgt ggc aag gcc ttc His Thr Gly Glu Lys Pro Tyr Gly Cys Ile Asp Cys Gly Lys Ala Phe 340 345 350 355	1353
agc cag aag tct tgc ctt gta gca cat cag aga tat cat aca gga aag Ser Gln Lys Ser Cys Leu Val Ala His Gln Arg Tyr His Thr Gly Lys 360 365 370	1401
act ccc ttt gta tgt cct gaa tgt ggg caa ccc tgt tca cag aag tca Thr Pro Phe Val Cys Pro Glu Cys Gly Gln Pro Cys Ser Gln Lys Ser 375 380 385	1449
gga ctc att aga cat cag aaa att cac tca gga gag aaa ccc tat aaa Gly Leu Ile Arg His Gln Lys Ile His Ser Gly Glu Lys Pro Tyr Lys 390 395 400	1497
tgc agt gac tgt ggg aaa gcc ttc ctt aca aag aca atg ctc att gta Cys Ser Asp Cys Gly Lys Ala Phe Leu Thr Lys Thr Met Leu Ile Val 405 410 415	1545
cat cac aga act cac acg gga gag aga ccc tat ggc tgt gat gag tgt His His Arg Thr His Thr Gly Glu Arg Pro Tyr Gly Cys Asp Glu Cys 420 425 430 435	1593

gag aaa gct tac ttc tat atg tct tgc ctt gtt aaa cat aag aga ata 1641  
 Glu Lys Ala Tyr Phe Tyr Met Ser Cys Leu Val Lys His Lys Arg Ile  
 440 445 450

cac tca agg gag aaa cgg ggg gat tca gtg aag gtg gaa aat cct tcc 1689  
 His Ser Arg Glu Lys Arg Gly Asp Ser Val Lys Val Glu Asn Pro Ser  
 455 460 465

aca gca agt cac agc tta agt cct agt gaa cat gtg cag ggg aaa agc 1737  
 Thr Ala Ser His Ser Leu Ser Pro Ser Glu His Val Gln Gly Lys Ser  
 470 475 480

cct gtt aat atg gta act gtg gca atg gtg gca ggg cag tgt gag ttt 1785  
 Pro Val Asn Met Val Thr Val Ala Met Val Ala Gly Gln Cys Glu Phe  
 485 490 495

gcc cac atc ctg cat tca tga ta aacagtttgc tgtttgatca tatagcctcc 1838  
 Ala His Ile Leu His Ser \*  
 500 505

agcggaatgc tgagtttgtc atgtcccatg ggcctttggc tccctgcact aatatgtata 1898  
 gtagggttta caagatatga aatatatttt acttttttat atcttataaa cctcactacc 1958  
 cctcccacaa tattgttttt catttactat cttgatcata gagtttggt ggggaggggg 2018  
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 <213> Homo sapiens

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 tgtggcgaat gctttgacct caaagtcaac cccacaggac ttccctgaat cttgtggagc 180  
 tggctgcaac atcactgaac agagcataga gaccctctcc ttgccaccog gcccttccca 240  
 cctggttggt gacaaatcac aaggtggtag aagttgccag ggacagataa c atg gca 297  
 Met Ala  
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gcc agc ggg aag acc agc aag tcc gaa ccg aac cat gtt atc ttc aag 345  
 Ala Ser Gly Lys Thr Ser Lys Ser Glu Pro Asn His Val Ile Phe Lys  
 5 10 15

aag atc tcc cgg gac aaa tcg gtg acc atc tac ctg ggg aac aga gac 393  
 Lys Ile Ser Arg Asp Lys Ser Val Thr Ile Tyr Leu Gly Asn Arg Asp  
 20 25 30



tac ata gac cat gtc agc caa gtc cag cct gtg gat ggt gtc gtg ttg	441
Tyr Ile Asp His Val Ser Gln Val Gln Pro Val Asp Gly Val Val Leu	
35 40 45 50	
gtt gat cct gat ctt gtg aag gga aag aaa gtg tat gtc act ctg acc	489
Val Asp Pro Asp Leu Val Lys Gly Lys Val Tyr Val Thr Leu Thr	
55 60 65	
tgc gcc ttc cgc tat ggc caa gag gac att gac gtg atc ggc ttg acc	537
Cys Ala Phe Arg Tyr Gly Gln Glu Asp Ile Asp Val Ile Gly Leu Thr	
70 75 80	
ttc cgc agg gac ctg tac ttc tcc cgg gtc cag gtg tat cct cct gtg	585
Phe Arg Arg Asp Leu Tyr Phe Ser Arg Val Gln Val Tyr Pro Pro Val	
85 90 95	
ggg gcc gcg agc acc ccc aca aaa ctg caa gag agc ctg ctt aaa aag	633
Gly Ala Ala Ser Thr Pro Thr Lys Leu Gln Glu Ser Leu Leu Lys Lys	
100 105 110	
ctg ggg agc aac acg tac ccc ttt ctc ctg acg ttt cct gac tac ttg	681
Leu Gly Ser Asn Thr Tyr Pro Phe Leu Leu Thr Phe Pro Asp Tyr Leu	
115 120 125 130	
ccc tgt tca gtg atg ttg cag cca gct cca caa gat tca ggg aag tcc	729
Pro Cys Ser Val Met Leu Gln Pro Ala Pro Gln Asp Ser Gly Lys Ser	
135 140 145	
tgt ggg gtt gac ttt gag gtc aaa gca ttc gcc aca gac agc acc gat	777
Cys Gly Val Asp Phe Glu Val Lys Ala Phe Ala Thr Asp Ser Thr Asp	
150 155 160	
gcc gaa gag gac aaa atc ccc aag aag agc tcc gtg cga tta ctg atc	825
Ala Glu Glu Asp Lys Ile Pro Lys Lys Ser Ser Val Arg Leu Leu Ile	
165 170 175	
cgc aaa gta cag cat gcc cca ctt gag atg ggt ccc cag ccc cga gct	873
Arg Lys Val Gln His Ala Pro Leu Glu Met Gly Pro Gln Pro Arg Ala	
180 185 190	
gag gcg gcc tgg cag ttc ttc atg tct gac aag ccc ctg cac ctt gcg	921
Glu Ala Ala Trp Gln Phe Phe Met Ser Asp Lys Pro Leu His Leu Ala	
195 200 205 210	
gtc tct ctc aac aaa gag atc tat ttc cat ggg gag ccc atc cct gtg	969
Val Ser Leu Asn Lys Glu Ile Tyr Phe His Gly Glu Pro Ile Pro Val	
215 220 225	
acc gtg act gtc acc aat aac aca gag aag acc gtg aag aag att aaa	1017
Thr Val Thr Val Thr Asn Asn Thr Glu Lys Thr Val Lys Lys Ile Lys	
230 235 240	
gca ttc gtg gaa cag gtg gcc aat gtg gtt ctc tac tcg agt gat tat	1065
Ala Phe Val Glu Gln Val Ala Asn Val Val Leu Tyr Ser Ser Asp Tyr	
245 250 255	
tac gtc aag ccc gtg gct atg gag gaa gcg caa gaa aaa gtg cca cca	1113
Tyr Val Lys Pro Val Ala Met Glu Glu Ala Gln Glu Lys Val Pro Pro	
260 265 270	
aac agc act ttg acc aag acg ctg acg ctg ctg ccc ttg ctg gct aac	1161
Asn Ser Thr Leu Thr Lys Thr Leu Thr Leu Leu Pro Leu Leu Ala Asn	
275 280 285 290	

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aat cga gaa agg aga ggc att gcc ctg gat ggg aaa atc aag cac gag      1209
Asn Arg Glu Arg Arg Gly Ile Ala Leu Asp Gly Lys Ile Lys His Glu
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gac aca aac ctt gcc tcc agc acc atc att aag gag ggc ata gac cgg      1257
Asp Thr Asn Leu Ala Ser Ser Thr Ile Ile Lys Glu Gly Ile Asp Arg
                310                      315                      320

acc gtc ctg gga atc ctg gtg tct tac cag atc aag gtg aag ctc aca      1305
Thr Val Leu Gly Ile Leu Val Ser Tyr Gln Ile Lys Val Lys Leu Thr
                325                      330                      335

gtg tca ggc ttt ctg gga gag ctc acc tcc agt gaa gtc gcc act gag      1353
Val Ser Gly Phe Leu Gly Glu Leu Thr Ser Ser Glu Val Ala Thr Glu
                340                      345                      350

gtc cca ttc cgc ctc atg cac cct cag cct gag gac cca gct aag gaa      1401
Val Pro Phe Arg Leu Met His Pro Gln Pro Glu Asp Pro Ala Lys Glu
                355                      360                      365                      370

agt tat cag gat gca aat tta gtt ttt gag gag ttt gct cgc cat aat      1449
Ser Tyr Gln Asp Ala Asn Leu Val Phe Glu Glu Phe Ala Arg His Asn
                375                      380                      385

ctg aaa gat gca gga gaa gct gag gag ggg aag aga gac aag aat gac      1497
Leu Lys Asp Ala Gly Glu Ala Glu Glu Gly Lys Arg Asp Lys Asn Asp
                390                      395                      400

att gat gag tga aga tgtcggctca ggatgccgga aaatgacctg tagttaccag      1552
Ile Asp Glu *
                405

tgcaacgagc aaagccccac agtttagtcc tttggagtta tgctgcgtat gaaaggatga      1612

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<210> 442  
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<220>  
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 <222> (259)..(1611)

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cggggcgggg ccgagtgcga acctgagccc caaatccga cccaggcagg gcgggggccc      180
ggagcggggc cttggaggcc cagcccgcgc ggcgacgtct ccgctggcg tcacggcacc      240
gactgacggc caccaccc atg gcc gca gac cag cgc ccg aag gcc gac acg      291
                Met Ala Ala Asp Gln Arg Pro Lys Ala Asp Thr
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ctg gcc ctg agg caa cgg ctc atc agc tct tcc tgc aga ctc ttt ttt      339
Leu Ala Leu Arg Gln Arg Leu Ile Ser Ser Ser Cys Arg Leu Phe Phe

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15	20	25	
ccc gag gat cct gtt aag att gtc cgg gcc caa ggg cag tac atg tac Pro Glu Asp Pro Val Lys Ile Val Arg Ala Gln Gly Gln Tyr Met Tyr 30 35 40			387
gat gaa cag ggg gca gaa tac atc gat tgc atc agc aat gtg gcg cac Asp Glu Gln Gly Ala Glu Tyr Ile Asp Cys Ile Ser Asn Val Ala His 45 50 55			435
gtt ggg cac tgc cac cct ctc gtg gtc caa gca gca cat gag cag aac Val Gly His Cys His Pro Leu Val Val Gln Ala Ala His Glu Gln Asn 60 65 70 75			483
cag gtg ctc aac acc aac agc cgg tac ctg cat gac aac atc gtg gac Gln Val Leu Asn Thr Asn Ser Arg Tyr Leu His Asp Asn Ile Val Asp 80 85 90			531
tat gcg cag agg ctg tca gag acc ctg ccg gag cag ctc tgt gtg ttc Tyr Ala Gln Arg Leu Ser Glu Thr Leu Pro Glu Gln Leu Cys Val Phe 95 100 105			579
tat ttc ctg aat tct ggg tca gaa gcc aat gac ctg gcc ctg agg ctg Tyr Phe Leu Asn Ser Gly Ser Glu Ala Asn Asp Leu Ala Leu Arg Leu 110 115 120			627
gct cgc cac tac acg gga cac cag gac gtg gtg gta tta gat cat gcg Ala Arg His Tyr Thr Gly His Gln Asp Val Val Leu Asp His Ala 125 130 135			675
tat cac ggc cac ctg agc tcc ctg att gac atc agt ccc tac aag ttc Tyr His Gly His Leu Ser Ser Leu Ile Asp Ile Ser Pro Tyr Lys Phe 140 145 150 155			723
cgc aac ctg gat ggc cag aag gag tgg gtc cac gtg gca cct ctc cca Arg Asn Leu Asp Gly Gln Lys Glu Trp Val His Val Ala Pro Leu Pro 160 165 170			771
gac acc tac cgg ggc ccc tac cgg gag gac cac ccc aac cca gct atg Asp Thr Tyr Arg Gly Pro Tyr Arg Glu Asp His Pro Asn Pro Ala Met 175 180 185			819
gcc tat gcc aac gag gtg aaa cgt gtg gtc agc agt gca cag gag aag Ala Tyr Ala Asn Glu Val Lys Arg Val Val Ser Ser Ala Gln Glu Lys 190 195 200			867
ggc agg aag att gca gcc ttc ttc gct gag tct ctg ccc agt gtg gga Gly Arg Lys Ile Ala Ala Phe Phe Ala Glu Ser Leu Pro Ser Val Gly 205 210 215			915
ggg cag atc att ccc cct gct ggc tac ttc tcc caa gtg gca gag cac Gly Gln Ile Ile Pro Pro Ala Gly Tyr Phe Ser Gln Val Ala Glu His 220 225 230 235			963
atc cgc aag gcc gga ggg gtc ttt gtt gca aat gag atc cag gtt ggc Ile Arg Lys Ala Gly Gly Val Phe Val Ala Asn Glu Ile Gln Val Gly 240 245 250			1011
ttt ggc cgg gta ggc aag cac ttc tgg gcc ttc cag ctc cag gga aaa Phe Gly Arg Val Gly Lys His Phe Trp Ala Phe Gln Leu Gln Gly Lys 255 260 265			1059
gac ttc gtc cct gac atc gtc acc atg ggc aag tcc att ggc aac ggc Asp Phe Val Pro Asp Ile Val Thr Met Gly Lys Ser Ile Gly Asn Gly 270 275 280 285			1107

270	275	280	
cac cct gtt gcc tgc gtg gcc gca acc cag cct gtg gcg agg gca ttt			1155
His Pro Val Ala Cys Val Ala Ala Thr Gln Pro Val Ala Arg Ala Phe			
285	290	295	
gaa gcc acc ggc gtt gag tac ttc aac acg ttt ggg ggc agc cca gtg			1203
Glu Ala Thr Gly Val Glu Tyr Phe Asn Thr Phe Gly Gly Ser Pro Val			
300	305	310	315
tcc tgc gct gtg ggg ctg gcc gtc ctg aat gtc ttg gag aag gag cag			1251
Ser Cys Ala Val Gly Leu Ala Val Leu Asn Val Leu Glu Lys Glu Gln			
320	325	330	
ctc cag gat cat gcc acc agt gta ggc agc ttc ctg atg cag ctc ctc			1299
Leu Gln Asp His Ala Thr Ser Val Gly Ser Phe Leu Met Gln Leu Leu			
335	340	345	
ggg cag caa aaa atc aaa cat ccc atc gtc ggg gat gtc agg ggt gtt			1347
Gly Gln Gln Lys Ile Lys His Pro Ile Val Gly Asp Val Arg Gly Val			
350	355	360	
ggg ctc ttc att ggt gtg gat ctg atc aaa gat gag gcc aca agg aca			1395
Gly Leu Phe Ile Gly Val Asp Leu Ile Lys Asp Glu Ala Thr Arg Thr			
365	370	375	
cca gca act gaa gag gct gcc tac ttg gta tca agg ctg aag gag aac			1443
Pro Ala Thr Glu Glu Ala Ala Tyr Leu Val Ser Arg Leu Lys Glu Asn			
380	385	390	395
tac gtt ttg ctg agc act gat ggc cct ggg agg aac atc ctg aag ttt			1491
Tyr Val Leu Leu Ser Thr Asp Gly Pro Gly Arg Asn Ile Leu Lys Phe			
400	405	410	
aag ccc cca atg tgc ttc agc ctg gac aat gca cgg cag gtg gtg gca			1539
Lys Pro Pro Met Cys Phe Ser Leu Asp Asn Ala Arg Gln Val Val Ala			
415	420	425	
aag ctg gat gcc att ctg act gac atg gaa gag aag gtg aga agt tgt			1587
Lys Leu Asp Ala Ile Leu Thr Asp Met Glu Glu Lys Val Arg Ser Cys			
430	435	440	
gaa acg ctg agg ctc cag ccc taa gccagccctg ctctgcctaa gtgtactcca			1641
Glu Thr Leu Arg Leu Gln Pro *			
445	450		
gaagaaactc atctcatcca aatacacgct attgagaagg cgagcctgac ctccctctta			1701
cagataaagt cagctttcag aggctcaggg tggggggggcc tgcccagggc cataatgcta			1761
cccaccccct cctcctaacc actggtctgt tggaataacc cagatgtctg catccccctca			1821
agtcagtcaa tttcctttct gtccactggg ggtggaatgg ggtaggggtgg gatacttta			1881
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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (73) .. (1245)

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (1570)

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&lt;400&gt; 443

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ggtgcggctg ca      atg ctg agc tcc cgg gcc gag gcg gcg atg acc gcg      108
                  Met Leu Ser Ser Arg Ala Glu Ala Ala Met Thr Ala
                   1              5              10

gcc gac agg gcc atc cag cgc ttc ctg cgg acc ggg gcg gcc gtc aga      156
Ala Asp Arg Ala Ile Gln Arg Phe Leu Arg Thr Gly Ala Ala Val Arg
                   15              20              25

tat aaa gtc atg aag aac tgg gga gtt ata ggt gga att gct gct gct      204
Tyr Lys Val Met Lys Asn Trp Gly Val Ile Gly Gly Ile Ala Ala Ala
                   30              35              40

ctt gca gca gga ata tat gtt att tgg ggt ccc att aca gaa aga aag      252
Leu Ala Ala Gly Ile Tyr Val Ile Trp Gly Pro Ile Thr Glu Arg Lys
                   45              50              55              60

aag cgt aga aaa ggg ctt gtg cct ggc ctt gtt aat tta ggg aac acc      300
Lys Arg Arg Lys Gly Leu Val Pro Gly Leu Val Asn Leu Gly Asn Thr
                   65              70              75

tgc ttc atg aac tcc ctg cta caa ggc ctg tct gcc tgt cct gct ttc      348
Cys Phe Met Asn Ser Leu Leu Gln Gly Leu Ser Ala Cys Pro Ala Phe
                   80              85              90

atc ggg tgg ctg gaa gag ttc acc tcc cag tac tcc agg gat cag aag      396
Ile Gly Trp Leu Glu Glu Phe Thr Ser Gln Tyr Ser Arg Asp Gln Lys
                   95              100              105

gag ccc ccc tca cac cag tat tta tcc tta aca ctc ttg cac ctt ctg      444
Glu Pro Pro Ser His Gln Tyr Leu Ser Leu Thr Leu Leu His Leu Leu
                   110              115              120

aaa gcc ttg tcc tgc caa gaa gtt act gat gat gag gtc tta cat gca      492
Lys Ala Leu Ser Cys Gln Glu Val Thr Asp Asp Glu Val Leu His Ala
                   125              130              135              140

agc tgc ttg ttg gat gtc tta aga atg tac aga tgg cag atc tca tca      540
Ser Cys Leu Leu Asp Val Leu Arg Met Tyr Arg Trp Gln Ile Ser Ser
                   145              150              155

ttt gaa gaa cag gat gct cac gaa tta ttc cat gtc att acc tcg tca      588
Phe Glu Glu Gln Asp Ala His Glu Leu Phe His Val Ile Thr Ser Ser
                   160              165              170

ttg gaa gat gag cga gac cgc cag cct cgg gtc aca cat ttg ttt gat      636
Leu Glu Asp Glu Arg Asp Arg Gln Pro Arg Val Thr His Leu Phe Asp
                   175              180              185

gtg cat tcc ctg gag cag cag tca gaa ata act ccc aaa caa att acc      684
Val His Ser Leu Glu Gln Gln Ser Glu Ile Thr Pro Lys Gln Ile Thr

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190	195	200	
tgc cgc aca aga ggg tca cct cac ccc aca tcc aat cac tgg aag tct			732
Cys Arg Thr Arg Gly Ser Pro His Pro Thr Ser Asn His Trp Lys Ser			
205	210	215	220
caa cat cct ttt cat gga aga ctc act agt aat atg gtc tgc aaa cac			780
Gln His Pro Phe His Gly Arg Leu Thr Ser Asn Met Val Cys Lys His			
225	230		235
tgt gaa cac cag agt cct gtt cga ttt gat acc ttt gat agc ctt tca			828
Cys Glu His Gln Ser Pro Val Arg Phe Asp Thr Phe Asp Ser Leu Ser			
240	245		250
cta agt att cca gcc gcc aca tgg ggt cac cca ttg acc ctg gac cac			876
Leu Ser Ile Pro Ala Ala Thr Trp Gly His Pro Leu Thr Leu Asp His			
255	260		265
tgc ctt cac cac ttc atc tca tca gaa tca gtg cgg gat gtt gtg tgt			924
Cys Leu His His Phe Ile Ser Ser Glu Ser Val Arg Asp Val Val Cys			
270	275		280
gac aac tgt aca aag att gaa gcc aag gga acg ttg aac ggg gaa aag			972
Asp Asn Cys Thr Lys Ile Glu Ala Lys Gly Thr Leu Asn Gly Glu Lys			
285	290		300
gtg gaa cac cag agg acc act ttt gtt aaa cag tta aaa cta ggg aag			1020
Val Glu His Gln Arg Thr Thr Phe Val Lys Gln Leu Lys Leu Gly Lys			
305	310		315
ctc cct cag tgt ctc tgc atc cac cta cag cgg ctg agc tgg tcc agc			1068
Leu Pro Gln Cys Leu Cys Ile His Leu Gln Arg Leu Ser Trp Ser Ser			
320	325		330
cac ggc acg cct ctg aag cgg cat gag cac gtg cag ttc aat gag ttc			1116
His Gly Thr Pro Leu Lys Arg His Glu His Val Gln Phe Asn Glu Phe			
335	340		345
ctg atg atg gac att tac aag tac cac ctc ctt gga cat aaa cct agt			1164
Leu Met Met Asp Ile Tyr Lys Tyr His Leu Leu Gly His Lys Pro Ser			
350	355		360
caa cac aac cct aaa ctg aac aag aac cca ggg cct aca ctg gag ctg			1212
Gln His Asn Pro Lys Leu Asn Lys Asn Pro Gly Pro Thr Leu Glu Leu			
365	370		380
cag gat ggg ccg gga gcc cca cac cag ttc tga atcagcca ggggccccca			1263
Gln Asp Gly Pro Gly Ala Pro His Gln Phe *			
385	390		
aaacacagat ttttatgaat ggcgcctgct ccccatcttt attgccaacg ctgtcagcgc			1323
cgatgccctt ccctctccca gttgttcccg actacagctc ctccacatac ctcttccggc			1383
tgatgggcag ttgtcgtcca ccatgggaga catggcactc tgggacactt tgttcattta			1443
ccgacggtcc ccaccttttt gccaggggaa cntcttttcc aattaggcan tcagttggct			1503
gttgggtttt ccgatggaca ttgttccgna aggccaggct tgcagggagg tctcgttctt			1563
tccagcg			1570

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 acttggaat gtgaacgcaa gaagcaggct tgattttttt ttctcccccc ttctctctct 180  
 ctctctctct ctctcttctt ctctccctct ttctctcttc tcacccacac tcacgcacac 240  
 ctccaaaccg cacaccaga cgcacacgca taccacagcg cccggcagtt atg tat 296  
 Met Tyr  
 1  
 tct ccg ctc tgt ctc acc cag gat gaa ttt cat cct ttc atc gaa gca 344  
 Ser Pro Leu Cys Leu Thr Gln Asp Glu Phe His Pro Phe Ile Glu Ala  
 5 10 15  
 ctt ctg ccc cac gtc cga gcc ttt gcc tac aca tgg ttc aac ctg cag 392  
 Leu Leu Pro His Val Arg Ala Phe Ala Tyr Thr Trp Phe Asn Leu Gln  
 20 25 30  
 gcc cga aaa cga aaa tac ttc aaa aaa cat gaa aag cgt atg tca aaa 440  
 Ala Arg Lys Arg Lys Tyr Phe Lys Lys His Glu Lys Arg Met Ser Lys  
 35 40 45 50  
 gaa gaa gag aga gcc gtg aag gat gaa ttg cta agt gaa aaa cca gag 488  
 Glu Glu Glu Arg Ala Val Lys Asp Glu Leu Leu Ser Glu Lys Pro Glu  
 55 60 65  
 gtc aag cag aag tgg gca tct cga ctt ctg gca aag ttg cgg aaa gat 536  
 Val Lys Gln Lys Trp Ala Ser Arg Leu Leu Ala Lys Leu Arg Lys Asp  
 70 75 80  
 atc cga ccc gaa tat cga gag gat ttt gtt ctt aca gtt aca ggg aaa 584  
 Ile Arg Pro Glu Tyr Arg Glu Asp Phe Val Leu Thr Val Thr Gly Lys  
 85 90 95  
 aaa cct cca tgt tgt gtt ctt tcc aac cca gac cag aaa ggc aag atg 632  
 Lys Pro Pro Cys Cys Val Leu Ser Asn Pro Asp Gln Lys Gly Lys Met  
 100 105 110  
 cga aga att gac tgc ctc cgc cag gca gat aaa gtc tgg agg ttg gac 680  
 Arg Arg Ile Asp Cys Leu Arg Gln Ala Asp Lys Val Trp Arg Leu Asp  
 115 120 125 130  
 ctt gtt atg gtg att ttg ttt aaa ggt att ccg ctg gaa agt act gat 728  
 Leu Val Met Val Ile Leu Phe Lys Gly Ile Pro Leu Glu Ser Thr Asp  
 135 140 145  
 ggc gag cgc ctt gta aag tcc cca caa tgc tct aat cca ggg ctc tgt 776  
 Gly Glu Arg Leu Val Lys Ser Pro Gln Cys Ser Asn Pro Gly Leu Cys  
 150 155 160  
 gtc caa ccc cat cac ata ggg gtt tct gtt aag gaa ctc gat tta tat 824

Val	Gln	Pro	His	His	Ile	Gly	Val	Ser	Val	Lys	Glu	Leu	Asp	Leu	Tyr	
	165						170					175				
ttg	gca	tac	ttt	gtg	cat	gca	gca	gat	tca	agt	caa	tct	gaa	agt	ccc	872
Leu	Ala	Tyr	Phe	Val	His	Ala	Ala	Asp	Ser	Ser	Gln	Ser	Glu	Ser	Pro	
	180					185					190					
agc	cag	cca	agt	gac	gct	gac	att	aag	gac	cag	cca	gaa	aat	gga	cat	920
Ser	Gln	Pro	Ser	Asp	Ala	Asp	Ile	Lys	Asp	Gln	Pro	Glu	Asn	Gly	His	
195					200					205				210		
ttg	ggc	ttc	cag	gac	agt	ttt	gtc	aca	tca	ggg	gtt	ttt	agt	gtc	act	968
Leu	Gly	Phe	Gln	Asp	Ser	Phe	Val	Thr	Ser	Gly	Val	Phe	Ser	Val	Thr	
			215					220				225				
gag	cta	gta	aga	gtg	tca	cag	aca	cca	ata	gct	gca	gga	act	ggc	cca	1016
Glu	Leu	Val	Arg	Val	Ser	Gln	Thr	Pro	Ile	Ala	Ala	Gly	Thr	Gly	Pro	
			230					235				240				
aat	ttt	tct	ctc	tca	gat	ttg	gaa	agt	tct	tca	tac	tac	agc	atg	agt	1064
Asn	Phe	Ser	Leu	Ser	Asp	Leu	Glu	Ser	Ser	Ser	Tyr	Tyr	Ser	Met	Ser	
	245					250					255					
cca	gga	gca	atg	agg	agg	tct	tta	ccc	agc	aca	tcc	tct	acg	agc	tcc	1112
Pro	Gly	Ala	Met	Arg	Arg	Ser	Leu	Pro	Ser	Thr	Ser	Ser	Thr	Ser	Ser	
	260					265					270					
aca	aag	cgc	ctc	aag	tct	gtg	gag	gat	gaa	atg	gac	agt	cct	ggg	gag	1160
Thr	Lys	Arg	Leu	Lys	Ser	Val	Glu	Asp	Glu	Met	Asp	Ser	Pro	Gly	Glu	
275					280					285				290		
gag	cca	ttt	tat	aca	ggc	caa	ggg	cgc	tcc	cca	gga	agt	ggc	agt	cag	1208
Glu	Pro	Phe	Tyr	Thr	Gly	Gln	Gly	Arg	Ser	Pro	Gly	Ser	Gly	Ser	Gln	
			295					300					305			
tca	agt	gga	tgg	cat	gaa	gtg	gag	cca	gga	atg	cca	tct	cca	acc	aca	1256
Ser	Ser	Gly	Trp	His	Glu	Val	Glu	Pro	Gly	Met	Pro	Ser	Pro	Thr	Thr	
			310					315				320				
ctg	aag	aag	tcg	gag	aag	tct	ggg	ttc	agc	agc	ccc	tcc	cct	tca	cag	1304
Leu	Lys	Lys	Ser	Glu	Lys	Ser	Gly	Phe	Ser	Ser	Pro	Ser	Pro	Ser	Gln	
	325						330					335				
acc	tcc	tcc	ctg	gga	acg	gcg	ttc	aca	cag	cat	cac	cga	cct	gtc	att	1352
Thr	Ser	Ser	Leu	Gly	Thr	Ala	Phe	Thr	Gln	His	His	Arg	Pro	Val	Ile	
	340					345					350					
aca	gga	ccc	aga	gca	agt	cca	cat	gca	aca	cca	tcg	act	ctt	cat	ttc	1400
Thr	Gly	Pro	Arg	Ala	Ser	Pro	His	Ala	Thr	Pro	Ser	Thr	Leu	His	Phe	
355					360					365				370		
ccg	aca	tca	ccc	att	atc	cag	cag	cct	ggg	cct	tac	ttc	tca	cac	cca	1448
Pro	Thr	Ser	Pro	Ile	Ile	Gln	Gln	Pro	Gly	Pro	Tyr	Phe	Ser	His	Pro	
			375					380					385			
gcc	atc	cgc	tat	cac	cct	cag	gag	acg	ctg	aaa	gaa	ttt	gtc	caa	ctt	1496
Ala	Ile	Arg	Tyr	His	Pro	Gln	Glu	Thr	Leu	Lys	Glu	Phe	Val	Gln	Leu	
			390					395				400				
gtc	tgc	cct	gat	gct	ggg	cag	cag	gct	gga	cag	ccc	aat	ggg	agc	agc	1544
Val	Cys	Pro	Asp	Ala	Gly	Gln	Gln	Ala	Gly	Gln	Pro	Asn	Gly	Ser	Ser	
	405					410					415					
caa	ggc	aag	gtg	cac	aac	cca	ttc	ctt	ccc	acc	cca	atg	ttg	cca	ccg	1592



Gln Gly Lys Val His Asn Pro Phe Leu Pro Thr Pro Met Leu Pro Pro	
420 425 430	
cca ccg cca cca ccg atg gcc agg cct gtg cct ctg ccg gtg cca gac	1640
Pro Pro Pro Pro Pro Met Ala Arg Pro Val Pro Leu Pro Val Pro Asp	
435 440 445 450	
aca aag cct cca acc acg tca aca gaa gga ggt gca gcc tcc ccc acg	1688
Thr Lys Pro Pro Thr Thr Ser Thr Glu Gly Gly Ala Ala Ser Pro Thr	
455 460 465	
tca cca acc tac tcg aca ccc agc acc tcc ccc gca aac cga ttc gtc	1736
Ser Pro Thr Tyr Ser Thr Pro Ser Thr Ser Pro Ala Asn Arg Phe Val	
470 475 480	
agt gtt gga cca ccg gat cca agc ttt gta aat atc cct caa cag aca	1784
Ser Val Gly Pro Arg Asp Pro Ser Phe Val Asn Ile Pro Gln Gln Thr	
485 490 495	
cag tcc tgg tac ctg gga taa aa gttgcagcgt cccaccatcc accagacaga	1837
Gln Ser Trp Tyr Leu Gly *	
500 505	
ccacctgac cctttctcaac tctgtaacat ggacgcaacc tcaaccacgc gcagttacaa	1897
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aagtgtttcc atgtagcgtg catttaaggt acgtggctag ggaggactac cctgctcact	2137
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ctggccacct gccatgccct cagccggctc caggacaccc ccgtgggcga ccccatggac	180
ttgaagatgg tggagtctac tggctgggtc ctggaggaag agccggctgc agactcagca	240
tttgggaccc aggtcttggc agtg atg aga ccc cca ctt tgg gag ccc cag	291
Met Arg Pro Pro Leu Trp Glu Pro Gln	
1 5	
ctg cag gca atg gag gag ccc ccg gtg cca gtc agc gtc ctc cac cgc	339
Leu Gln Ala Met Glu Glu Pro Pro Val Pro Val Ser Val Leu His Arg	
10 15 20 25	

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Phe Pro Phe Ser Ser Ala Leu Gln Arg Met Ser Val Val Val Ala Trp	
30 35 40	
cca ggg gcc act cag ccc gag gcc tac gtc aaa ggc tcc ccg gag ctg	435
Pro Gly Ala Thr Gln Pro Glu Ala Tyr Val Lys Gly Ser Pro Glu Leu	
45 50 55	
gtg gca ggg ctc tgc aac ccc gag aca gtg ccc acc gac ttc gcc cag	483
Val Ala Gly Leu Cys Asn Pro Glu Thr Val Pro Thr Asp Phe Ala Gln	
60 65 70	
atg ctg cag agc tat aca gct gct ggc tac cgt gtc gtg gcc ctg gcc	531
Met Leu Gln Ser Tyr Thr Ala Ala Gly Tyr Arg Val Val Ala Leu Ala	
75 80 85	
agc aag cca ctg ccc act gtg ccc agc ctg gag gca gcc cag caa ctg	579
Ser Lys Pro Leu Pro Thr Val Pro Ser Leu Glu Ala Ala Gln Gln Leu	
90 95 100 105	
acg agg gac act gtg gaa gga gac ctg agc ctc ctg ggg ctg ctg gtc	627
Thr Arg Asp Thr Val Glu Gly Asp Leu Ser Leu Leu Gly Leu Leu Val	
110 115 120	
atg agg aac cta ctg aag ccg cag aca acg cca gtt atc cag gct ctg	675
Met Arg Asn Leu Leu Lys Pro Gln Thr Thr Pro Val Ile Gln Ala Leu	
125 130 135	
cga agg acc cgc atc cgc gcc gtc atg gtg aca ggg gac aac ctg cag	723
Arg Arg Thr Arg Ile Arg Ala Val Met Val Thr Gly Asp Asn Leu Gln	
140 145 150	
aca gcg gtg act gtg gcc cgg ggc tgt ggc atg gtg gcc ccc cag gag	771
Thr Ala Val Thr Val Ala Arg Gly Cys Gly Met Val Ala Pro Gln Glu	
155 160 165	
cat ctg atc atc gtc cac gcc acc cac cct gag cgg ggt cag cct gcc	819
His Leu Ile Ile Val His Ala Thr His Pro Glu Arg Gly Gln Pro Ala	
170 175 180 185	
tct ctc gag ttc ctg ccg atg gag tcc ccc aca gcc gtg aat ggc gtt	867
Ser Leu Glu Phe Leu Pro Met Glu Ser Pro Thr Ala Val Asn Gly Val	
190 195 200	
aag gat cct gac cag gct gca agc tac acc gtg gag cca gac ccc cga	915
Lys Asp Pro Asp Gln Ala Ala Ser Tyr Thr Val Glu Pro Asp Pro Arg	
205 210 215	
tcc agg cac ctg gcc ctc agc ggg ccc acc ttt ggt atc att gtg aag	963
Ser Arg His Leu Ala Leu Ser Gly Pro Thr Phe Gly Ile Ile Val Lys	
220 225 230	
cac ttc ccc aag ctg ctg ccc aag gtc ctg gtc cag ggc act gtc ttt	1011
His Phe Pro Lys Leu Leu Pro Lys Val Leu Val Gln Gly Thr Val Phe	
235 240 245	
gcc cgc atg gcc cct gag cag aag aca gag ctg gtg tgc gag cta cag	1059
Ala Arg Met Ala Pro Glu Gln Lys Thr Glu Leu Val Cys Glu Leu Gln	
250 255 260 265	
aag ctt cag tac tgc gtg ggc atg tgc gga gac ggt gcc aat gac tgt	1107
Lys Leu Gln Tyr Cys Val Gly Met Cys Gly Asp Gly Ala Asn Asp Cys	
270 275 280	

ggg gcc ctg aag gcg gct gat gtc ggc atc tcg ctg tcc cag gca gaa	1155
Gly Ala Leu Lys Ala Ala Asp Val Gly Ile Ser Leu Ser Gln Ala Glu	
285 290 295	
gcc tca gtg gtc tca ccc ttc acc tcg agc atg gcc agt att gag tgc	1203
Ala Ser Val Val Ser Pro Phe Thr Ser Ser Met Ala Ser Ile Glu Cys	
300 305 310	
gtg ccc atg gtc atc agg gag ggg cgc tgt tcc ctt gac act tcg ttc	1251
Val Pro Met Val Ile Arg Glu Gly Arg Cys Ser Leu Asp Thr Ser Phe	
315 320 325	
agc gtc ttc aag tac atg gct ctg tac agc ctg acc cag ttc atc tcc	1299
Ser Val Phe Lys Tyr Met Ala Leu Tyr Ser Leu Thr Gln Phe Ile Ser	
330 335 340 345	
gtc ctg atc ctc tac acg atc aac acc aac ctg ggt gac ctg cag ttc	1347
Val Leu Ile Leu Tyr Thr Ile Asn Thr Asn Leu Gly Asp Leu Gln Phe	
350 355 360	
ctg gcc atc gac ctg gtc atc acc acc aca gtg gca gtg ctc atg agc	1395
Leu Ala Ile Asp Leu Val Ile Thr Thr Thr Val Ala Val Leu Met Ser	
365 370 375	
cgc acg ggg cca gcg ctg gtc ctg gga cgg gtg cgg cca ccg ggg gcg	1443
Arg Thr Gly Pro Ala Leu Val Leu Gly Arg Val Arg Pro Pro Gly Ala	
380 385 390	
ctg ctc agc gtg ccc gtg ctc agc agc ctg ctg ctg cag atg gtc ctg	1491
Leu Leu Ser Val Pro Val Leu Ser Ser Leu Leu Leu Gln Met Val Leu	
395 400 405	
gtg acc ggc gtg cag cta ggg ggc tac ttc ctg acc ctg gcc cag cca	1539
Val Thr Gly Val Gln Leu Gly Gly Tyr Phe Leu Thr Leu Ala Gln Pro	
410 415 420 425	
tgg ttc gtg cct ctg aac agg aca gtg gcc gca cca gac aac ctg ccc	1587
Trp Phe Val Pro Leu Asn Arg Thr Val Ala Ala Pro Asp Asn Leu Pro	
430 435 440	
aac tac gag aac acc gtg gtc ttc tct ctg tcc agc ttc cag tac ctc	1635
Asn Tyr Glu Asn Thr Val Val Phe Ser Leu Ser Ser Phe Gln Tyr Leu	
445 450 455	
atc ctg gct gca gcc gtg tcc aag ggg gcg ccc ttc cgc cgg ccg ctc	1683
Ile Leu Ala Ala Ala Val Ser Lys Gly Ala Pro Phe Arg Arg Pro Leu	
460 465 470	
tac acc aat gag cgt gct aga cca gtg cct ccc cgc ctg cct gcg ccg	1731
Tyr Thr Asn Glu Arg Ala Arg Pro Val Pro Pro Arg Leu Pro Ala Pro	
475 480 485	
cct ccg gcc caa gcg ggc ctc caa gaa gcg ctt caa gca gct gga acg	1779
Pro Pro Ala Gln Ala Gly Leu Gln Glu Ala Leu Gln Ala Ala Gly Thr	
490 495 500 505	
aga gct ggc cga gca gcc ctg gcc gcc gct gcc cgc cgg ccc cct gag	1827
Arg Ala Gly Arg Ala Ala Leu Ala Ala Ala Ala Arg Arg Pro Pro Glu	
510 515 520	
gta gtg cag gcc cac ggg cac ccc aga cac tgg aac tcc ctg cct ctg	1875
Val Val Gln Ala His Gly His Pro Arg His Trp Asn Ser Leu Pro Leu	
525 530 535	

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agc cac caa ctg gac ccc tct cca gca aca cca ccg cca cca cct ccc 1923
Ser His Gln Leu Asp Pro Ser Pro Ala Thr Pro Pro Pro Pro Pro
      540                545                550

aca tcc ctg agg ttg gcg act gtc tac act cct ccc ccg aga cca ccc 1971
Thr Ser Leu Arg Leu Ala Thr Val Tyr Thr Pro Pro Pro Arg Pro Pro
      555                560                565

cca ccc tgg gga agc gtt gac tac tgt ccc cta cct tgg acc atc ccg 2019
Pro Pro Trp Gly Ser Val Asp Tyr Cys Pro Leu Pro Trp Thr Ile Pro
      570                575                580                585

cgt agg ggt ggc agc ccc cag ctc ccc tca gtg ctg ctg tca gtg tag 2067
Arg Arg Gly Gly Ser Pro Gln Leu Pro Ser Val Leu Leu Ser Val *
      590                595                600

caaataaagt catgatattt tcctggcaaa aaaaaaaaaa 2106

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<210> 446
<211> 1555
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (808)..(966)

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<220>
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<222> (1)...(1555)
<223> n = a,t,c or g

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gctgcaagaa atccagatcc caggcgacac ctgctgcctt gcctgctgcc cccgcaaaat 120
ccctgcatct ggagccaccc acctggagga actcatcggtg cttcctctgt agacgggaaa 180
aaacaaacgc accacaaacc gacaatcaaa gccatggcgg atgcggggcc gccaccagtt 240
catctccctg gagccaggcg gctccaggcc tctctcacct ttcttgtgtg gaacgcaggc 300
ttgcaatggt ctgagcccac ctgtcctcgg gctagtccca ttttcaaaag ttctgagtac 360
gcaggtgaga agacaccccc acaaaacccc aaaactagcc ttaggctggt tttccccaac 420
acaacgcacc tccacacccc acaccgccag cagccacact gggtagccaa agtgagctgc 480
caggggggtc cgaggaccct gcctggtgcc ttccagctca taaggagagg ccaagagcca 540
tgaggagagg gccacacggc ccagcgtca gggcttgtca tccaagagtg agagaagtgg 600
ggagagaggt gacggagggt ggagtgtgt gtggcgtcna aataggctag ccagagagag 660
agggtcctgt gggattctgc tggctggagc caggaggtaa gtgtgaacag ggaggccaaa 720
gatgaaagtt atctgaaaga gcccgtaccc cctataaaca cggcagagga atgtcttaag 780
agccaccaac agtaattccc tttccgg atg tta aca ggt tat ttg tat ctt 831
Met Leu Thr Gly Tyr Leu Tyr Leu

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1

5

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atg tgg cgt cgt aaa gca ttc tgg agt ggc aca caa cgt cat ccc ctt      879
Met Trp Arg Arg Lys Ala Phe Trp Ser Gly Thr Gln Arg His Pro Leu
   10                      15                      20

ccc ggt ggt ctg aag agg agg agg aga cca ggg agg ggt cct tgg cca      927
Pro Gly Gly Leu Lys Arg Arg Arg Pro Gly Arg Gly Pro Trp Pro
   25                      30                      35                      40

gcc cct ggc ggc caa ggg gtg ggt cct tct gct cta tag aaggcaggaa      976
Ala Pro Gly Gly Gln Gly Val Gly Pro Ser Ala Leu *
          45                      50

gcccgccagc taaccgcccg ggtcaggggg agcaggcctg atctctccca agcctgtgac      1036

cgagggtcctg cctgatgtcc aagggggcccc tgtgccagta cccccaacttc ccacgcccc      1096

cagccttcct cacctccaga atcagccgcc caggtgcagc actatctcct ttctttttct      1156

tggaagccgt ctcagggggc tgagtgaagg gctgaccgt ccccgctacc gctgctgcc      1216

atgcgaccag atggctgacc cggcccggct tctcagggcc cagaccagcc tggcctcgtg      1276

cccacctgct tcgctcccaa cctcaccacc aggcaagggt ttccagaaaa ccgagacacg      1336

caaacaccca ccaccacgac aacaacacaa accaaagtgc actgcgaacc gccctttggc      1396

ctccttcttg taggtgcctt gaaacttcaa tgttgagatg aatgtgatta actacttggt      1456

cctattttct gtttgtctat ttcatagaa aatgtccaag tccacttgcc ttgttctttc      1516

ttgaaataaa tagaaagatt taactttaaa aaaaaaaaaa      1555

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<210> 447  
 <211> 2205  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(2205)

<400> 447

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Met His Glu Ser Val His Val Gly Phe Leu Ser Ile Pro Ser Lys Glu
   1                      5                      10                      15

aaa ggc ctt ggc ctc ctc cag ctg ggt ctg ctc ctt cct ttg aac ccc      96
Lys Gly Leu Gly Leu Leu Gln Leu Gly Leu Leu Leu Pro Leu Asn Pro
   20                      25                      30

atc ggt acc tat gcc cac acc ttt cag agc ttt cct gat cag tgt caa      144
Ile Gly Thr Tyr Ala His Thr Phe Gln Ser Phe Pro Asp Gln Cys Gln
   35                      40                      45

cat gct gct ctt cct ctt aca aaa tgt acc atc aat aca gcc cag gca      192
His Ala Ala Leu Pro Leu Thr Lys Cys Thr Ile Asn Thr Ala Gln Ala
   50                      55                      60

cat ggc tcc cac aaa gct agc cac tta tat agt atg ggt cac atc aaa      240

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1158

Arg Phe Ser Ser Tyr Arg Thr Leu Leu His His His His His His His	
325 330 335	
ctg gtt gct ttt ggc aag caa ggt tca gta gct aca gaa ctc tcc atc	1056
Leu Val Ala Phe Gly Lys Gln Gly Ser Val Ala Thr Glu Leu Ser Ile	
340 345 350	
atc atc atc atc atc atc atc atc atc atc atc atc atc tgg ttg ctt ttg	1104
Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Trp Leu Leu Leu	
355 360 365	
gca agg ttc agt agc tac aga act ctc ctt cat cat cat cat cat cat	1152
Ala Arg Phe Ser Ser Tyr Arg Thr Leu Leu His His His His His His	
370 375 380	
cat ctg gtt gct ttt ggc aag gcc ctg gca aga att att tgg ctt tac	1200
His Leu Val Ala Phe Gly Lys Ala Leu Ala Arg Ile Ile Trp Leu Tyr	
385 390 395 400	
cga aac acc tat tcc ata ggt aac caa ttc cag tca aaa atg cca gag	1248
Arg Asn Thr Tyr Ser Ile Gly Asn Gln Phe Gln Ser Lys Met Pro Glu	
405 410 415	
tat tac tcc tca acc caa tgc cct atc tcc tta gtg gat tat aaa ctt	1296
Tyr Tyr Ser Ser Thr Gln Cys Pro Ile Ser Leu Val Asp Tyr Lys Leu	
420 425 430	
act acg aca acc tgt ctt ctt tgg atc caa tcc ccg ccc aag tct gag	1344
Thr Thr Thr Thr Cys Leu Leu Trp Ile Gln Ser Pro Pro Lys Ser Glu	
435 440 445	
tct tct ctc cca ggc tac aag ccc cca agt cct ggc agc tct atg ctt	1392
Ser Ser Leu Pro Gly Tyr Lys Pro Pro Ser Pro Gly Ser Ser Met Leu	
450 455 460	
gac agc tcg ctg acc tcc acc tca tca gac cat tgg gtc gcc ctt ctc	1440
Asp Ser Ser Leu Thr Ser Thr Ser Ser Asp His Trp Val Ala Leu Leu	
465 470 475 480	
gcc gtc ctc cag cct tct tcc cgc tca gac act cat cca ctg tcc ggg	1488
Ala Val Leu Gln Pro Ser Ser Arg Ser Asp Thr His Pro Leu Ser Gly	
485 490 495	
gag cct cga ccc ctc cta tac ccc ctc ccc gat ccc gca gtc ccc ttc	1536
Glu Pro Arg Pro Leu Leu Tyr Pro Leu Pro Asp Pro Ala Val Pro Phe	
500 505 510	
tgg acc ttg cgg acc cct ctc agc ccc cgt acc ccc tac cgc ctc ttc	1584
Trp Thr Leu Arg Thr Pro Leu Ser Pro Arg Thr Pro Tyr Arg Leu Phe	
515 520 525	
ctc ctc cac tcc cac aac tcc gcc cga gct cca ctg cgc ctg tgc ggc	1632
Leu Leu His Ser His Asn Ser Ala Arg Ala Pro Leu Arg Leu Cys Gly	
530 535 540	
caa cga ggc cgc gcg cag gcg atc ggg gca gaa gag ctt ccg gtt cct	1680
Gln Arg Gly Arg Ala Gln Ala Ile Gly Ala Glu Glu Leu Pro Val Pro	
545 550 555 560	
gct gtc aat aag acg tgg acc tgc gag ccg ggg caa aag ggc ttc ccg	1728
Ala Val Asn Lys Thr Trp Thr Cys Glu Pro Gly Gln Lys Gly Phe Arg	
565 570 575	
tct gcg gga aac tgg agg cta gcg gtg ggc gtg gac cgt cga ggt gac	1776

Ser Ala Gly Asn Trp Arg Leu Ala Val Gly Val Asp Arg Arg Gly Asp  
580 585 590

tgg cgg ttg tgc gat ctg ctg ttg ttt gct gac cag gca gcc gta ggt 1824  
Trp Arg Leu Ser Asp Leu Leu Leu Phe Ala Asp Gln Ala Ala Val Gly  
595 600 605

aat gac gga tgc cca gac cct gtg ggc gga gta aag gaa tca tgc act 1872  
Asn Asp Gly Cys Pro Asp Pro Val Gly Gly Val Lys Glu Ser Cys Thr  
610 615 620

gat aca cgc aca ctc acc gag ggg cgc gtc cgt ctg cgt gcc cct cat 1920  
Asp Thr Arg Thr Leu Thr Glu Gly Arg Val Arg Leu Arg Ala Pro His  
625 630 635 640

ctc gta gcc gaa agg agc gcg ttc cgg ggc agg cct ccg ggt act tcc 1968  
Leu Val Ala Glu Arg Ser Ala Phe Arg Gly Arg Pro Pro Gly Thr Ser  
645 650 655

cgc aga gga ccg ggc ttt ata ctc ttt gct cct ttt cct ccc cta aaa 2016  
Arg Arg Gly Pro Gly Phe Ile Leu Phe Ala Pro Phe Pro Pro Leu Lys  
660 665 670

gct gtg ctt gac ttc ttg gtg tac atg gat aaa ggc tac aat gaa gga 2064  
Ala Val Leu Asp Phe Leu Val Tyr Met Asp Lys Gly Tyr Asn Glu Gly  
675 680 685

aac att tta gaa ata ctc gcc tac ctg gta gtc cac aga tct tta gat 2112  
Asn Ile Leu Glu Ile Leu Ala Tyr Leu Val Val His Arg Ser Leu Asp  
690 695 700

ttc att ggc cag caa aat ctc aaa gga aga gaa aga gag aac aag aga 2160  
Phe Ile Gly Gln Gln Asn Leu Lys Gly Arg Glu Arg Glu Asn Lys Arg  
705 710 715 720

gac cat cat atg gaa gac aaa ttt gat gcc atc act tca aaa tga 2205  
Asp His His Met Glu Asp Lys Phe Asp Ala Ile Thr Ser Lys \*  
725 730 735

<210> 448  
<211> 1832  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (131)..(1513)

<220>  
<221> misc\_feature  
<222> (1)...(1832)  
<223> n = a,t,c or g

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aagctnnnnc cttccctttg ccagcttggg gcccgagcct gtcccccgtg gctgccagga 120  
gcctgaggag atg agc tgg ccg cca tgc ggg gag att gcc agc cca cca 169  
Met Ser Trp Pro Pro Ser Gly Glu Ile Ala Ser Pro Pro



	1	5	10	
gag ctg cca agc agc cca cct cct ggg ctt ccc gaa gtg gcc cca gat				217
Glu Leu Pro Ser Ser Pro Pro Pro Gly Leu Pro Glu Val Ala Pro Asp				
15	20	25		
gca acc tcc act ggc ctc cct gat acc ccc gca gct cca gaa acc agc				265
Ala Thr Ser Thr Gly Leu Pro Asp Thr Pro Ala Ala Pro Glu Thr Ser				
30	35	40	45	
acc aac tac cca gtg gag tgc acc gag ggg tct gca ggc ccc cag tct				313
Thr Asn Tyr Pro Val Glu Cys Thr Glu Gly Ser Ala Gly Pro Gln Ser				
50	55	60		
ctc ccc ttg cct att ctg gag ccg gtc aaa aac ccc tgc tct gtc aaa				361
Leu Pro Leu Pro Ile Leu Glu Pro Val Lys Asn Pro Cys Ser Val Lys				
65	70	75		
gac cag acg cca ctc caa ctt tct gta gaa gat acc acc tct cca aat				409
Asp Gln Thr Pro Leu Gln Leu Ser Val Glu Asp Thr Thr Ser Pro Asn				
80	85	90		
acc aag ccg tgc cca cct act ccc acc acc cca gaa aca tcc cct cct				457
Thr Lys Pro Cys Pro Pro Thr Pro Thr Thr Pro Glu Thr Ser Pro Pro				
95	100	105		
cct cct cct cct cct cct tca tct act cct tgt tca gct cac ctg acc				505
Pro Pro Pro Pro Pro Pro Ser Ser Thr Pro Cys Ser Ala His Leu Thr				
110	115	120	125	
ccc tcc tcc ctg ttc cct tcc tcc ctg gaa tca tca tcc gaa cag aaa				553
Pro Ser Ser Leu Phe Pro Ser Ser Leu Glu Ser Ser Ser Glu Gln Lys				
130	135	140		
ttc tat aac ttt gtg atc ctc cac gcc agg gca gac gaa cac atc gcc				601
Phe Tyr Asn Phe Val Ile Leu His Ala Arg Ala Asp Glu His Ile Ala				
145	150	155		
ctg cgg gtt cgg gag aag ctg gag gcc ctt ggc gtg ccc gac ggg gcc				649
Leu Arg Val Arg Glu Lys Leu Glu Ala Leu Gly Val Pro Asp Gly Ala				
160	165	170		
acc ttc tgc gag gat ttc cag gtg ccg ggg cgc ggg gag ctg agc tgc				697
Thr Phe Cys Glu Asp Phe Gln Val Pro Gly Arg Gly Glu Leu Ser Cys				
175	180	185		
ctg cag gac gcc ata gac cac tca gct ttc atc atc cta ctt ctc acc				745
Leu Gln Asp Ala Ile Asp His Ser Ala Phe Ile Ile Leu Leu Leu Thr				
190	195	200	205	
tcc aac ttc gac tgt cgc ctg agc ctg cac cag gtg aac caa gcc atg				793
Ser Asn Phe Asp Cys Arg Leu Ser Leu His Gln Val Asn Gln Ala Met				
210	215	220		
atg agc aac ctc acg cga cag ggg tcc cca gac tgt gtc atc ccc ttc				841
Met Ser Asn Leu Thr Arg Gln Gly Ser Pro Asp Cys Val Ile Pro Phe				
225	230	235		
ctg ccc ctg gag agc tcc ccg gcc cgg ctc agc tcc gac acg gcc agc				889
Leu Pro Leu Glu Ser Ser Pro Ala Arg Leu Ser Ser Asp Thr Ala Ser				
240	245	250		
ctg ctc tcc ggg ctg gtg cgg ctg gac gaa cac tcc cag atc ttc gcc				937
Leu Leu Ser Gly Leu Val Arg Leu Asp Glu His Ser Gln Ile Phe Ala				

255	260	265	
agg aag gtg gcc aac acc ttc aag ccc cac agg ctt cag gcc cga aag			985
Arg Lys Val Ala Asn Thr Phe Lys Pro His Arg Leu Gln Ala Arg Lys			
270	275	280	285
gcc atg tgg agg aag gaa cag gac acc cga gcc ctg cgg gaa cag agc			1033
Ala Met Trp Arg Lys Glu Gln Asp Thr Arg Ala Leu Arg Glu Gln Ser			
	290	295	300
caa cac ctg gat ggt gag cgg atg cag gcg gcg gca ctg aac gca gcc			1081
Gln His Leu Asp Gly Glu Arg Met Gln Ala Ala Ala Leu Asn Ala Ala			
	305	310	315
tac tca gcc tac ctc cag agc tac ttg tcc tac cag gca cag atg gag			1129
Tyr Ser Ala Tyr Leu Gln Ser Tyr Leu Ser Tyr Gln Ala Gln Met Glu			
	320	325	330
cag ctc cag gtg gct ttt ggg agc cac atg tca ttt ggg act ggg gcg			1177
Gln Leu Gln Val Ala Phe Gly Ser His Met Ser Phe Gly Thr Gly Ala			
	335	340	345
ccc tat ggg gct cga atg ccc ttt ggg ggc cag gtg ccc ctg gga gcc			1225
Pro Tyr Gly Ala Arg Met Pro Phe Gly Gly Gln Val Pro Leu Gly Ala			
	350	355	360
ccg cca ccc ttt ccc act tgg ccg ggg tgc ccg cag ccg cca ccc ctg			1273
Pro Pro Pro Phe Pro Thr Trp Pro Gly Cys Pro Gln Pro Pro Pro Leu			
	370	375	380
cac gca tgg cag gct ggc acc ccc cca ccg ccc tcc cca cag cca gca			1321
His Ala Trp Gln Ala Gly Thr Pro Pro Pro Pro Ser Pro Gln Pro Ala			
	385	390	395
gcc ttt cca cag tca ctg ccc ttc ccg cag tcc cca gcc ttc cct acg			1369
Ala Phe Pro Gln Ser Leu Pro Phe Pro Gln Ser Pro Ala Phe Pro Thr			
	400	405	410
gcc tca ccc gca ccc cct cag agc cca ggg ctg caa ccc ctc att atc			1417
Ala Ser Pro Ala Pro Pro Gln Ser Pro Gly Leu Gln Pro Leu Ile Ile			
	415	420	425
cac cac gca cag atg gta cag ctg ggg ctg aac aac cac atg tgg aac			1465
His His Ala Gln Met Val Gln Leu Gly Leu Asn Asn His Met Trp Asn			
	430	435	440
cag aga ggg tcc cag gcg ccc gag gac aag acg cag gag gca gaa tga			1513
Gln Arg Gly Ser Gln Ala Pro Glu Asp Lys Thr Gln Glu Ala Glu *			
	450	455	460
ccgcgtgtcc ttgcctgacc acctggggaa cacccttgga cccaggcatc ggccaggacc			1573
ccatagagca ccccggtctg ccctgtgccc tgtggacagt ggaagatgag gtcattctgcc			1633
actttcagga cattgtccgg gagcccttca tttaggacaa aacgggcgcg atgatgccct			1693
ggctttcagg gtggtcagaa ctggatacgg tgtttacaat tccaatctct ctattttctgg			1753
gtgaagggtc ttggtggtgg ggggtattgct acggtctttt aattataata aatattttatt			1813
gaatgctaaa aaaaaaaaaa			1832

<400> 449																
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gagggcgagg	ccgaggacca	ggaatcacct	tcaagcctat	gtcgtgaggc	tttggcagaa										120	
attaagaagg	aaatatctcc	attgttcatt	ggc	atg	gaa	aaa	tgt	tca	gtg	gga					174	
					Met	Glu	Lys	Cys	Ser	Val	Gly					
						1				5						
gga	tta	gag	ttg	act	gaa	cag	act	cct	gct	tta	tta	ggg	aat	atg	gcc	222
Gly	Leu	Glu	Leu	Thr	Glu	Gln	Thr	Pro	Ala	Leu	Leu	Gly	Asn	Met	Ala	
		10					15					20				
atg	gca	act	agt	ctc	atg	gac	ata	ggg	gat	tca	ttt	ggg	cat	cca	gct	270
Met	Ala	Thr	Ser	Leu	Met	Asp	Ile	Gly	Asp	Ser	Phe	Gly	His	Pro	Ala	
		25				30					35					
tgt	cct	tta	gtc	agt	aga	tct	agg	aac	tca	cca	gtg	gaa	gat	gat	gat	318
Cys	Pro	Leu	Val	Ser	Arg	Ser	Arg	Asn	Ser	Pro	Val	Glu	Asp	Asp	Asp	
	40				45					50					55	
gat	gat	gat	gat	gtt	gtg	ttt	att	gaa	tct	ata	caa	cct	cct	tca	att	366
Asp	Asp	Asp	Asp	Val	Val	Phe	Ile	Glu	Ser	Ile	Gln	Pro	Pro	Ser	Ile	
				60				65						70		
tct	gct	cca	gca	ata	gct	gat	caa	aga	aac	ttc	ata	ttt	gca	tca	tca	414
Ser	Ala	Pro	Ala	Ile	Ala	Asp	Gln	Arg	Asn	Phe	Ile	Phe	Ala	Ser	Ser	
			75				80						85			
aaa	aat	gaa	aag	cct	caa	gga	aat	tat	tct	gta	att	cct	cct	tct	tca	462
Lys	Asn	Glu	Lys	Pro	Gln	Gly	Asn	Tyr	Ser	Val	Ile	Pro	Pro	Ser	Ser	
		90				95						100				
aga	gat	ttg	gca	tct	cag	aaa	gga	aat	ata	agt	gag	aca	att	gtt	att	510
Arg	Asp	Leu	Ala	Ser	Gln	Lys	Gly	Asn	Ile	Ser	Glu	Thr	Ile	Val	Ile	
		105				110					115					
gat	gat	gaa	gag	gac	ata	gaa	aca	aat	gga	gga	gca	gag	aaa	aag	tct	558
Asp	Asp	Glu	Glu	Asp	Ile	Glu	Thr	Asn	Gly	Gly	Ala	Glu	Lys	Lys	Ser	
		120			125					130					135	
tcc	tgt	ttt	atc	gaa	tgg	gga	ctt	cct	gga	act	aaa	aac	aaa	acc	aac	606
Ser	Cys	Phe	Ile	Glu	Trp	Gly	Leu	Pro	Gly	Thr	Lys	Asn	Lys	Thr	Asn	
			140						145					150		
gat	ttg	gat	ttc	tcc	act	tcc	agt	ctt	tca	aga	agt	aag	acc	aag	act	654
Asp	Leu	Asp	Phe	Ser	Thr	Ser	Ser	Leu	Ser	Arg	Ser	Lys	Thr	Lys	Thr	
			155					160					165			
gga	gta	aga	cct	ttt	aac	cct	ggg	aga	atg	aat	gtg	gca	gga	gac	tta	702
Gly	Val	Arg	Pro	Phe	Asn	Pro	Gly	Arg	Met	Asn	Val	Ala	Gly	Asp	Leu	
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Phe Gln Asn Gly Glu Phe Ala Thr His His Ser Pro Asp Ser Trp Ile	
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tct tta tca cca gtg gcc tta ctt cgt aag cag aat ttc cag cct aca	846
Ser Leu Ser Pro Val Ala Leu Leu Arg Lys Gln Asn Phe Gln Pro Thr	
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gcc caa caa caa ctt act aaa cca gct aaa atc act tgt gca aat tgc	894
Ala Gln Gln Gln Leu Thr Lys Pro Ala Lys Ile Thr Cys Ala Asn Cys	
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aaa aag cct tta cag aag gga cag aca gct tat caa cga aaa gga tca	942
Lys Lys Pro Leu Gln Lys Gly Gln Thr Ala Tyr Gln Arg Lys Gly Ser	
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gct cac ctc ttt tgc tct acc acc tgc ctt tct tcc ttc tct cat aaa	990
Ala His Leu Phe Cys Ser Thr Thr Cys Leu Ser Ser Phe Ser His Lys	
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cgt act caa aac aca cga agc ata ata tgt aaa aaa gat gca tct aca	1038
Arg Thr Gln Asn Thr Arg Ser Ile Ile Cys Lys Lys Asp Ala Ser Thr	
	280 285 290 295
aag aag gct aat gtc att ctt cca gta gaa tca agc aaa tcc ttc caa	1086
Lys Lys Ala Asn Val Ile Leu Pro Val Glu Ser Ser Lys Ser Phe Gln	
	300 305 310
gaa ttt tat agt aca tct tgt ttg tct ccc tgt gaa aac aac tgg aat	1134
Glu Phe Tyr Ser Thr Ser Cys Leu Ser Pro Cys Glu Asn Asn Trp Asn	
	315 320 325
ctt aaa aaa gga gtt ttt aat aag tca aga tgt aca att tgt agt aaa	1182
Leu Lys Lys Gly Val Phe Asn Lys Ser Arg Cys Thr Ile Cys Ser Lys	
	330 335 340
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Leu Ala Glu Val Trp Ile Phe Ile Pro Lys Leu Leu Phe Arg Leu Thr	
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Val Ile Ile Leu Thr Phe Lys Cys Tyr Tyr Val Leu Phe His Leu His	
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1165

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235	240	245	
aaa tta gca gag gtc tgg att ttt ata cct aag ttg ttg ttt agg cta			942
Lys Leu Ala Glu Val Trp Ile Phe Ile Pro Lys Leu Leu Phe Arg Leu			
250	255	260	
aca gtg ata att tta act ttt aag tgc tat tat gga ctc ttt cat cta			990
Thr Val Ile Ile Leu Thr Phe Lys Cys Tyr Tyr Gly Leu Phe His Leu			
265	270	275	
cat aat gca cgt gtt ctg gat gta taa catga agctgaaagg aagaataagg			1042
His Asn Ala Arg Val Leu Asp Val *			
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aaaaaaaaa a			1113

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Tyr His Pro Phe Leu Pro His Arg Ala Pro Asp Phe Ala Met Ser Ala	
20 25 30	
gtg ctg ggt cac cag ccg ccg ttc ttc ccc gcg ctg acg ctg cct ccc	144
Val Leu Gly His Gln Pro Pro Phe Phe Pro Ala Leu Thr Leu Pro Pro	
35 40 45	
aac ggc gcg gcg gcg ctc tcg ctg ccg ggc gcc ctg gcc aag ccg atc	192
Asn Gly Ala Ala Ala Leu Ser Leu Pro Gly Ala Leu Ala Lys Pro Ile	
50 55 60	
atg gat caa ttg gtg ggg gcg gcc gag acc ggc atc ccg ttc tcc tcc	240
Met Asp Gln Leu Val Gly Ala Ala Glu Thr Gly Ile Pro Phe Ser Ser	
65 70 75 80	
ctg ggg ccc cag gcg cat ctg agg cct ttg aag acc atg gag ccc gaa	288
Leu Gly Pro Gln Ala His Leu Arg Pro Leu Lys Thr Met Glu Pro Glu	
85 90 95	
gaa gag gtg gag gac gac ccc aag gtg cac ctg gag gct aaa gaa ctt	336
Glu Glu Val Glu Asp Asp Pro Lys Val His Leu Glu Ala Lys Glu Leu	
100 105 110	
tgg gat cag ttt cac aag ccg ggc acc gag atg gtc att acc aag tcg	384

Trp Asp Gln Phe His Lys Arg Gly Thr Glu Met Val Ile Thr Lys Ser	
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Gly Arg Arg Met Phe Pro Pro Phe Lys Val Arg Cys Ser Gly Leu Asp	
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Lys Lys Ala Lys Tyr Ile Leu Leu Met Asp Ile Ile Ala Ala Asp Asp	
145 150 155 160	
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Cys Arg Tyr Lys Phe His Asn Ser Arg Trp Met Val Ala Gly Lys Ala	
165 170 175	
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Asp Pro Glu Met Pro Lys Arg Met Tyr Ile His Pro Asp Ser Pro Ala	
180 185 190	
act ggg gaa cag tgg atg tcc aaa gtc gtc act ttc cac aaa ctg aaa	624
Thr Gly Glu Gln Trp Met Ser Lys Val Val Thr Phe His Lys Leu Lys	
195 200 205	
ctc acc aac aac att tca gac aaa cat gga ttt act ata ttg aac tcc	672
Leu Thr Asn Asn Ile Ser Asp Lys His Gly Phe Thr Ile Leu Asn Ser	
210 215 220	
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Met His Lys Tyr Gln Pro Arg Phe His Ile Val Arg Ala Asn Asp Ile	
225 230 235 240	
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Leu Lys Leu Pro Tyr Ser Thr Phe Arg Thr Tyr Leu Phe Pro Glu Thr	
245 250 255	
gaa ttc atc gct gtg act gca tac cag aat gat aag ata acc cag tta	816
Glu Phe Ile Ala Val Thr Ala Tyr Gln Asn Asp Lys Ile Thr Gln Leu	
260 265 270	
aaa ata gac aac aac cct ttt gca aaa ggt ttc cgg gac act gga aat	864
Lys Ile Asp Asn Asn Pro Phe Ala Lys Gly Phe Arg Asp Thr Gly Asn	
275 280 285	
ggc cga aga gaa aaa aga aaa cag ctc acc ctg cag tcc atg agg gtg	912
Gly Arg Arg Glu Lys Arg Lys Gln Leu Thr Leu Gln Ser Met Arg Val	
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Phe Asp Glu Arg His Lys Lys Glu Asn Gly Thr Ser Asp Glu Ser Ser	
305 310 315 320	
agt gaa caa gca gct ttc aac tgc ttc gcc cag gct tct tct cca gcc	1008
Ser Glu Gln Ala Ala Phe Asn Cys Phe Ala Gln Ala Ser Ser Pro Ala	
325 330 335	
gcc tcc act gta ggg aca tcg aac ctc aaa gat tta tgt ccc agc gag	1056
Ala Ser Thr Val Gly Thr Ser Asn Leu Lys Asp Leu Cys Pro Ser Glu	
340 345 350	
ggt gag agc gac gcc gag gcc gag agc aaa gag gag cat ggc ccc gag	1104
Gly Glu Ser Asp Ala Glu Ala Glu Ser Lys Glu Glu His Gly Pro Glu	
355 360 365	
gcc tgc gac gcg gcc aag atc tcc acc acc acg tcg gag gag ccc tgc	1152

Ala Cys Asp Ala Ala Lys Ile Ser Thr Thr Thr Ser Glu Glu Pro Cys	
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Arg Asp Lys Gly Ser Pro Ala Val Lys Ala His Leu Phe Ala Ala Glu	
385 390 395 400	
cgg ccc cgg gac agc ggg cgg ctg gac aaa gcg tcg ccc gac tca cgc	1248
Arg Pro Arg Asp Ser Gly Arg Leu Asp Lys Ala Ser Pro Asp Ser Arg	
405 410 415	
cat agc ccc gcc acc atc tcg tcc agc act cgc ggc ctg ggc gcg gag	1296
His Ser Pro Ala Thr Ile Ser Ser Ser Thr Arg Gly Leu Gly Ala Glu	
420 425 430	
gag cgc agg agc ccg gtt cgc gag ggc aca gcg ccg gcc aag gtg gaa	1344
Glu Arg Arg Ser Pro Val Arg Glu Gly Thr Ala Pro Ala Lys Val Glu	
435 440 445	
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Glu Ala Arg Ala Leu Pro Gly Lys Glu Ala Phe Ala Pro Leu Thr Val	
450 455 460	
cag acg gac gcg gcc gcc gcg cac ctg gcc cag ggc ccc ctg cct ggc	1440
Gln Thr Asp Ala Ala Ala Ala His Leu Ala Gln Gly Pro Leu Pro Gly	
465 470 475 480	
ctc ggc ttc gcc ccg ggc ctg gcg ggc caa cag ttc ttc aac ggg cac	1488
Leu Gly Phe Ala Pro Gly Leu Ala Gly Gln Gln Phe Phe Asn Gly His	
485 490 495	
ccg ctc ttc ctg cac ccc agc cag ttt gcc atg ggg ggc gcc ttc tcc	1536
Pro Leu Phe Leu His Pro Ser Gln Phe Ala Met Gly Gly Ala Phe Ser	
500 505 510	
agc atg gcg gcc gct ggc atg ggt ccc ctc ctg gcc acg gtt tct ggg	1584
Ser Met Ala Ala Ala Gly Met Gly Pro Leu Leu Ala Thr Val Ser Gly	
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gcc tcc acc ggt gtc tcg ggc ctg gat tcc acg gcc atg gcc tct gcc	1632
Ala Ser Thr Gly Val Ser Gly Leu Asp Ser Thr Ala Met Ala Ser Ala	
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gct gcg gcg cag gga ctg tcc ggg gcg tcc gcg gcc acc ctg ccc ttc	1680
Ala Ala Ala Gln Gly Leu Ser Gly Ala Ser Ala Ala Thr Leu Pro Phe	
545 550 555 560	
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His Leu Gln Gln His Val Leu Ala Ser Gln Gly Leu Ala Met Ser Pro	
565 570 575	
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Phe Gly Ser Leu Phe Pro Tyr Pro Tyr Thr Tyr Met Ala Ala Ala Ala	
580 585 590	
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Ala Ala Ser Leu Arg Gln Pro Gln Leu Arg Cys Thr Ala Pro Leu Leu	
595 600 605	
aat ctg aac acc atg cgc ccg cgg ttg cgc tac agc ccc tac tcc atc	1872
Asn Leu Asn Thr Met Arg Pro Arg Leu Arg Tyr Ser Pro Tyr Ser Ile	
610 615 620	
ccg gtg ccg gtc ccg gac ggc agc agt ctg ctc acc acc gcc ctg ccc	1920



Pro Val Pro Val Pro Asp Gly Ser Ser Leu Leu Thr Thr Ala Leu Pro	
625 630 635 640	
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Ser Met Ala Ala Ala Ala Gly Pro Leu Asp Gly Lys Val Ala Ala Leu	
645 650 655	
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Ala Ala Ser Pro Ala Ser Val Ala Val Asp Ser Gly Ser Glu Leu Thr	
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Ser Arg Ser Ser Thr Leu Ser Ser Ser Ser Met Ser Leu Ser Pro Lys	
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ctc tgc gcg gag aaa gag gcg gcc acc agc gaa ctg cag agc atc cag	2112
Leu Cys Ala Glu Lys Glu Ala Ala Thr Ser Glu Leu Gln Ser Ile Gln	
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Arg Leu Val Ser Gly Leu Glu Ala Lys Pro Asp Arg Ser Arg Ser Ala	
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Ser Pro *	
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&lt;222&gt; (465)..(1493)

&lt;400&gt; 452

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gtcaacgtca gctctgttgc gagggcgggtt ctcccaacaa tagccacac catttccagg 180  
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Met Ala Gln Val  
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ctg atc gtg ggc gcc ggg atg aca gga agc ttg tgc gct gcg ctg ctg 524  
Leu Ile Val Gly Ala Gly Met Thr Gly Ser Leu Cys Ala Ala Leu Leu  
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agg agg cag acg tcc ggt ccc ttg tac ctt gct gtg tgg gac aag gct 572  
Arg Arg Gln Thr Ser Gly Pro Leu Tyr Leu Ala Val Trp Asp Lys Ala  
25 30 35

gag gac tca ggg gga aga atg act aca gcc tgc agt cct cat aat cct 620  
Glu Asp Ser Gly Gly Arg Met Thr Thr Ala Cys Ser Pro His Asn Pro  
40 45 50

cag tgc aca gct gac ttg ggt gct cag tac atc acc tgc act cct cat 668  
Gln Cys Thr Ala Asp Leu Gly Ala Gln Tyr Ile Thr Cys Thr Pro His  
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tat gcc aaa aaa cac caa cgt ttt tat gat gaa ctg tta gcc tat ggc 716  
Tyr Ala Lys Lys His Gln Arg Phe Tyr Asp Glu Leu Leu Ala Tyr Gly  
70 75 80

gtt ttg agg cct cta agc tcg cct att gaa gga atg gtg atg aaa gaa 764  
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85 90 95 100

gga gac tgt aac ttt gtg gca cct caa gga att tct tca att att aag 812  
Gly Asp Cys Asn Phe Val Ala Pro Gln Gly Ile Ser Ser Ile Ile Lys  
105 110 115

cat tac ttg aaa gaa tca ggt gca gaa gtc tac ttc aga cat cgt gtg 860  
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120 125 130

aca cag atc aac cta aga gat gac aaa tgg gaa gta tcc aaa caa aca 908  
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Gly Ser Pro Glu Gln Phe Asp Leu Ile Val Leu Thr Met Pro Val Pro  
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Glu Ile Leu Gln Leu Gln Gly Asp Ile Thr Thr Leu Ile Ser Glu Cys  
165 170 175 180

caa agg cag caa ctg gag gct gtg agc tac tcc tct cga tat gct ctg 1052  
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cac acc act gtc cca ttt gga gtt aca tac ttg gaa cac agc att gag His Thr Thr Val Pro Phe Gly Val Thr Tyr Leu Glu His Ser Ile Glu 245 250 255 260			1244
gat gtg caa gag tta gtc ttc cag cag ctg gaa aac att ttg ccg ggt Asp Val Gln Glu Leu Val Phe Gln Gln Leu Glu Asn Ile Leu Pro Gly 265 270 275			1292
ttg cct cag cca att gct acc aaa tgc caa aaa tgg aga cat tca cag Leu Pro Gln Pro Ile Ala Thr Lys Cys Gln Lys Trp Arg His Ser Gln 280 285 290			1340
gtt aca aat gct gct gcc aac tgt cct ggc caa atg act ctg cat cac Val Thr Asn Ala Ala Ala Asn Cys Pro Gly Gln Met Thr Leu His His 295 300 305			1388
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gat ggc tgc atc act tct gcc cta tgt gtt ctg gaa gct tta aag aat Asp Gly Cys Ile Thr Ser Ala Leu Cys Val Leu Glu Ala Leu Lys Asn 325 330 335 340			1484
tat att tag tgcctat atccttattc tctacatgtg tattggggttt ttattttcac Tyr Ile *			1540
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ttcttcactt attatcattt ttcatgtgga gtataaaatc aattttgtaa ttttgatagt			1660
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&lt;222&gt; (95)..(862)

&lt;220&gt;

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&lt;400&gt; 453

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                                         Met Leu Ser Val Ala Ala
                                           1           5

cgc tcg ggc ccg ttc gcg ccc gtc ctg tcg gcc acc ccg gag cag cct      160
Arg Ser Gly Pro Phe Ala Pro Val Leu Ser Ala Thr Pro Glu Gln Pro
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gtg ttg gac ctg aag cgg ccc ttc ctc agc cgg gag tcg ctg agc ggc      208
Val Leu Asp Leu Lys Arg Pro Phe Leu Ser Arg Glu Ser Leu Ser Gly
                25           30           35

cag gcc gtg cgc cgg cct ttg gtc gcc tcc gtg ggc ctc aat gtc cct      256
Gln Ala Val Arg Arg Pro Leu Val Ala Ser Val Gly Leu Asn Val Pro
                40           45           50

gct tct gtt tgt tat tcc cac aca gac atc aag gtg cct gac ttc tct      304
Ala Ser Val Cys Tyr Ser His Thr Asp Ile Lys Val Pro Asp Phe Ser
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Ser Ser Glu Ala Arg Lys Gly Phe Ser Tyr Leu Val Thr Gly Val Thr
                90           95           100

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Thr Val Gly Val Ala Tyr Ala Ala Lys Asn Ala Val Thr Gln Phe Val
                105           110           115

tcc agc atg agt gct tct gct gat gtg ttg gcc ctg gcg aaa atc gaa      496
Ser Ser Met Ser Ala Ser Ala Asp Val Leu Ala Leu Ala Lys Ile Glu
                120           125           130

atc aag tta tcc gat att cca gaa ggc aag aac atg gct ttc aaa tgg      544
Ile Lys Leu Ser Asp Ile Pro Glu Gly Lys Asn Met Ala Phe Lys Trp
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Arg Gly Lys Pro Leu Phe Val Arg His Arg Thr Gln Lys Glu Ile Glu
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cag gaa gct gca gtt gaa tta tca cag ttg agg gac cca cag cat gat      640
Gln Glu Ala Ala Val Glu Leu Ser Gln Leu Arg Asp Pro Gln His Asp
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Leu Asp Arg Val Lys Lys Pro Glu Trp Val Ile Leu Ile Gly Val Cys
                185           190           195

act cat ctt ggc tgt gta ccc att gca aat gca gga gat ttt ggt ggt      736
Thr His Leu Gly Cys Val Pro Ile Ala Asn Ala Gly Asp Phe Gly Gly

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215	220	225	230
aga ttg ggt cct gct cct ctc aac ctt gaa gtc ccc acg tat gag ttc			832
Arg Leu Gly Pro Ala Pro Leu Asn Leu Glu Val Pro Thr Tyr Glu Phe			
	235	240	245
acc agt gac gat atg gtg att gtt ggt taa g agacttggac tcaagtcata			883
Thr Ser Asp Asp Met Val Ile Val Gly *			
	250	255	
ggcttctttc agtctttatg tcacctcagg agacttattt gagaggaagc cttctgtact			943
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aaaaaaaaaaaa			1078
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Trp Val Gly Arg Gln Arg Asp Ser Gly Val Leu Ser Arg Pro Cys Pro			
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tcg act gcg gcc ttg ccc gaa gcc ctt ttg tgc agc tcc gcg ccc gca			151
Ser Thr Ala Ala Leu Pro Glu Ala Leu Leu Cys Ser Ser Ala Pro Ala			
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gcc cga cgc ccc agc ttg tgc ggg gcc acg gga ggg tca tgc gcg gat			199
Ala Arg Arg Pro Ser Leu Cys Gly Ala Thr Gly Gly Ser Cys Ala Asp			
	35	40	45
ttc gac tcg ggt gtg gat ttc gtc cgt aga gag agc agc ggt ctg tgg			247
Phe Asp Ser Gly Val Asp Phe Val Arg Arg Glu Ser Ser Gly Leu Trp			
	50	55	60
ggc cca cag cct cca ctt tct cct gtt aaa aat tat act gag atg ttt			295
Gly Pro Gln Pro Pro Leu Ser Pro Val Lys Asn Tyr Thr Glu Met Phe			
	70	75	80
cag gac cca gtg gct ttt aag gat gtg gct gtg aac ttc acc cag gag			343
Gln Asp Pro Val Ala Phe Lys Asp Val Ala Val Asn Phe Thr Gln Glu			
	85	90	95
gag tgg gct ttg ctg gat att tcc cag aag aat ctc tac agg gaa gtg			391

Glu Trp Ala Leu Leu Asp Ile Ser Gln Lys Asn Leu Tyr Arg Glu Val	
100 105 110	
atg ctg gaa act ttc tgg aac ctg acc tct ata gga aaa aag tgg aaa	439
Met Leu Glu Thr Phe Trp Asn Leu Thr Ser Ile Gly Lys Lys Trp Lys	
115 120 125	
gac cag aac att gaa tat gag tac caa aac ccc agg aga aac ttc agg	487
Asp Gln Asn Ile Glu Tyr Glu Tyr Gln Asn Pro Arg Arg Asn Phe Arg	
130 135 140 145	
agt gtc aca gaa gag aaa gtc aat gaa att aaa gaa gac agt cat tgt	535
Ser Val Thr Glu Glu Lys Val Asn Glu Ile Lys Glu Asp Ser His Cys	
150 155 160	
gga gaa act ttt acc cca gtt cca gat gac agg ctg aac ttc cag aag	583
Gly Glu Thr Phe Thr Pro Val Pro Asp Asp Arg Leu Asn Phe Gln Lys	
165 170 175	
aag aaa gct tct cct gaa gta aaa tca tgt gac agc ttt gtg tgt gaa	631
Lys Lys Ala Ser Pro Glu Val Lys Ser Cys Asp Ser Phe Val Cys Glu	
180 185 190	
gtt ggc cta ggt aac tca tct tct aat atg aac atc aga ggt gac act	679
Val Gly Leu Gly Asn Ser Ser Ser Asn Met Asn Ile Arg Gly Asp Thr	
195 200 205	
gga cac aag gca tgt gaa tgt cag gaa tat gga cca aag cca tgg aag	727
Gly His Lys Ala Cys Glu Cys Gln Glu Tyr Gly Pro Lys Pro Trp Lys	
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Ser Gln Gln Pro Lys Lys Ala Phe Arg Tyr His Pro Ser Leu Arg Thr	
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caa gaa agg gat cac act gga aag aaa ccc tat gct tgt aaa gaa tgt	823
Gln Glu Arg Asp His Thr Gly Lys Lys Pro Tyr Ala Cys Lys Glu Cys	
245 250 255	
gga aaa aac att att tac cat tca agc att caa aga cac atg gta gtg	871
Gly Lys Asn Ile Ile Tyr His Ser Ser Ile Gln Arg His Met Val Val	
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cac agt ggg gat gga cct tat aaa tgt aag ttt tgt ggg aaa gca ttc	919
His Ser Gly Asp Gly Pro Tyr Lys Cys Lys Phe Cys Gly Lys Ala Phe	
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His Cys Leu Ser Leu Tyr Leu Ile His Glu Arg Thr His Thr Gly Glu	
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aaa ccg tat gaa tgt aaa caa tgt ggt aaa tct ttt agt tat tct gct	1015
Lys Pro Tyr Glu Cys Lys Gln Cys Gly Lys Ser Phe Ser Tyr Ser Ala	
310 315 320	
acc cat cga ata cat gaa aga act cac att gga gaa aag cct tat gaa	1063
Thr His Arg Ile His Glu Arg Thr His Ile Gly Glu Lys Pro Tyr Glu	
325 330 335	
tgt cag gaa tgt ggg aaa gca ttc cat agt ccc aga tcc tgt cac aga	1111
Cys Gln Glu Cys Gly Lys Ala Phe His Ser Pro Arg Ser Cys His Arg	
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cat gaa agg agt cac atg gga gag aag gct tat caa tgt aag gaa tgt	1159

His	Glu	Arg	Ser	His	Met	Gly	Glu	Lys	Ala	Tyr	Gln	Cys	Lys	Glu	Cys		
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gga	aaa	gca	ttc	atg	tgt	ccc	cgt	tat	gtt	cgt	aga	cat	gaa	agg	acc	1207	
Gly	Lys	Ala	Phe	Met	Cys	Pro	Arg	Tyr	Val	Arg	Arg	His	Glu	Arg	Thr		
370					375					380					385		
cac	tct	agg	aaa	aaa	ctt	tat	gaa	tgt	aag	cag	tgt	ggg	aaa	gca	tta	1255	
His	Ser	Arg	Lys	Lys	Leu	Tyr	Glu	Cys	Lys	Gln	Cys	Gly	Lys	Ala	Leu		
				390						395				400			
tcc	tct	ctt	aca	agt	ttt	caa	aca	cac	ata	aga	atg	cac	tct	gga	gaa	1303	
Ser	Ser	Leu	Thr	Ser	Phe	Gln	Thr	His	Ile	Arg	Met	His	Ser	Gly	Glu		
			405					410						415			
aga	cct	tat	gaa	tgt	aag	aca	tgt	ggg	aaa	ggc	ttt	tat	tct	gcc	aag	1351	
Arg	Pro	Tyr	Glu	Cys	Lys	Thr	Cys	Gly	Lys	Gly	Phe	Tyr	Ser	Ala	Lys		
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tca	ttt	caa	aga	cat	gaa	aaa	act	cac	agt	gga	gag	aaa	ccg	tat	aaa	1399	
Ser	Phe	Gln	Arg	His	Glu	Lys	Thr	His	Ser	Gly	Glu	Lys	Pro	Tyr	Lys		
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tgc	aag	caa	tgt	ggt	aaa	gcc	ttc	act	cgt	tcc	ggt	tcc	ttt	cga	tat	1447	
Cys	Lys	Gln	Cys	Gly	Lys	Ala	Phe	Thr	Arg	Ser	Gly	Ser	Phe	Arg	Tyr		
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cat	gaa	agg	act	cac	act	gga	gag	aaa	ccc	tat	gag	tgt	aag	caa	tgt	1495	
His	Glu	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Lys	Gln	Cys		
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ggg	aaa	gcc	ttc	aga	tct	gcc	cca	aat	ctt	caa	tcg	cat	ggt	agg	act	1543	
Gly	Lys	Ala	Phe	Arg	Ser	Ala	Pro	Asn	Leu	Gln	Ser	His	Gly	Arg	Thr		
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cac	act	gga	gag	aaa	ccg	tat	caa	tgt	aag	gaa	tgt	ggg	aaa	gct	ttc	1591	
His	Thr	Gly	Glu	Lys	Pro	Tyr	Gln	Cys	Lys	Glu	Cys	Gly	Lys	Ala	Phe		
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aga	tct	gcc	tca	caa	ctt	cga	atc	cat	cgt	agg	att	cac	act	gga	gag	1639	
Arg	Ser	Ala	Ser	Gln	Leu	Arg	Ile	His	Arg	Arg	Ile	His	Thr	Gly	Glu		
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aaa	ccc	tat	gaa	tgt	aag	aaa	tgt	ggg	aaa	gcc	ttc	aga	tat	gtc	cag	1687	
Lys	Pro	Tyr	Glu	Cys	Lys	Lys	Cys	Gly	Lys	Ala	Phe	Arg	Tyr	Val	Gln		
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aac	ttt	cga	ttt	cat	gaa	agg	aca	cac	aat	gga	gag	aaa	ccc	tat	gaa	1735	
Asn	Phe	Arg	Phe	His	Glu	Arg	Thr	His	Asn	Gly	Glu	Lys	Pro	Tyr	Glu		
				550					555					560			
tgt	aaa	gaa	tgc	aga	aaa	gca	ttc	agc	ttg	cct	act	tcc	ttt	cat	aga	1783	
Cys	Lys	Glu	Cys	Arg	Lys	Ala	Phe	Ser	Leu	Pro	Thr	Ser	Phe	His	Arg		
			565					570					575				
cat	gaa	aag	aca	ttg	gaa	gga	aac	cct	atg	aag	gca	agc	aat	gtg	gca	1831	
His	Glu	Lys	Thr	Leu	Glu	Gly	Asn	Pro	Met	Lys	Ala	Ser	Asn	Val	Ala		
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aag	ctt	tca	ctt	ctt	cca	gtt	ctt	ttc	aat	atc	atg	aaa	gaa	ttc	aca	1879	
Lys	Leu	Ser	Leu	Leu	Pro	Val	Leu	Phe	Asn	Ile	Met	Lys	Glu	Phe	Thr		
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ctg	ggg	aga	aac	cct	atc	agt	gta	agc	aat	gtg	cga	aag	cct	tta	ttt	1927	

Leu Gly Arg Asn Pro Ile Ser Val Ser Asn Val Arg Lys Pro Leu Phe  
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 630 635 640  
 cct atg agt gta tgc cat gtg gga aag cct tca ttt ttc tag ttgcttt 2024  
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 645 650 655  
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 Met Leu Leu  
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 Gly Ser Leu Leu Pro Val Lys Ile Ile Glu Thr Asp Phe Glu Lys Ala  
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 His Arg Ser Lys Lys Ile Leu Ser Leu Cys Asn Thr Phe Gly Gly Gly  
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 Val Phe Leu Ala Thr Cys Phe Asn Ala Leu Leu Pro Ala Val Arg Glu  
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 aag ctc cag aag gtc ctg agc ctc ggc cac atc agc acc gac tac ccg 546



Lys	Leu	Gln	Lys	Val	Leu	Ser	Leu	Gly	His	Ile	Ser	Thr	Asp	Tyr	Pro	
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ctg	gcc	gaa	acc	atc	ctc	ctg	ctg	ggc	ttc	ttc	atg	acc	gtc	ttc	ctg	594
Leu	Ala	Glu	Thr	Ile	Leu	Leu	Leu	Gly	Phe	Phe	Met	Thr	Val	Phe	Leu	
		70					75					80				
gag	cag	ctg	atc	ctg	acc	ttc	cgc	aag	gag	aag	ccg	tcc	ttc	atc	gac	642
Glu	Gln	Leu	Ile	Leu	Thr	Phe	Arg	Lys	Glu	Lys	Pro	Ser	Phe	Ile	Asp	
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ctg	gag	acc	ttc	aac	gcc	gga	tcg	gac	gtg	ggc	agc	gac	tcg	gag	tat	690
Leu	Glu	Thr	Phe	Asn	Ala	Gly	Ser	Asp	Val	Gly	Ser	Asp	Ser	Glu	Tyr	
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gag	agc	ccc	ttc	atg	ggg	ggc	gcg	cgg	ggc	cac	gcg	ctg	tac	gtg	gag	738
Glu	Ser	Pro	Phe	Met	Gly	Gly	Ala	Arg	Gly	His	Ala	Leu	Tyr	Val	Glu	
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ccc	cac	ggc	cac	ggc	ccc	agc	ctg	agc	gtg	cag	ggc	ctc	tcg	cgc	gcc	786
Pro	His	Gly	His	Gly	Pro	Ser	Leu	Ser	Val	Gln	Gly	Leu	Ser	Arg	Ala	
			135						140				145			
agc	ccc	gtg	cgc	ctg	ctc	agc	ctg	gcc	ttc	gcg	ctg	tcg	gcc	cac	tcg	834
Ser	Pro	Val	Arg	Leu	Leu	Ser	Leu	Ala	Phe	Ala	Leu	Ser	Ala	His	Ser	
		150					155					160				
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Val	Phe	Glu	Gly	Leu	Ala	Leu	Gly	Leu	Gln	Glu	Glu	Gly	Glu	Lys	Val	
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gtg	agc	ctg	ttc	gtg	ggg	gtg	gcc	gtc	cac	gag	aca	ctg	gtg	gcc	gtg	930
Val	Ser	Leu	Phe	Val	Gly	Val	Ala	Val	His	Glu	Thr	Leu	Val	Ala	Val	
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gcc	ctg	ggc	atc	agc	atg	gcc	cgg	agt	gcc	atg	ccc	ctg	cgg	gac	gcg	978
Ala	Leu	Gly	Ile	Ser	Met	Ala	Arg	Ser	Ala	Met	Pro	Leu	Arg	Asp	Ala	
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gcc	aag	ctg	gcg	gtc	acc	gta	agc	gcc	atg	atc	ccc	ctg	ggc	atc	ggc	1026
Ala	Lys	Leu	Ala	Val	Thr	Val	Ser	Ala	Met	Ile	Pro	Leu	Gly	Ile	Gly	
			215					220					225			
ctg	ggc	ctg	ggc	att	gag	agc	gcc	cag	ggc	gtg	ccg	ggc	agc	gtg	gcg	1074
Leu	Gly	Leu	Gly	Ile	Glu	Ser	Ala	Gln	Gly	Val	Pro	Gly	Ser	Val	Ala	
		230					235					240				
tcc	gtg	ctg	ctg	cag	ggc	ctg	gcg	ggc	ggc	acc	ttc	ctc	ttc	atc	acc	1122
Ser	Val	Leu	Leu	Gln	Gly	Leu	Ala	Gly	Gly	Thr	Phe	Leu	Phe	Ile	Thr	
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ttc	ctg	gag	atc	ctg	gcc	aag	gag	ctg	gag	gag	aag	agt	gac	cgt	ctg	1170
Phe	Leu	Glu	Ile	Leu	Ala	Lys	Glu	Leu	Glu	Glu	Lys	Ser	Asp	Arg	Leu	
260					265					270					275	
ctc	aag	gtc	ctc	ttc	ctg	gtg	ctg	ggc	tac	acc	gtc	ctg	gcc	ggg	atg	1218
Leu	Lys	Val	Leu	Phe	Leu	Val	Leu	Gly	Tyr	Thr	Val	Leu	Ala	Gly	Met	
				280					285					290		
gtc	ttc	ctc	aag	tgg	tga	gcggcc	ttgccattgt	ccctgccgcc	ggagccccgcc							1272
Val	Phe	Leu	Lys	Trp	*											
			295													
gggagccccg	ggccggacac	aggccgcgtc	ccccggccgc	gcgtccccca	agagcgagca											1332

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 Gln Phe Pro His Leu Glu Ser Arg Asn Asp Asn Arg Thr Cys His Trp  
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tgt gac aca gag att cat ata gtg aac gcc acc atc agt gac act gat 145  
 Cys Asp Thr Glu Ile His Ile Val Asn Ala Thr Ile Ser Asp Thr Asp  
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tgc atg aaa tct gcc atg gtg gtg gcc ctt agt aag aga agt cag gag 193  
 Cys Met Lys Ser Ala Met Val Val Ala Leu Ser Lys Arg Ser Gln Glu  
 45 50 55 60

gcg gag gct gct ttt ctg agt gtt tac aag caa tta att gaa gca cca 241  
 Ala Glu Ala Ala Phe Leu Ser Val Tyr Lys Gln Leu Ile Glu Ala Pro  
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gcc ctg tgg gaa ctc aag ctc aag tcc agg cct gcc ctt gga gac tct 289  
 Ala Leu Trp Glu Leu Lys Leu Lys Ser Arg Pro Ala Leu Gly Asp Ser  
 80 85 90

cgg gtt cag caa gga caa cat gac cca aag aca gac aac cag aat aca 337  
 Arg Val Gln Gln Gly Gln His Asp Pro Lys Thr Asp Asn Gln Asn Thr  
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caa cag aaa gca ggc ttc aag gaa gga tgg ctg gca gag gcc tca gag 385  
 Gln Gln Lys Ala Gly Phe Lys Glu Gly Trp Leu Ala Glu Ala Ser Glu  
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agg gag gcc ttt gga cct ggt ttt aaa gac ccc gtg cct gtg ttt gag 433  
 Arg Glu Ala Phe Gly Pro Gly Phe Lys Asp Pro Val Pro Val Phe Glu  
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gcg gca cgc agc cta gac gac aga ctg cag ccc ccc agc ttt gac ccc 481  
 Ala Ala Arg Ser Leu Asp Asp Arg Leu Gln Pro Pro Ser Phe Asp Pro  
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agt ggg cag ccc cgg cga gac ctc cac act tcg tgg aag agg aac ccc 529  
 Ser Gly Gln Pro Arg Arg Asp Leu His Thr Ser Trp Lys Arg Asn Pro  
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Glu Leu Leu Ser Pro Lys Ala Leu Lys Ala Thr Gln Ala Glu Leu Leu	
175 180 185	
gag ctg cgg cgg aag tac gac gag gag gca gca tcc aag gca gat gaa	625
Glu Leu Arg Arg Lys Tyr Asp Glu Glu Ala Ala Ser Lys Ala Asp Glu	
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gtc ggc ctg atc atg acc aac ctg gag aaa gct aat cag cga gct gag	673
Val Gly Leu Ile Met Thr Asn Leu Glu Lys Ala Asn Gln Arg Ala Glu	
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Ala Ala Gln Arg Glu Val Glu Ser Leu Arg Glu Gln Leu Ala Ser Val	
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Asn Ser Ser Ile Arg Leu Ala Cys Cys Ser Pro Gln Gly Pro Ser Gly	
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Asp Lys Val Asn Phe Thr Leu Cys Ser Gly Pro Arg Leu Glu Ala Ala	
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Leu Ala Ser Lys Asp Arg Glu Ile Leu Arg Leu Leu Lys Asp Val Gln	
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His Leu Gln Ser Ser Leu Gln Glu Leu Glu Glu Ala Ser Ala Asn Gln	
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Ile Ala Asp Leu Glu Arg Gln Leu Thr Ala Lys Ser Glu Ala Ile Glu	
305 310 315	
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Lys Leu Glu Glu Lys Leu Gln Ala Gln Ser Asp Tyr Glu Glu Ile Lys	
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Thr Glu Leu Ser Ile Leu Lys Ala Met Lys Leu Ala Ser Ser Thr Cys	
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Ser Leu Pro Gln Gly Met Ala Lys Pro Glu Asp Ser Leu Leu Ile Ala	
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aag gag gcc ttc ttc ccc acg cag aaa ttc ctt ctg gag aag ccc agc	1153
Lys Glu Ala Phe Phe Pro Thr Gln Lys Phe Leu Leu Glu Lys Pro Ser	
365 370 375 380	
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Leu Leu Ala Ser Pro Glu Glu Asp Pro Ser Glu Asp Asp Ser Ile Lys	
385 390 395	
gat tca ctg ggc acg gag cag tcc tac ccc tcc cct cag cag ctc cca	1249
Asp Ser Leu Gly Thr Glu Gln Ser Tyr Pro Ser Pro Gln Gln Leu Pro	
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cct cca cca ggg cca gaa gac ccc ctg tct ccc agc ccc ggg cag ccc	1297
Pro Pro Pro Gly Pro Glu Asp Pro Leu Ser Pro Ser Pro Gly Gln Pro	
415 420 425	

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Leu Leu Gly Pro Ser Leu Gly Pro Asp Gly Thr Arg Thr Phe Ser Leu	
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Ser Pro Phe Pro Ser Leu Ala Ser Gly Glu Arg Leu Met Met Pro Pro	
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Phe Tyr Gly Ala Lys Pro Pro Thr Ala Pro Ala Thr Pro Ala Pro Gly	
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Pro Glu Pro Leu Gly Gly Pro Glu Pro Ala Asp Gly Gly Gly Gly Gly	
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Ala Ala Gly Pro Gly Ala Glu Glu Glu Gln Leu Asp Thr Ala Glu Ile	
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Ala Phe Gln Val Lys Glu Gln Leu Leu Lys His Asn Ile Gly Gln Arg	
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Val Phe Gly His Tyr Val Leu Gly Leu Ser Gln Gly Ser Val Ser Glu	
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Ile Leu Ala Arg Pro Lys Pro Trp Arg Lys Leu Thr Val Lys Gly Lys	
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Arg Ile Arg Thr Pro Glu Thr Gly Ser Asp Asp Ala Ile Lys Ser Ile	
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Lys Thr Ser Val Ala Pro Leu Ser Ile Ala Asn Gly Thr Thr Pro Ala	
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Ser Thr Ser Glu Asp Ala Ile Lys Ser Ile Leu Glu Gln Ala Arg Arg	
655 660 665	
gag atg cag gcg caa cag cag gcg ctg ctg gag atg gag gtg gcg ccc	2065
Glu Met Gln Ala Gln Gln Gln Ala Leu Leu Glu Met Glu Val Ala Pro	
670 675 680	

agg ggc cgc tcg gtg ccc ccc tcg ccc ccg gag cgg cca tca ctg gcc	2113
Arg Gly Arg Ser Val Pro Pro Ser Pro Pro Glu Arg Pro Ser Leu Ala	
685 690 695 700	
acc gcg agc cag aac ggg gcc ccg gcc ttg gtg aag cag gag gag ggc	2161
Thr Ala Ser Gln Asn Gly Ala Pro Ala Leu Val Lys Gln Glu Glu Gly	
705 710 715	
agc ggg ggc ccc gcg cag gcg ccg ctc ccg gtc ctg tcc ccc gcc gcc	2209
Ser Gly Gly Pro Ala Gln Ala Pro Leu Pro Val Leu Ser Pro Ala Ala	
720 725 730	
ttc gtg cag agc atc atc cgc aag gtc aag tcc gag atc ggc gac gcc	2257
Phe Val Gln Ser Ile Ile Arg Lys Val Lys Ser Glu Ile Gly Asp Ala	
735 740 745	
ggc tac ttc gac cac cac tgg gcc tcc gac cgc ggc ctg ctc agc cgc	2305
Gly Tyr Phe Asp His His Trp Ala Ser Asp Arg Gly Leu Leu Ser Arg	
750 755 760	
ccc tac gcc tcc gtg tcg ccc tcg ctg tcc tcc tcc tcc tcc tcc ggc	2353
Pro Tyr Ala Ser Val Ser Pro Ser Leu Ser Ser Ser Ser Ser Ser Gly	
765 770 775 780	
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Tyr Ser Gly Gln Pro Asn Gly Arg Ala Trp Pro Arg Gly Asp Glu Ala	
785 790 795	
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Pro Val Pro Pro Glu Asp Glu Ala Ala Ala Gly Ala Glu Asp Glu Pro	
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Pro Arg Thr Gly Glu Leu Lys Ala Glu Gly Ala Thr Ala Glu Ala Gly	
815 820 825	
gcg cgg ctg ccc tac tac ccg gcc tac gtg ccg cgc acc ctg aag ccc	2545
Ala Arg Leu Pro Tyr Tyr Pro Ala Tyr Val Pro Arg Thr Leu Lys Pro	
830 835 840	
acc gtg ccg ccg ctg acc ccc gag cag tac gag ctg tac atg tac cgt	2593
Thr Val Pro Pro Leu Thr Pro Glu Gln Tyr Glu Leu Tyr Met Tyr Arg	
845 850 855 860	
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Glu Val Asp Thr Leu Glu Leu Thr Arg Gln Val Lys Glu Lys Leu Ala	
865 870 875	
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Lys Asn Gly Ile Cys Gln Arg Ile Phe Gly Glu Lys Val Leu Gly Leu	
880 885 890	
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Ser Gln Gly Ser Val Ser Asp Met Leu Ser Arg Pro Lys Pro Trp Ser	
895 900 905	
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Lys Leu Thr Gln Lys Gly Arg Glu Pro Phe Ile Arg Met Gln Leu Trp	
910 915 920	
ctc tct gac cag ctc ggc cag gca gtg ggc cag cag cct ggt gcc tcc	2833
Leu Ser Asp Gln Leu Gly Gln Ala Val Gly Gln Gln Pro Gly Ala Ser	
925 930 935 940	

cag gcc agt ccc	aca gaa cca	agg tcc tca	cca tcc cca	ccc ccc agc	2881
Gln Ala Ser Pro	Thr Glu Pro	Arg Ser Ser	Pro Ser Pro	Pro Pro Ser	
	945	950		955	
ccc aca gag cct	gag aag agc	tcc cag gag	cgc ttg agc	ctg tcc ctg	2929
Pro Thr Glu Pro	Glu Lys Ser	Ser Ser Glu	Pro Leu Ser	Leu Ser Leu	
	960	965		970	
gag agc agc aag	gag aac cag	cag cca gag	ggc cgc tcc	agc tcc tcg	2977
Glu Ser Ser Lys	Glu Asn Gln	Gln Pro Glu	Gly Arg Ser	Ser Ser Ser	
	975	980		985	
ttg agc ggg aag	atg tac tca	ggc agc cag	gcc cca ggg	ggc atc cag	3025
Leu Ser Gly Lys	Met Tyr Ser	Gly Ser Gln	Ala Pro Gly	Gly Ile Gln	
	990	995		1000	
gag atc gtg gcc	atg tcc ccc	gag ctg gac	acg tac tcc	atc acc aag	3073
Glu Ile Val Ala	Met Ser Pro	Glu Leu Asp	Thr Tyr Ser	Ile Thr Lys	
1005	1010		1015	1020	
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Arg Val Lys Glu	Val Leu Thr	Asp Asn Asn	Leu Gly Gln	Arg Leu Phe	
	1025	1030		1035	
ggg gaa agc atc	ctg ggt ctg	aca cag ggc	tcc gtg tct	gac ctg ctg	3169
Gly Glu Ser Ile	Leu Gly Leu	Thr Gln Gly	Ser Val Ser	Asp Leu Leu	
	1040	1045		1050	
tcc cgg ccc aaa	ccc tgg cac	aag ctg agc	ctg aag ggg	cgg gag cct	3217
Ser Arg Pro Lys	Pro Trp His	Lys Leu Ser	Leu Lys Gly	Arg Glu Pro	
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ttt gtc cgc atg	cag ctg tgg	ctc aat gac	ccc cat aac	gtg gag aag	3265
Phe Val Arg Met	Gln Leu Trp	Leu Asn Asp	Pro His Asn	Val Glu Lys	
	1070	1075		1080	
ctg agg gat atg	aag aag ctg	gag aag aaa	gcc tac ctg	aaa cgt cgc	3313
Leu Arg Asp Met	Lys Lys Leu	Glu Lys Lys	Ala Tyr Leu	Lys Arg Arg	
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tat ggc ctc atc	agc acc ggc	tca gac agt	gag tcc ccg	gcc acc cgc	3361
Tyr Gly Leu Ile	Ser Thr Gly	Ser Asp Ser	Glu Ser Pro	Ala Thr Arg	
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tca gag tgc ccc	agc ccc tgc	ctg cag ccc	cag gac ctg	agc ctc ctg	3409
Ser Glu Cys Pro	Ser Pro Cys	Leu Gln Pro	Gln Asp Leu	Ser Leu Leu	
	1120	1125		1130	
cag atc aag aag	ccc cgg gtg	gtg ctg gca	ccc gag gag	aag gag gca	3457
Gln Ile Lys Lys	Pro Arg Val	Val Leu Ala	Pro Glu Glu	Lys Glu Ala	
	1135	1140		1145	
ctg cgg aag gcc	tat cag ctg	gaa ccc tac	ccc tcg cag	cag acc atc	3505
Leu Arg Lys Ala	Tyr Gln Leu	Glu Pro Tyr	Pro Ser Gln	Gln Thr Ile	
	1150	1155		1160	
gag ctc ctc tcc	ttc cag ctc	aac ctc aag	acc aac acc	gtc atc aac	3553
Glu Leu Leu Ser	Phe Gln Leu	Asn Leu Lys	Thr Asn Thr	Val Ile Asn	
1165	1170		1175	1180	
tgg ttc cac aac	tac agg tcc	cgg atg cgc	cgg gag atg	ttg gtg gag	3601
Trp Phe His Asn	Tyr Arg Ser	Arg Met Arg	Glu Met Leu	Val Glu	
	1185	1190		1195	

ggg acc cag gat gag cca gac ctt gat cca agc ggg ggt cct gga atc Gly Thr Gln Asp Glu Pro Asp Leu Asp Pro Ser Gly Gly Pro Gly Ile 1200 1205 1210	3649
cta ccg cca ggc cac tcc cac cca gac ccc acc ccg cag agc cct gac Leu Pro Pro Gly His Ser His Pro Asp Pro Thr Pro Gln Ser Pro Asp 1215 1220 1225	3697
tct gag act gag gac cag aag cca acc gtg aag gaa ctg gag ctt cag Ser Glu Thr Glu Asp Gln Lys Pro Thr Val Lys Glu Leu Glu Leu Gln 1230 1235 1240	3745
gag ggc cct gag gag aac agc aca ccc ctg acc acc cag gac aag gcc Glu Gly Pro Glu Glu Asn Ser Thr Pro Leu Thr Thr Gln Asp Lys Ala 1245 1250 1255 1260	3793
caa gtg agg atc aag cag gaa cag atg gag gag gac gct gag gaa gag Gln Val Arg Ile Lys Gln Glu Gln Met Glu Glu Asp Ala Glu Glu Glu 1265 1270 1275	3841
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ccc ccc aaa gag gag cat ccc gac cct ccg ggt aat gat gga ctc cca Pro Pro Lys Glu Glu His Pro Asp Pro Pro Gly Asn Asp Gly Leu Pro 1295 1300 1305	3937
aaa gtg gct ccc ggg ccc ctc ctt cca ggt gga tcc acc cca gac tgt Lys Val Ala Pro Gly Pro Leu Leu Pro Gly Gly Ser Thr Pro Asp Cys 1310 1315 1320	3985
ccc tca ctt cat ccc caa cag gag agt gag gcc ggg gag cga ctt cac Pro Ser Leu His Pro Gln Gln Glu Ser Glu Ala Gly Glu Arg Leu His 1325 1330 1335 1340	4033
ccg gac cct tta agt ttt aag tca gcc tca gag tcc tca cgc tgc agc Pro Asp Pro Leu Ser Phe Lys Ser Ala Ser Glu Ser Ser Arg Cys Ser 1345 1350 1355	4081
ctg gag gtg tca ctg aac tcg ccc tcg gcc gcc tcc tca cca ggc ctc Leu Glu Val Ser Leu Asn Ser Pro Ser Ala Ala Ser Ser Pro Gly Leu 1360 1365 1370	4129
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tcc cca cct ggc gcc ccc cct gcc aaa gtg ccg agt gcc agc ccc act Ser Pro Pro Gly Ala Pro Pro Ala Lys Val Pro Ser Ala Ser Pro Thr 1390 1395 1400	4225
gct gac atg gct gga gcc ttg cac ccc agt gcc aag gtg aac ccc aac Ala Asp Met Ala Gly Ala Leu His Pro Ser Ala Lys Val Asn Pro Asn 1405 1410 1415 1420	4273
ttg cag cgg cgg cat gag aag atg gcc aat ctg aac aac atc att tac Leu Gln Arg Arg His Glu Lys Met Ala Asn Leu Asn Asn Ile Ile Tyr 1425 1430 1435	4321
cga cta gag cgg gct gcc aat cgg gag gag gcc ctg gag tgg gag ttc Arg Leu Glu Arg Ala Ala Asn Arg Glu Glu Ala Leu Glu Trp Glu Phe 1440 1445 1450	4369

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tattttgaca ataggaaaca gtgaccattt tcagagtaat caaatctgga acaaatgaaa 6229  
catcttttag ccaccaccac cctgttgcaa ttaagacaac cgtgggggaa cacaccactt 6289



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tttactgttg aaaccaacac aacgttgaaa tccaggctta tacgcagact ccgattccta 6349
gagaactaaa tttggcttta gtgtgacggg atttgattaa gcacttagta tagtcttttg 6409
aacacggaaa tctgtttgta cttaaagcta gcggaccctg gaacaacttt gtcaggttca 6469
cgtcctataa cggttaaaaa acacacacac acatacacia accgtttcta tgagagattg 6529
atgaactttg tttaaaattt taaaaaagg aacacgttct gtaaacgagt cgctaaatac 6589
agaattgtat aataaaaaaa aaaaaaa 6616

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<210> 457  
 <211> 1461  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (262) .. (1323)

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tcaccggatc agagatagca gagcgccgag ttggggccac gaaggcgtga ggggagtcgt 120
cgtccctcct gcacgaaagc gtctaagcct tggcgacgcc gccctggggg acccagctca 180
ggcctgggat agggaccgct gtccccgggt cctaccaat gtcgcccgtc gctcccggcc 240
cagctctacc cgcagagtct g atg gca gcg gcc act ctg agg acg cca act 291
                        Met Ala Ala Ala Thr Leu Arg Thr Pro Thr
                        1 5 10

cag ggc act gtg acc ttt gaa gat gtg gcc gta cac ttc tcc tgg gag 339
Gln Gly Thr Val Thr Phe Glu Asp Val Ala Val His Phe Ser Trp Glu
                        15 20 25

gaa tgg ggt ctc ctt gat gag gct caa aga tgc ctg tac cgt gat gtg 387
Glu Trp Gly Leu Leu Asp Glu Ala Gln Arg Cys Leu Tyr Arg Asp Val
                        30 35 40

atg ctg gag aac ttg gct ctt tta acc tct cta gat gtt cat cat cag 435
Met Leu Glu Asn Leu Ala Leu Leu Thr Ser Leu Asp Val His His Gln
                        45 50 55

aag cag cac ctt gga gaa aaa cat ttc ata agc aat gtg ggc cga gcc 483
Lys Gln His Leu Gly Glu Lys His Phe Ile Ser Asn Val Gly Arg Ala
                        60 65 70

ttg ttt gtg aag acc tgc aca ttc cat gtg tca ggg gag cct tcc acc 531
Leu Phe Val Lys Thr Cys Thr Phe His Val Ser Gly Glu Pro Ser Thr
                        75 80 85 90

tgc aga gaa ttt ggg aag gac ttc ctg gcc aag ttg gga ttt ctc cat 579
Cys Arg Glu Phe Gly Lys Asp Phe Leu Ala Lys Leu Gly Phe Leu His
                        95 100 105

caa cag gct gct cac act ggg gag caa tcc aat agc aaa agc gac ggt 627
Gln Gln Ala Ala His Thr Gly Glu Gln Ser Asn Ser Lys Ser Asp Gly
                        110 115 120

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ggg gcc atc agt cac aga gga aaa act cat tac aac tgt gga gaa cac Gly Ala Ile Ser His Arg Gly Lys Thr His Tyr Asn Cys Gly Glu His 125 130 135	675
aca aaa gca ttc agc ggt aaa cac aca ctt gtt cag cag cag aga acc Thr Lys Ala Phe Ser Gly Lys His Thr Leu Val Gln Gln Gln Arg Thr 140 145 150	723
ctc act aca gaa aga tgt tac ata tgc agt gaa tgt ggg aaa tcc ttt Leu Thr Thr Glu Arg Cys Tyr Ile Cys Ser Glu Cys Gly Lys Ser Phe 155 160 165 170	771
agc aaa agc tac agt ctc aat gac cat tgg aga ctt cac act gga gaa Ser Lys Ser Tyr Ser Leu Asn Asp His Trp Arg Leu His Thr Gly Glu 175 180 185	819
aag cct tat gaa tgt cga gag tgt ggg aag tcc ttt agg caa agc tct Lys Pro Tyr Glu Cys Arg Glu Cys Gly Lys Ser Phe Arg Gln Ser Ser 190 195 200	867
agt ctc att caa cac cgg aga ggt cac act gca gta cga cct cat gag Ser Leu Ile Gln His Arg Arg Gly His Thr Ala Val Arg Pro His Glu 205 210 215	915
ggg gat gaa tgt gga aaa tta ttt agc aac ccg tct aac ctc att aaa Gly Asp Glu Cys Gly Lys Leu Phe Ser Asn Pro Ser Asn Leu Ile Lys 220 225 230	963
cat cgg aga gtt cac act ggg gaa agg cca tat gag tgc agc gaa tgt His Arg Arg Val His Thr Gly Glu Arg Pro Tyr Glu Cys Ser Glu Cys 235 240 245 250	1011
ggg aaa tcc ttt aac caa agg tct gca ctc ctt caa cat cgg gga ggt Gly Lys Ser Phe Asn Gln Arg Ser Ala Leu Leu Gln His Arg Gly Gly 255 260 265	1059
cac act ggg gag agg cct tat gag tgc agt gaa tgt ggg aag ttt ttt His Thr Gly Glu Arg Pro Tyr Glu Cys Ser Glu Cys Gly Lys Phe Phe 270 275 280	1107
ccc tac agc tcc agt ctc cga aaa cac cag aga gtt cac act gga tca Pro Tyr Ser Ser Ser Leu Arg Lys His Gln Arg Val His Thr Gly Ser 285 290 295	1155
aga ccc tat gag tgc agt gaa tgt ggg aaa tcc ttt act caa aat tcc Arg Pro Tyr Glu Cys Ser Glu Cys Gly Lys Ser Phe Thr Gln Asn Ser 300 305 310	1203
ggc ctc att aag cac agg agg gtt cac act ggg gag aag cct tat gag Gly Leu Ile Lys His Arg Arg Val His Thr Gly Glu Lys Pro Tyr Glu 315 320 325 330	1251
tgc acg gaa tgt ggg aaa tcc ttt agc cat aac tcc agc ctt att aaa Cys Thr Glu Cys Gly Lys Ser Phe Ser His Asn Ser Ser Leu Ile Lys 335 340 345	1299
cat cag aga att cat agt cga taa aaggcttatg agtggcaa at gtggaaaatc His Gln Arg Ile His Ser Arg *	1353
tgtagcacc ctggagaaag tccttgagta cacagtgaat gtcagaaagc ttcagctgaa	1413
ggccatatct cattgagtgc cacacagggtc acaagggaaa gacacttt	1461

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<222> (206) .. (1009)
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1187

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170                      175                      180                      185

gtg gcc tcc tcc tcc agg cat gga ggt ctg tcc act act ggg ctt ctg      808
Val Ala Ser Ser Ser Arg His Gly Gly Leu Ser Thr Thr Gly Leu Leu
                      190                      195                      200

ggc tat ttg ccc ctg att tgc tcc ctg gta cgg gct ctt gtt aac agg      856
Gly Tyr Leu Pro Leu Ile Cys Ser Leu Val Arg Ala Leu Val Asn Arg
                      205                      210                      215

cag gca agg ggt gcg ggg acc agg caa ggg ctt caa agg gta cag tac      904
Gln Ala Arg Gly Ala Gly Thr Arg Gln Gly Leu Gln Arg Val Gln Tyr
                      220                      225                      230

caa atc ttc caa act cag cac ttg tgc cct ggg gtc tcc aaa ctg tct      952
Gln Ile Phe Gln Thr Gln His Leu Cys Pro Gly Val Ser Lys Leu Ser
                      235                      240                      245

tct gcc cta gga ttt att cat act gtt aaa tta cca gtt tat gca aat      1000
Ser Ala Leu Gly Phe Ile His Thr Val Lys Leu Pro Val Tyr Ala Asn
250                      255                      260                      265

gat atg taa ataaagctca attttttgaa aaaaaa      1035
Asp Met *
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<210> 459  
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 <212> DNA  
 <213> Homo sapiens

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 <222> (49)..(756)

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gct ctg ctc ctc ctg acc ctc ctc act cac tct gca gtg tca gtg gtc      105
Ala Leu Leu Leu Leu Thr Leu Leu Thr His Ser Ala Val Ser Val Val
5                      10                      15

cag gca ggg ctg act cag cca ccc tcg gtg tcc aag ggc ttg aga cag      153
Gln Ala Gly Leu Thr Gln Pro Pro Ser Val Ser Lys Gly Leu Arg Gln
20                      25                      30                      35

acc gcc aca ctc acc tgc act ggg aac agc aac aat gtt ggc gac caa      201
Thr Ala Thr Leu Thr Cys Thr Gly Asn Ser Asn Asn Val Gly Asp Gln
                      40                      45                      50

gga gca tct tgg ctg cag cag cac cag ggc cac cct ccc aaa ctc ctc      249
Gly Ala Ser Trp Leu Gln Gln His Gln Gly His Pro Pro Lys Leu Leu
55                      60                      65

tcc tac agg aat aac aac cgg ccc tca ggg atc tca gag aga tta tct      297
Ser Tyr Arg Asn Asn Asn Arg Pro Ser Gly Ile Ser Glu Arg Leu Ser
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70	75	80	
gca tcc agg tca gga aac aca gcc tcc ctg acc att act gga ctc cag			345
Ala Ser Arg Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Leu Gln			
85	90	95	
cct gag gac gag gct gac tat tac tgc tca gca tgg gac agc agc ctc			393
Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ala Trp Asp Ser Ser Leu			
100	105	110	115
agt gct tgg gtg ttc ggc gga ggg acc aag ctg acc gtc cta ggt cag			441
Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln			
	120	125	130
ccc aag gct gcc ccc tcg gtc act ctg ttc ccg ccc tcc tct gag gag			489
Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu			
	135	140	145
ctt caa gcc aac aag gcc aca ctg gtg tgt ctc ata agt gac ttc tac			537
Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr			
	150	155	160
ccg gga gcc gtg aca gtg gcc tgg aag gca gat agc agc ccc gtc aag			585
Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys			
	165	170	175
gcg gga gtg gag acc acc aca ccc tcc aaa caa agc aac aac aag tac			633
Ala Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr			
180	185	190	195
gcg gcc agc agc tac ctg agc ctg acg cct gag cag tgg aag tcc cac			681
Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His			
	200	205	210
aga agc tac agc tgc cag gtc acg cat gaa ggg agc acc gtg gag aag			729
Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys			
	215	220	225
aca gtg gcc cct aca gaa tgt tca tag gttct caaccctcac cccaccacg			781
Thr Val Ala Pro Thr Glu Cys Ser *			
	230	235	
ggagactaga gctgcaggat cccaggggag gggctctctcc tcccacccca aggcacaaag			841
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aaaaa			906

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<220>  
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 <222> (203)..(1588)

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ctctgcttgcc tccagaggcc tcgtcctaata ccacctcgcc tgacggcgcg ggatccctgg	180
ctccgcgagc ctcagcctca cc atg tgt gtc agg agc tgt ttc cag tcc ccc	232
Met Cys Val Arg Ser Cys Phe Gln Ser Pro	
1 5 10	
cgt ctc cag tgg gtg tgg aga aca gcc ttc ctg aaa cac acc cag cgc	280
Arg Leu Gln Trp Val Trp Arg Thr Ala Phe Leu Lys His Thr Gln Arg	
15 20 25	
agg cac cag ggg tcc cac cga tgg aca cac ctt gga ggc agc acc tac	328
Arg His Gln Gly Ser His Arg Trp Thr His Leu Gly Gly Ser Thr Tyr	
30 35 40	
aga gcg gtg att ttc gac atg ggc gga gtt ctc att cct tct cca ggg	376
Arg Ala Val Ile Phe Asp Met Gly Gly Val Leu Ile Pro Ser Pro Gly	
45 50 55	
aga gtc gct gca gaa tgg gag gta cag aat cgt atc cct tct gga act	424
Arg Val Ala Ala Glu Trp Glu Val Gln Asn Arg Ile Pro Ser Gly Thr	
60 65 70	
ata tta aag gcc ttg atg gaa ggt ggt gaa aat ggg ccc tgg atg aga	472
Ile Leu Lys Ala Leu Met Glu Gly Gly Glu Asn Gly Pro Trp Met Arg	
75 80 85 90	
ttt atg aga gca gaa ata aca gca gag ggt ttt tta cga gaa ttt ggg	520
Phe Met Arg Ala Glu Ile Thr Ala Glu Gly Phe Leu Arg Glu Phe Gly	
95 100 105	
aga ctt tgc tct gaa atg tta aag acc tcc gtg cct gtg gac tca ttt	568
Arg Leu Cys Ser Glu Met Leu Lys Thr Ser Val Pro Val Asp Ser Phe	
110 115 120	
ttc tct ctg ttg acc agt gag cga gtg gca aag cag ttc cca gtg atg	616
Phe Ser Leu Leu Thr Ser Glu Arg Val Ala Lys Gln Phe Pro Val Met	
125 130 135	
act gag gcc ata act caa att cgg gca aaa ggt ctt cag act gca gtc	664
Thr Glu Ala Ile Thr Gln Ile Arg Ala Lys Gly Leu Gln Thr Ala Val	
140 145 150	
ttg agc aat aat ttt tat ctt ccc aac cag aaa agc ttt ttg ccc ctg	712
Leu Ser Asn Asn Phe Tyr Leu Pro Asn Gln Lys Ser Phe Leu Pro Leu	
155 160 165 170	
gac cgg aaa cag ttt gat gtg att gtg gag tcc tgc atg gaa ggg atc	760
Asp Arg Lys Gln Phe Asp Val Ile Val Glu Ser Cys Met Glu Gly Ile	
175 180 185	
tgt aag cca gac cct agg atc tac aag ctg tgc ttg gag cag ctc ggc	808
Cys Lys Pro Asp Pro Arg Ile Tyr Lys Leu Cys Leu Glu Gln Leu Gly	
190 195 200	
ctg cag ccc tct gag tcc atc ttt ctt gat gac ctt gga aca aat cta	856
Leu Gln Pro Ser Glu Ser Ile Phe Leu Asp Asp Leu Gly Thr Asn Leu	
205 210 215	
aaa gaa gct gcc aga ctt ggt att cac acc att aag gtt aat gac cca	904
Lys Glu Ala Ala Arg Leu Gly Ile His Thr Ile Lys Val Asn Asp Pro	
220 225 230	
gag act gca gta aag gaa tta gaa gct ctc ttg ggt ttt aca ttg aga	952

Glu Thr Ala Val Lys	Glu Leu Glu Ala Leu Leu Gly Phe Thr Leu Arg	
235	240 245 250	
gta ggt gtt cca aac act cgg cct gtg aaa aag acg atg gaa att ccg		1000
Val Gly Val Pro Asn Thr Arg Pro Val Lys Lys Thr Met Glu Ile Pro		
	255 260 265	
aaa gat tcc ttg cag aag tac ctc aaa gac tta ctg ggt atc cag acc		1048
Lys Asp Ser Leu Gln Lys Tyr Leu Lys Asp Leu Leu Gly Ile Gln Thr		
	270 275 280	
aca ggc cca ttg gaa cta ctt cag ttt gat cac ggg cag tca aat cca		1096
Thr Gly Pro Leu Glu Leu Leu Phe Asp His Gly Gln Ser Asn Pro		
	285 290 295	
act tac tac atc agg ctg gct aat cgt gat cta gtt ctg agg aag aag		1144
Thr Tyr Tyr Ile Arg Leu Ala Asn Arg Asp Leu Val Leu Arg Lys Lys		
	300 305 310	
ccc cca ggg aca ctc ctt cca tct gcc cat gcc ata gag agg gag ttc		1192
Pro Pro Gly Thr Leu Leu Pro Ser Ala His Ala Ile Glu Arg Glu Phe		
	315 320 325 330	
agg att atg aaa gcc ctt gca aat gct gga gta cct gtc cct aac gtt		1240
Arg Ile Met Lys Ala Leu Ala Asn Ala Gly Val Pro Val Pro Asn Val		
	335 340 345	
ctt gat ctc tgt gaa gat tca agt gtc att ggc acc ccc ttc tat gtg		1288
Leu Asp Leu Cys Glu Asp Ser Ser Val Ile Gly Thr Pro Phe Tyr Val		
	350 355 360	
atg gag tac tgc cca ggt ctc atc tac aaa gac cct tcc ctg cca ggc		1336
Met Glu Tyr Cys Pro Gly Leu Ile Tyr Lys Asp Pro Ser Leu Pro Gly		
	365 370 375	
ttg gag ccc agc cac aga cga gcc ata tac act gcc atg aac aca gtc		1384
Leu Glu Pro Ser His Arg Arg Ala Ile Tyr Thr Ala Met Asn Thr Val		
	380 385 390	
ctg tgc aaa att cac agt gtg gat ctg cag gct gtg gga ctt gaa gac		1432
Leu Cys Lys Ile His Ser Val Asp Leu Gln Ala Val Gly Leu Glu Asp		
	395 400 405 410	
tat ggg aag caa ggc tgc aca acc tgg tgt ttc atc cag aag agc cag		1480
Tyr Gly Lys Gln Gly Ser Thr Thr Trp Cys Phe Ile Gln Lys Ser Gln		
	415 420 425	
agg tgc ttg ctg tcc ttg act ggg aac ttt cta cct tgg gcg acc ccc		1528
Arg Cys Leu Leu Ser Leu Thr Gly Asn Phe Leu Pro Trp Ala Thr Pro		
	430 435 440	
ttg ctg atg tgg cct aca gct gcc tgg ctc att acc tgc cat cca gtt		1576
Leu Leu Met Trp Pro Thr Ala Ala Trp Leu Ile Thr Cys His Pro Val		
	445 450 455	
ttc ccg tgc tga gag gtattaatga ctgtgacttg acacagctgg gaatccctgc		1631
Phe Pro Cys *		
	460	
tgcagaggag tatttcagga tgtactgtct ccaaattgggg ctccctcca ctgagaactg		1691
gaactttctat atggcttttt cctttttccg tgtggctgca atcctacagg gagtctacaa		1751
gcgatcactc acaggtaatg ggatggctgc cctgaagagc cactgcgggc attctgccga		1811

1192



135	140	145	150	
gat gaa agc ttt ggg gca gtg aag aag aaa ttc tgt acc ttt cga gaa				715
Asp Glu Ser Phe Gly Ala Val Lys Lys Lys Phe Cys Thr Phe Arg Glu				
	155	160	165	
gat tat gat gac att tcc aat cag ata gac ttc atc atc tgc ctg ggg				763
Asp Tyr Asp Asp Ile Ser Asn Gln Ile Asp Phe Ile Ile Cys Leu Gly				
	170	175	180	
gga gac ggg acg ctg ctg tac gct tcc tgc ctt ttc cag gga acg cag				811
Gly Asp Gly Thr Leu Leu Tyr Ala Ser Ser Leu Phe Gln Gly Thr Gln				
	185	190	195	
ctg ttg ttc tcc gga gtc ggc tga aggtcagggt ggtgaaggag ctccggggga				865
Leu Leu Phe Ser Gly Val Gly *				
	200	205		
agaagacggc cgtgcacaat gggctgggtg agaaaggctc gcaggctgca ggcttgaca				925
tggtatgtcgg gaagcaggcc atgcagtacc aggtcctgaa tgaggtgggtg attgacagag				985
gccctcctc ctacctgtcc aatgtggatg tctacctgga cggacacctc atcaccacgg				1045
tgcagggcga cggagtgatc gtgtccacc cgcagggcag cacggcgtat gcggccgcaa				1105
gctta				1110

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 <212> DNA  
 <213> Homo sapiens

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ttatgggtct ttcaactctc gtatatatatt aaatgcaatt ggagccccgc agggaatacc	180
agatcaattt aaagcttgaa atcaaatagt tacaggactg aagtcaatat tttggtagat	240
gacagtcaat aaaaatgtaa attagataca ctacatctat tacaaccaac agcaacgagc	300
ttttcatgag ttaaaaagaa aaactcatgt cggccccagc cctggggcta cctgacctga	360
caaaactctt tacactccat gtgtcaaaaa gagaaaaaat ggcagttgga gttttaaccc	420
agactgtggg gccctggcca aggccagtgg cctatctctc aaaacaacta gatgggtttc	480
caaaggtgg ccactatgtc taaggaccct ggcagcaaca gccctgttag cacaagaagc	540
agataaacta acccttgggc aaaacctgaa tataaaggcc ccccatgctg tggttaacttt	600
g atg act acc gaa gga cat cat tgg cta aca aat gct aga tta acc	646
Met Thr Thr Glu Gly His His Trp Leu Thr Asn Ala Arg Leu Thr	
1 5 10 15	

aag tac caa agc ttg cca tgt gaa aat ccc cac ata act att gaa gtc	694
Lys Tyr Gln Ser Leu Pro Cys Glu Asn Pro His Ile Thr Ile Glu Val	
20 25 30	
tgt aac acc cta aat ccc acc acc ctg ctc cca gta tca gag agc ccg	742
Cys Asn Thr Leu Asn Pro Thr Thr Leu Leu Pro Val Ser Glu Ser Pro	
35 40 45	
ggc gag cat aac tgt gta gag gtg ttg gac tca gtc tat tct agc aga	790
Gly Glu His Asn Cys Val Glu Val Leu Asp Ser Val Tyr Ser Ser Arg	
50 55 60	
cct gac ctt cgg gac cag cca tgg gca tca tca gta gac tgg gag tta	838
Pro Asp Leu Arg Asp Gln Pro Trp Ala Ser Ser Val Asp Trp Glu Leu	
65 70 75	
tac atg gac ggg agc agc ttc atc aac tca caa gga gaa aga tgt gca	886
Tyr Met Asp Gly Ser Ser Phe Ile Asn Ser Gln Gly Glu Arg Cys Ala	
80 85 90 95	
gga tat gcg gtg gta act ttg gat gct gtc att aaa gcc aaa ctg tgg	934
Gly Tyr Ala Val Val Thr Leu Asp Ala Val Ile Lys Ala Lys Leu Trp	
100 105 110	
cta cag ggc act tca gcc cag aag gct gag ctc att gct tta act cgg	982
Leu Gln Gly Thr Ser Ala Gln Lys Ala Glu Leu Ile Ala Leu Thr Arg	
115 120 125	
gct gta gaa ctc agt gaa ggg caa gag tca ctt gaa gaa ttg tta ggc	1030
Ala Val Glu Leu Ser Glu Gly Gln Glu Ser Leu Glu Glu Leu Leu Gly	
130 135 140	
cgg tac ttc tac gtc tca cac ttg cca gcc ttt gcc aaa gca gta gca	1078
Arg Tyr Phe Tyr Val Ser His Leu Pro Ala Phe Ala Lys Ala Val Ala	
145 150 155	
caa ctg tgc att aca tgc cga cag cac aat gcg agg caa agc ccc act	1126
Gln Leu Cys Ile Thr Cys Arg Gln His Asn Ala Arg Gln Ser Pro Thr	
160 165 170 175	
gtt tcg ccc cac ata caa gct tat gga gca gct cct ttt gag gat ctt	1174
Val Ser Pro His Ile Gln Ala Tyr Gly Ala Ala Pro Phe Glu Asp Leu	
180 185 190	
cag gtg gat ttc aca gaa atg cca aaa tgt gga ggt aac aag tat ttg	1222
Gln Val Asp Phe Thr Glu Met Pro Lys Cys Gly Gly Asn Lys Tyr Leu	
195 200 205	
ctg gtt ctt acg tgt act tac tct ggg tgg gtg gag gct tat cca aca	1270
Leu Val Leu Thr Cys Thr Tyr Ser Gly Trp Val Glu Ala Tyr Pro Thr	
210 215 220	
cga act gaa aag gcc tac gaa gta acc cgt gtg ctt ctc cga gat ctt	1318
Arg Thr Glu Lys Ala Tyr Glu Val Thr Arg Val Leu Leu Arg Asp Leu	
225 230 235	
att cct agg ttt gga ctg ccc tta cga att ggc tca cat aac ggg ccg	1366
Ile Pro Arg Phe Gly Leu Pro Leu Arg Ile Gly Ser His Asn Gly Pro	
240 245 250 255	
gtg ttt gtg gct gac ttg gac tgt gtg gaa atc aat gtg gat act ggt	1414
Val Phe Val Ala Asp Leu Asp Cys Val Glu Ile Asn Val Asp Thr Gly	
260 265 270	

gtc att tgg gcc act tgg ata aaa aat gaa aag gat cca gtg cag ctt	1462
Val Ile Trp Ala Thr Trp Ile Lys Asn Glu Lys Asp Pro Val Gln Leu	
275 280 285	
cag aaa gga aaa agt ggc cct tcc tgt act aag gga caa tgt aac ccc	1510
Gln Lys Gly Lys Ser Gly Pro Ser Cys Thr Lys Gly Gln Cys Asn Pro	
290 295 300	
tta gag cta gta ata acc aat ccc ctt gat cct cgc tgg aaa aaa ggg	1558
Leu Glu Leu Val Ile Thr Asn Pro Leu Asp Pro Arg Trp Lys Lys Gly	
305 310 315	
gag cgt gtg acc tta gga atc aat ggg gct gga ctg aat ccc cga gta	1606
Glu Arg Val Thr Leu Arg Ile Asn Gly Ala Gly Leu Asn Pro Arg Val	
320 325 330 335	
aat atc ttg gtt cga gga gaa gtt tac aaa tgc tct ctt gag cca gtg	1654
Asn Ile Leu Val Arg Gly Glu Val Tyr Lys Cys Ser Leu Glu Pro Val	
340 345 350	
ttt caa act ttc tat gat gaa cta aat gtg cca ata aca gaa ttt cca	1702
Phe Gln Thr Phe Tyr Asp Glu Leu Asn Val Pro Ile Thr Glu Phe Pro	
355 360 365	
gga aaa aca aga aat ttg ttt ttg caa tta gcc gag cat gta gcc cag	1750
Gly Lys Thr Arg Asn Leu Phe Leu Gln Leu Ala Glu His Val Ala Gln	
370 375 380	
tct ctc act gtc act tca tgt tat gta tgt gga gga act gta ata gca	1798
Ser Leu Thr Val Thr Ser Cys Tyr Val Cys Gly Gly Thr Val Ile Ala	
385 390 395	
gat caa tgg cca tgg gaa gcc cga gaa tta gta cct aca gac cca gtt	1846
Asp Gln Trp Pro Trp Glu Ala Arg Glu Leu Val Pro Thr Asp Pro Val	
400 405 410 415	
cct gat gaa ttc cca gct caa aag aat cac cct gat aat ttc tgg gtc	1894
Pro Asp Glu Phe Pro Ala Gln Lys Asn His Pro Asp Asn Phe Trp Val	
420 425 430	
cta aaa gcc tca atc att aga caa tac tat ata gca aga gtg gag aag	1942
Leu Lys Ala Ser Ile Ile Arg Gln Tyr Tyr Ile Ala Arg Val Glu Lys	
435 440 445	
gac ttc acc ctt cct gta gga aga cta cat ggt gga gtt caa acc aca	1990
Asp Phe Thr Leu Pro Val Gly Arg Leu His Gly Gly Val Gln Thr Thr	
450 455 460	
cag aga aaa atc cat tca gta aat ttc caa agt tgc aga ccg ttt agg	2038
Gln Arg Lys Ile His Ser Val Asn Phe Gln Ser Cys Arg Pro Phe Arg	
465 470 475	
ccc acc cag aat ccc acc ggg act gga cag ccc cca ctg ggc tat act	2086
Pro Thr Gln Asn Pro Thr Gly Thr Gly Gln Pro Pro Leu Gly Tyr Thr	
480 485 490 495	
gga tat gtg gac ata gag cct aca cta agc tgc ctg aca agt agt tgt	2134
Gly Tyr Val Asp Ile Glu Pro Thr Leu Ser Cys Leu Thr Ser Ser Cys	
500 505 510	
gtt att ggc act att aaa cca tct ttc ttc cta ctg tcc ata aaa aca	2182
Val Ile Gly Thr Ile Lys Pro Ser Phe Phe Leu Leu Ser Ile Lys Thr	
515 520 525	

gga gaa ctc ctg ggc ttc cct gtc tat gct tcc cgt gaa aag cat agc 2230  
 Gly Glu Leu Leu Gly Phe Pro Val Tyr Ala Ser Arg Glu Lys His Ser  
 530 535 540

tat aag aaa ttg aaa caa tga ta aatggccccc tgagagaatc atacagtatt 2283  
 Tyr Lys Lys Leu Lys Gln \*  
 545 550

atgggcctgc tacttaggca caagatggct cgtggggata ccggatcccc atttatatga 2343  
 tcaaccgaat catacgggta caagctgtct taaaaataat cactgcaacc ggcagagcct 2403  
 tgactattct ggcccagcaa gaaactcaga tgagaaatgc tatctatcaa aatagattag 2463  
 ctctcgacta cttgctagca gctgaaggag aggtctgtag gaaatttaac cttactaatt 2523  
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 aagtggcaca tgtgcccgtg caagtgtggc atggatttga tcctggggcc atgttttagaa 2643  
 aatggttccc agcgctagga ggatttaaaa ctcttataat aagagggtata atagtaaatag 2703  
 gaacctactt actgctccct cgtttgctac ctgtacttct tcaaatgata aaaagcttca 2763  
 tcgctacctt agtgtaccaa aatgcatcat cacagggtga ctatataaat cactattgat 2823  
 ctgtctagca cgaagacatg ggtagtaaac atgaaacaac tcctgctatt gagtggaggt 2883  
 ctcaaagtgg gggaataagg gaggagacca ccctcatat tgtcttatgc ccaatttctg 2943  
 cctccaaaga aagaaaaagt aaaaactaaa aggcagaaat gaaatccaca agcagacagc 3003  
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 tcaatcgatc acgacctct caccacacc cccttagact tgtgagtcct taaaagggac 3243  
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 ggcctaataa accccttct tctttaaaaa aaaaaaaaaa a 3344

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 <213> Homo sapiens

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 <222> (240)..(575)

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 tgcctcagtg tgcattgtca ctgggcatct tcccttcgac ccctttgccc acgtggtgac 120  
 cgctggggag ctgtgagagt gtgaggggca cgttcacgcc gtctggactc tttctctcct 180

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actgagacgc agcctatagg tccgcaggcc agtcctccca ggaactgaaa tagtgaaat      239
atg agt tgg cga gga aga tca aca tat agg cct agg cca aga aga agt      287
Met Ser Trp Arg Gly Arg Ser Thr Tyr Arg Pro Arg Pro Arg Arg Ser
  1             5             10             15

tta cag cct cct gag ctg att ggg gct atg ctt gaa ccc act gat gaa      335
Leu Gln Pro Pro Glu Leu Ile Gly Ala Met Leu Glu Pro Thr Asp Glu
             20             25             30

gag cct aaa gaa gag aaa cca ccc act aaa agt cgg aat cct aca cct      383
Glu Pro Lys Glu Glu Lys Pro Pro Thr Lys Ser Arg Asn Pro Thr Pro
             35             40             45

gat cag aag aga gaa gat gat cag ggt gca gct gag att caa gtg cct      431
Asp Gln Lys Arg Glu Asp Asp Gln Gly Ala Ala Glu Ile Gln Val Pro
             50             55             60

gac ctg gaa gcc gat ctc cag gag cta tgt cag aca aag act ggg gat      479
Asp Leu Glu Ala Asp Leu Gln Glu Leu Cys Gln Thr Lys Thr Gly Asp
             65             70             75             80

gga tgt gaa ggt ggt act gat gtc aag ggg aag att cta cca aaa gca      527
Gly Cys Glu Gly Gly Thr Asp Val Lys Gly Lys Ile Leu Pro Lys Ala
             85             90             95

gag cac ttt aaa atg cca gaa gca ggt gaa ggg aaa tca cag gtt taa      575
Glu His Phe Lys Met Pro Glu Ala Gly Glu Gly Lys Ser Gln Val *
             100             105             110

aggaagataa gctgaaacaa cacaaaactgt ttttatatta gatattttac tttaaaatat      635

cttaataaag ttttaagctt ttctccaaaa aaaaaaaaaa      673

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<210> 464  
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 <212> DNA  
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 <222> (1)...(987)  
 <223> n = a,t,c or g

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ggttctcttc ttgctcttgc ctgtgacctt ggctggtgtg aggactggag ctgctgcctg      180
gtacaggggtg gaggagatct tgttgatgta gtacagacca accatggaga agatgaagca      240
ggtggtgaca cagactcggg ggatgaggcc agatgcaaag agagccaaca ggaggcacag      300
gagaatctca ggggaagatct ttgcttgaa tcctttgccc aagacaagat tttccaaatt      360
attgaaggca gtgagcgaga acacgaagag accctaacca agcagggcgc cttggatggt      420

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gagccactcg gtggaggcca gctgacggct gtacatctgc atcccagcaa agagcagcag      480
ggacaggagg gaggagagcg ccagcgaggt gcccgtaccc accactggag gggatgggag      540
aagggacgga gagtcaggct ccgccctccc tccggcaagc tacgggcaga tcagccggtc      600
cggaagctcg gtgggcccgc cccctccaag aactcccggg actgcagcca cagcccccac      660
ctccccacac cgcgcgggcaa cccctacgta ttcccagcc ccggacaccc cgaacctcc      720
cgtccggtag aa      atg ccc gct ccc ggt gga acc cag gac acg tca gct      768
                        Met Pro Ala Pro Gly Gly Thr Gln Asp Thr Ser Ala
                        1          5          10

ctg tcg gga gag gac gag gaa agc ttg tcc acc caa acc ccg acc ccc      816
Leu Ser Gly Glu Asp Glu Glu Ser Leu Ser Thr Gln Thr Pro Thr Pro
                        15          20          25

tct agg act tcc tgg gga ccc cac cgg tcc tgt tac cca tca tgc ccc      864
Ser Arg Thr Ser Trp Gly Pro His Arg Ser Cys Tyr Pro Ser Cys Pro
                        30          35          40

gcc cgt gag tcc aac cgg cgc ctc tgg cca aga aag gcg agc tga acc      912
Ala Arg Glu Ser Asn Arg Arg Leu Trp Pro Arg Lys Ala Ser *
                        45          50          55

gggtgcgggtt agctatgcgc atgcgtcagc gacgaaatcg tcgaccggg aattccggac      972
cggtacctca ggcgt                                           987

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<210> 465  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (255)..(809)

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tgtccccacc ccaggggtca gagcaccac aggtgccgag ctggcccagg agacccccac      180
gctgctgacg ctgtttgcct tgtgtctgca caggcctcta ctaaactctc ccacacaatt      240
agtgctcttaa atat      atg tac acg tat ata ttt tgt ccc aac tgt gtc agt      290
                        Met Tyr Thr Tyr Ile Phe Cys Pro Asn Cys Val Ser
                        1          5          10

tat aaa atg aaa act gac cac ttc tcc tta cgt tat ctt cac agt agc      338
Tyr Lys Met Lys Thr Asp His Phe Ser Leu Arg Tyr Leu His Ser Ser
                        15          20          25

tgt gca gaa gac aac aaa tcc agt gtt gat agc tca ggg cag gct gcc      386
Cys Ala Glu Asp Asn Lys Ser Ser Val Asp Ser Ser Gly Gln Ala Ala
                        30          35          40

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cac ccc agc aaa ggg aag ttc ttc ccc cat ggg acc cac tgg ggg acc	434
His Pro Ser Lys Gly Lys Phe Phe Pro His Gly Thr His Trp Gly Thr	
45 50 55 60	
cag tgc cgc ggc cac atc tcc gtg ctt ggg tgg cag tgt agc tgc cca	482
Gln Cys Arg Gly His Ile Ser Val Leu Gly Trp Gln Cys Ser Cys Pro	
65 70 75	
tct acg ggg tgc cgg gtt ggc ttg ggc ctt gcc atg tgc cag acg cat	530
Ser Thr Gly Cys Arg Val Gly Leu Gly Leu Ala Met Cys Gln Thr His	
80 85 90	
gca tac ata cac aca cac aca cac aca cac aca cac acc cca ccc gat	578
Ala Tyr Ile His Thr His Thr His Thr His Thr His Thr Pro Pro Asp	
95 100 105	
tat gga gca cat cac acc gat ccc ttg cag agg tgg ggg ctg ggg ccc	626
Tyr Gly Ala His His Thr Asp Pro Leu Gln Arg Trp Gly Leu Gly Pro	
110 115 120	
agg aca atc aga agc agg gcc cct ccc cca gct gtc tcg aga cca aag	674
Arg Thr Ile Arg Ser Arg Ala Pro Pro Pro Ala Val Ser Arg Pro Lys	
125 130 135 140	
cca tcc agg gcc tct gag ccc tgg ggc atc acc cag aag cgc tgg gct	722
Pro Ser Arg Ala Ser Glu Pro Trp Gly Ile Thr Gln Lys Arg Trp Ala	
145 150 155	
ccc agg ctg gca ccc agc aca cca gga gcc cag ggc gcg tgg gag atg	770
Pro Arg Leu Ala Pro Ser Thr Pro Gly Ala Gln Gly Ala Trp Glu Met	
160 165 170	
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Ile Val Gln His Arg Leu Leu Ser Arg Gln Glu Glu Leu Lys Glu Arg	
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Gly Asn Lys His Asn Thr Asn Thr Ala Thr Pro Phe Cys Asn Arg Gln	
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Leu Ser Asp Gln Gln Asp Glu Glu Arg Arg Gln Leu Arg Glu Arg	
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aag ctc cta gaa gtt cag cca cag gtg gca aat tca ccc tcc agt gct Lys Leu Leu Glu Val Gln Pro Gln Val Ala Asn Ser Pro Ser Ser Ala 755 760 765 770	2359
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ctt cag tct ttc agc caa tat att gag aat aga cca gag atg aaa agg Leu Gln Ser Phe Ser Gln Tyr Ile Glu Asn Arg Pro Glu Met Lys Arg 820 825 830	2551
cag aga tca ata cag gaa gat aca aag aaa gga aat gag gag aag gca Gln Arg Ser Ile Gln Glu Asp Thr Lys Lys Gly Asn Glu Glu Lys Ala 835 840 845 850	2599
gcg ata act gaa act cag agg aag cca tca gaa gat gaa gtg ctt aat Ala Ile Thr Glu Thr Gln Arg Lys Pro Ser Glu Asp Glu Val Leu Asn 855 860 865	2647
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tta ata agg aga atg aat cag ctc tct ctt ctg gaa aaa gaa cat gat Leu Ile Arg Arg Met Asn Gln Leu Ser Leu Leu Glu Lys Glu His Asp 935 940 945	2887
tta gaa cga cgg tat gag ctg ctg aac cgg gaa ttg agg gca atg cta Leu Glu Arg Arg Tyr Glu Leu Leu Asn Arg Glu Leu Arg Ala Met Leu 950 955 960	2935



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His Leu Glu Arg Thr Leu Glu Gln Asn Lys Gly Lys Met Ala Lys Lys  
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Glu Glu Lys Cys Val Leu Gln \*  
1030

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Arg Arg Thr Ala Leu Ile Leu Gly Ser Gly Leu Leu Ser Phe Val Ala		
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Phe Trp Asn Ser Val Thr Trp His Leu Gln Arg Phe Trp Gly Ala Ser		
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Gly Tyr Phe Trp Gln Ala Gln Trp Glu Arg Leu Leu Thr Thr Phe Glu		
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Gly Lys Glu Trp Ile Leu Phe Phe Ile Gly Ala Ile Gln Val Pro Cys		
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Leu Phe Phe Trp Ser Phe Asn Gly Leu Leu Leu Val Val Asp Thr Thr		
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Glu Pro Val Asp Pro Val Lys Leu His Gln Cys Met Ile Ser Phe Pro		
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Met Val Val Phe Leu Tyr Pro Phe Leu Lys Trp Trp Arg Asp Pro Cys		
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Arg Arg Glu Leu Pro Thr Phe His Trp Phe Leu Leu Glu Leu Ala Ile		
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Phe Thr Leu Ile Glu Glu Val Leu Phe Tyr Tyr Ser His Arg Leu Leu		
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His His Pro Thr Phe Tyr Lys Lys Ile His Lys Lys His His Glu Trp		
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Ala Val Ser Asn Met Leu Pro Val Ile Val Gly Pro Leu Val Met Gly		
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Ser His Leu Ser Ser Ile Thr Met Trp Phe Ser Leu Ala Leu Ile Ile		
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acc acc atc tcc cac tgt ggc tac cac ctt ccc ttc ctg cct tgc cct		776

Thr Thr Ile Ser His Cys Gly Tyr His Leu Pro Phe Leu Pro Ser Pro	
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Glu Phe His Asp Tyr His His Leu Lys Phe Asn Gln Cys Tyr Gly Val	
245 250 255	
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Leu Gly Val Leu Asp His Leu His Gly Thr Asp Thr Met Phe Lys Gln	
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acc aag gcc tac gag aga cat gtc ctc ctg ctg ggc ttc acc ccg ctc	920
Thr Lys Ala Tyr Glu Arg His Val Leu Leu Leu Gly Phe Thr Pro Leu	
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tct gag agc atc cca gac tcc cca aag agg atg gag tga gagacagcct	969
Ser Glu Ser Ile Pro Asp Ser Pro Lys Arg Met Glu *	
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acctgtggag gcaacactgg ccaagaagag gaaagtctta gagtttgaaa gagtctatct	300
tgataatctc cccagtgcac cc atg tat gag cgc agt tac atg cat aga gat	352
Met Tyr Glu Arg Ser Tyr Met His Arg Asp	
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Val Ile Thr His Val Val Cys Thr Lys Thr Asp Phe Ile Ile Thr Ala	
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agt cat gat gga cat gtc aag ttc tgg aaa aaa ata gaa gag gga att	448
Ser His Asp Gly His Val Lys Phe Trp Lys Lys Ile Glu Glu Gly Ile	
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Glu Phe Val Lys His Phe Arg Ser His Leu Gly Val Ile Glu Ser Ile	
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gca gtt agc tct gag gga gca ttg ttc tgt tct gtg ggt gat gat aaa	544
Ala Val Ser Ser Glu Gly Ala Leu Phe Cys Ser Val Gly Asp Asp Lys	
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gca atg aag gtg ttt gat gta gtg aac ttt gac atg atc aac atg ctg	592
Ala Met Lys Val Phe Asp Val Val Asn Phe Asp Met Ile Asn Met Leu	
75 80 85 90	
aaa ctt ggc tat ttt cct gga cag tgt gag tgg atc tat tgc cca ggg	640
Lys Leu Gly Tyr Phe Pro Gly Gln Cys Glu Trp Ile Tyr Cys Pro Gly	
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gat gca att tct tca gtt gct gct tcc gaa aag agt aca gga aaa att	688
Asp Ala Ile Ser Ser Val Ala Ala Ser Glu Lys Ser Thr Gly Lys Ile	
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ttc att tat gat ggc cga gga gat aac cag cca ctt cat att ttt gac	736
Phe Ile Tyr Asp Gly Arg Gly Asp Asn Gln Pro Leu His Ile Phe Asp	
125 130 135	
aaa ctc cat aca tca cct ctt act cag ata cgg cta aac cca gtt tac	784
Lys Leu His Thr Ser Pro Leu Thr Gln Ile Arg Leu Asn Pro Val Tyr	
140 145 150	
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Lys Ala Val Val Ser Ser Asp Lys Ser Gly Met Ile Glu Tyr Trp Thr	
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ggg cct cct cat gaa tat aaa ttc ccc aaa aat gtg aac tgg gaa tat	880
Gly Pro Pro His Glu Tyr Lys Phe Pro Lys Asn Val Asn Trp Glu Tyr	
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Lys Thr Asp Thr Asp Leu Tyr Glu Phe Ala Lys Cys Lys Ala Tyr Pro	
190 195 200	
acc agc gta tgt ttt tca cca gat ggg aag aaa ata gct act att ggt	976
Thr Ser Val Cys Phe Ser Pro Asp Gly Lys Lys Ile Ala Thr Ile Gly	
205 210 215	
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Ser Asp Arg Lys Val Arg Ile Phe Arg Phe Val Thr Gly Lys Leu Met	
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Arg Val Phe Asp Glu Ser Leu Ser Met Phe Thr Glu Leu Gln Gln Met	
235 240 245 250	
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Arg Gln Gln Leu Pro Asp Met Glu Phe Gly Arg Arg Met Ala Val Glu	
255 260 265	
cgt gag ttg gag aag gtt gat gct gta aga tta att aat ata gtt ttt	1168
Arg Glu Leu Glu Lys Val Asp Ala Val Arg Leu Ile Asn Ile Val Phe	
270 275 280	

gat gaa act gga cac ttc gtg ctg tat gga aca atg ctg ggc att aaa	1216
Asp Glu Thr Gly His Phe Val Leu Tyr Gly Thr Met Leu Gly Ile Lys	
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Val Ile Asn Val Glu Thr Asn Arg Cys Val Arg Ile Leu Gly Lys Gln	
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Glu Asn Ile Arg Val Met Gln Leu Ala Leu Phe Gln Gly Ile Ala Lys	
315 320 325 330	
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Lys His Arg Ala Thr Ile Glu Met Lys Ala Ser Glu Asn Pro	
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Val Leu Gln Asn Ile Gln Ala Asp Pro Thr Ile Val Cys Thr Ser Phe	
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Lys Lys Asn Arg Phe Tyr Met Phe Thr Lys Arg Glu Pro Glu Asp Thr	
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Lys Ser Ala Asp Ser Asp Arg Asp Val Phe Asn Glu Lys Pro Ser Lys	
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395 400 405 410	
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Asp Ser Ala Ile Ile His Thr Ser Met Gly Asp Ile His Thr Lys Leu	
415 420 425	
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Phe Pro Val Glu Cys Pro Lys Thr Val Glu Asn Phe Cys Val His Ser	
430 435 440	
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Arg Asn Gly Tyr Tyr Asn Gly His Thr Phe His Arg Ile Ile Lys Gly	
445 450 455	
ttt atg att cag act gga gat cca aca ggt act ggt atg gga gga gaa	1744
Phe Met Ile Gln Thr Gly Asp Pro Thr Gly Thr Gly Met Gly Gly Glu	
460 465 470	
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Ser Ile Trp Gly Gly Glu Phe Glu Asp Glu Phe His Ser Thr Leu Arg	
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cat gac agg cca tac aca ctc agc atg gct aac gcg gga tca aat act	1840
His Asp Arg Pro Tyr Thr Leu Ser Met Ala Asn Ala Gly Ser Asn Thr	
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aat gga tcc cag ttt ttc ata acg gta gta cca acg cct tgg ctt gat	1888
Asn Gly Ser Gln Phe Phe Ile Thr Val Val Pro Thr Pro Trp Leu Asp	
510 515 520	
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Asn Lys His Thr Val Phe Gly Arg Val Thr Lys Gly Met Glu Val Val	
525 530 535	

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Gln Arg Ile Ser Asn Val Lys Val Asn Pro Lys Thr Asp Lys Pro Tyr
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gag gat gtc agc atc ata aat att act gtc aag taa aata agatttgttt      2034
Glu Asp Val Ser Ile Ile Asn Ile Thr Val Lys *
      555                      560                      565

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Met Ala Ala Ser Arg Lys Pro Pro Arg Val Arg Val
      1                      5                      10

aat cac cag gat ttt caa ctg aga aat tta aga ata att gaa cct aac      159
Asn His Gln Asp Phe Gln Leu Arg Asn Leu Arg Ile Ile Glu Pro Asn
      15                      20                      25

gag gtg aca cac tca gga gac aca ggt gtg gaa aca gac ggc aga atg      207
Glu Val Thr His Ser Gly Asp Thr Gly Val Glu Thr Asp Gly Arg Met
      30                      35                      40

cct cca aag gtg act tca gag ctg ctt cgg cag ctg aga caa gcc atg      255
Pro Pro Lys Val Thr Ser Glu Leu Leu Arg Gln Leu Arg Gln Ala Met
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agg aac tct gag tat gtg acc gaa ccg atc cag gcc tac atc atc cca      303
Arg Asn Ser Glu Tyr Val Thr Glu Pro Ile Gln Ala Tyr Ile Ile Pro
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Ser Gly Asp Ala His Gln Ser Glu Tyr Ile Ala Pro Cys Asp Cys Arg
      80                      85                      90

cgg gct ttt gtc tct gga ttc gat ggc tct gcg ggc aca gcc atc atc      399
Arg Ala Phe Val Ser Gly Phe Asp Gly Ser Ala Gly Thr Ala Ile Ile
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Thr Glu Glu His Ala Ala Met Trp Thr Asp Gly Arg Tyr Phe Leu Gln

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125	130	135	140
aag gac aca cca act cag gaa gac tgg ctg gtg agt gtg ctt cct gaa			543
Lys Asp Thr Pro Thr Gln Glu Asp Trp Leu Val Ser Val Leu Pro Glu			
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gga tcc agg gtt ggt gtg gac ccc ttg atc att cct aca gat tat tgg			591
Gly Ser Arg Val Gly Val Asp Pro Leu Ile Ile Pro Thr Asp Tyr Trp			
	160	165	170
aag aaa atg gcc aaa gtt ctg aga agt gcc ggc cat cac ctc att cct			639
Lys Lys Met Ala Lys Val Leu Arg Ser Ala Gly His His Leu Ile Pro			
	175	180	185
gtc aag gag aac ctc gtt gac aaa atc tgg aca gac cgt cct gag cgc			687
Val Lys Glu Asn Leu Val Asp Lys Ile Trp Thr Asp Arg Pro Glu Arg			
	190	195	200
cct tgc aag cct ctc ctc aca ctg ggc ctg gat tac aca ggc atc tcc			735
Pro Cys Lys Pro Leu Leu Thr Leu Gly Leu Asp Tyr Thr Gly Ile Ser			
	205	210	215
tgg aag gac aag gtt gca gac ctt cgg ttg aaa atg gct gag agg aac			783
Trp Lys Asp Lys Val Ala Asp Leu Arg Leu Lys Met Ala Glu Arg Asn			
	225	230	235
gtc atg tgg ttt gtg gtc act gcc ttg gat gag att gcg tgg cta ttt			831
Val Met Trp Phe Val Val Thr Ala Leu Asp Glu Ile Ala Trp Leu Phe			
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Asn Leu Arg Gly Ser Asp Val Glu His Asn Pro Val Phe Phe Ser Tyr			
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Ile Asp Ala Pro Ser Val Lys Glu His Leu Leu Leu Asp Leu Gly Leu			
	285	290	295
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	305	310	315
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Glu Leu Lys Ala Leu Cys Ala Asp Leu Ser Pro Arg Glu Lys Val Trp			
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gtc agt gac aag gcc agc tat gct gtg agc gag acc atc ccc aag gac			1119
Val Ser Asp Lys Ala Ser Tyr Ala Val Ser Glu Thr Ile Pro Lys Asp			
	335	340	345
cac cgc tgc tgt atg cct tac acc ccc atc tgc atc gcc aaa gct gtg			1167
His Arg Cys Cys Met Pro Tyr Thr Pro Ile Cys Ile Ala Lys Ala Val			
	350	355	360
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aaa ggt ggt gtg aca gag atc tca gct gct gac aaa gct gag gag ttt				1311
Lys Gly Gly Val Thr Glu Ile Ser Ala Ala Asp Lys Ala Glu Glu Phe				
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cgc agg caa cag gca gac ttt gtg gac ctg agc ttc cca aca att tcc				1359
Arg Arg Gln Gln Ala Asp Phe Val Asp Leu Ser Phe Pro Thr Ile Ser				
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agt acg gga ccc aac ggc gcc atc att cac tac gcg cca gtc cct gag				1407
Ser Thr Gly Pro Asn Gly Ala Ile Ile His Tyr Ala Pro Val Pro Glu				
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acg aat agg acc ttg tcc ctg gat gag gtg tac ctt att gac tcg ggt				1455
Thr Asn Arg Thr Leu Ser Leu Asp Glu Val Tyr Leu Ile Asp Ser Gly				
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gct caa tac aag gat ggc acc aca gat gtg acg cgg aca atg cat ttt				1503
Ala Gln Tyr Lys Asp Gly Thr Thr Asp Val Thr Arg Thr Met His Phe				
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ggg acc cct aca gcc tac gag aag gaa tgc ttc aca tat gtc ctc aag				1551
Gly Thr Pro Thr Ala Tyr Glu Lys Glu Cys Phe Thr Tyr Val Leu Lys				
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Gly His Ile Ala Val Ser Ala Ala Val Phe Pro Thr Gly Thr Lys Gly				
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His Leu Leu Asp Ser Phe Ala Arg Ser Ala Leu Trp Asp Ser Gly Leu				
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gat tac ttg cac ggg act gga cat ggt gtt ggg tct ttt ttg aat gtc				1695
Asp Tyr Leu His Gly Thr Gly His Gly Val Gly Ser Phe Leu Asn Val				
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cat gag ggt cct tgc ggc atc agt tac aaa aca ttc tct gat gag ccc				1743
His Glu Gly Pro Cys Gly Ile Ser Tyr Lys Thr Phe Ser Asp Glu Pro				
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Leu Glu Ala Gly Met Ile Val Thr Asp Glu Pro Gly Tyr Tyr Glu Asp				
	560	565	570	
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Gly Ala Phe Gly Ile Arg Ile Glu Asn Val Val Leu Val Val Pro Val				
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aag acc aag tat aat ttt aat aac cgg gga agc ctg acc ttt gaa cct				1887
Lys Thr Lys Tyr Asn Phe Asn Asn Arg Gly Ser Leu Thr Phe Glu Pro				
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cta aca ttg gtt cca att cag acc aaa atg ata gat gtg gat tct ctt				1935
Leu Thr Leu Val Pro Ile Gln Thr Lys Met Ile Asp Val Asp Ser Leu				
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aca gac aaa gag tgc gac tgg ctc aac aat tac cac ctg acc tgc agg				1983
Thr Asp Lys Glu Cys Asp Trp Leu Asn Asn Tyr His Leu Thr Cys Arg				



625

630

635

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 Asp Val Ile Gly Lys Glu Leu Gln Lys Gln Gly Arg Gln Glu Ala Leu  
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gag tgg ctc atc aga gag acg caa ccc atc tcc aaa cag cat taa taa 2079  
 Glu Trp Leu Ile Arg Glu Thr Gln Pro Ile Ser Lys Gln His \*  
 655 660 665

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 Met Pro Glu Asn Pro Ala  
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aca gat aaa ctg cag gtg ctg cag gta ctt gat cgc ctg aaa atg aaa 220  
 Thr Asp Lys Leu Gln Val Leu Gln Val Leu Asp Arg Leu Lys Met Lys  
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 Leu Gln Glu Lys Gly Asp Thr Ser Gln Asn Glu Lys Leu Ser Met Phe  
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 Tyr Glu Thr Leu Lys Ser Pro Leu Phe Asn Gln Ile Leu Thr Leu Gln  
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 Gln Ser Ile Lys Gln Leu Lys Gly Gln Leu Asn His Ile Pro Ser Asp  
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 Cys Ser Ala Asn Phe Asp Phe Ser Arg Lys Gly Leu Leu Val Phe Thr  
 75 80 85

gat ggt tcc att act aat gga aat gtc cac agg ccc tct aat aac tcg 460  
 Asp Gly Ser Ile Thr Asn Gly Asn Val His Arg Pro Ser Asn Asn Ser  
 90 95 100

act gta tct ggg tta ttt ccg tgg acc ccg aag ttg gga aat gaa gac 508

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Phe	Asn	Ser	Val	Ile	Gln	Gln	Met	Ala	Gln	Gly	Arg	Gln	Ile	Glu	Tyr	
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Ile	Asp	Ile	Glu	Arg	Pro	Ser	Thr	Gly	Gly	Leu	Gly	Phe	Ser	Val	Val	
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His	Gln	Gln	Ala	Ile	Ala	Leu	Leu	Gln	Gln	Thr	Thr	Gly	Ser	Leu	Arg	
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Leu	Ile	Val	Ala	Arg	Glu	Pro	Val	His	Thr	Lys	Ser	Ser	Thr	Ser	Ser	
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Lys	Ile	Gly	Gly	Thr	Asn	Val	Gln	Gly	Met	Thr	Ser	Glu	Gln	Val	Ala	
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Gln	Val	Leu	Arg	Asn	Cys	Gly	Asn	Ser	Val	Arg	Met	Leu	Val	Ala	Arg	
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Asp	Pro	Ala	Gly	Asp	Ile	Ser	Val	Thr	Pro	Pro	Ala	Pro	Ala	Ala	Leu	
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Pro	Val	Ala	Leu	Pro	Thr	Val	Ala	Ser	Lys	Gly	Pro	Gly	Ser	Asp	Ser	
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Ser	Leu	Phe	Glu	Thr	Tyr	Asn	Val	Glu	Leu	Val	Arg	Lys	Asp	Gly	Gln	
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Tyr	His	Asn	Gly	His	Ile	Gln	Val	Asn	Asp	Lys	Ile	Val	Ala	Val	Asp	
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Arg	Asn	Ala	Gly	Gln	Val	Val	His	Leu	Thr	Leu	Val	Arg	Arg	Lys	Thr	
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Gln	Pro	Glu	Asp	Glu	Leu	Leu	Glu	Val	Asn	Gly	Met	Gln	Leu	Tyr	Gly	
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